



PvuI (7)
SgfI (6)
1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAGGTGGCGCGGGTAAACTGGAAAAGTATGCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) HindIII (245) Bsu36I (291)
201 GTGAACGTTCTTTTTTCGAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGGCTTTCGCGCCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

AgeI (552) BspHI (560)
501 TCTGTTTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTATCATGACTCCTCTGCCTCAATTGCTCTGCCTCCCTGG

1 M T P L C L N C S V L P G
Bsu36I (670)
601 AGACCTGTACCCAGGGGTGCAAGGAACCCCATGGCTTGAATGGCAGTGGGCCAGGGGCACTTTGACCTGAGGACTTGAACCTGACTGACGAGGCA

13 D L Y P G G A R N P M A C N G S A A R G H F D P E D L N L T D E A
701 CTGAGACTCAAGTACCTGGGGCCCGAGCAGACAGAGCTGTTATGCCATCTGTGCCACATACCTGCTGATCTTCGTGGTGGGCGCTGTGGCAATGGGC

47 L R L K Y L G P Q Q T E L F M P I C A T Y L L I F V V G A V G N G

FspI (833)
801 TGACCTGTCTGGTCATCCTGCGCCACAAGGCCATGCGCACGCCTACCAACTACTACCTTTACGCTGGCCGTGTCGGACCTGCTGGTGTCTGGTGGG

80 L T C L V I L R H K A M R T P T N Y Y L F S L A V S D L L V L L V G
901 CCTGCCCTGGAGCTCTATGAGATGTGGCACAACCTACCCCTTCTGCTGGGCGTTGGTGGCTGCTATTTCCGACGCTACTGTTTGAAGTGGTCTGCCTG

113 L P L E L Y E M W H N Y P F L L G V G G C Y F R T L L F E M V C L

BstXI (1067)
1001 GCCTCAGTGCTAACGTCACCTGCCCTGAGCGTGAACGCTATGTGGCCGTGGTGACCCACTCCAGGCCAGGTCATGGTGACGCGGGCCCATGTGCGCC

147 A S V L N V T A L S V E R Y V A V V H P L Q A R S M V T R A H V R

BbrPI (1177)
1101 GAGTGCTTGGGGCGTCTGGGGTCTTGCCATGCTCTGCTCCCTGCCAACACCAGCCTGCACGGCATCCGGCAGCTGCACGTCGCCCTGCCGGGCCAGT

180 R V L G A V W G L A M L C S L P N T S L H G I R Q L H V P C R G P V

BspHI (1298)
SphI (1217) SapI (1272) MscI (1292)
1201 GCCAGACTCAGCTGTTTGCATGCTGGTCCGCCACGGCCCTCTACAACATGGTAGTGACAGACCACCGCGTCTCTTCTTCTGCCATGGCCATC

213 P D S A V C M L V R P R A L Y N M V V Q T T A L L F F C L P M A I
1301 ATGAGCGTGCTCTACCTGCTCATTGGGCTGCGACTGCGGCGGAGAGGCTGCTGCTCATGACGAGGCCAAGGGCAGGGGCTCTGCAGCAGCCAGGTC

247 M S V L Y L L I G L R L R R E R L L L M Q E A K G R G S A A A R S

SdaI (1406) PvuI (1425)
1401 GATACACCTGCAGGCTCCAGCAGCAGATCGGGGCCGAGACAAGTGACCAAGATGCTGTTTGTCTGGTCTGTTGGCATCTGCTGGGCCCGTT

280 R Y T C R L Q Q H D R G R R Q V T K M L F V L V V V F G I C W A P F

Tth111I (1507) BbrPI (1567)
1501 CCACGCCGACCGTGTGGAGCGTGTGTACAGTGGACAGATGGCCTGCACCTGGCCTTCCAGCACGTGCACGTCTCCGGCATCTTCTTCTAC

313 H A D R V T M W S V V S Q W T D G L H L A F Q H V H V I S G I F F Y
1601 CTGGGCTCGGGGCCAACCCCGTCTATAGCCTCATGTCCAGCCGCTTCCGAGAGACCTTCCAGGAGGCCCTGTGCTCGGGCCCTGCTGCCATCGCC

347 L G S A A N P V L Y S L M S S R F R E T F Q E A L C L G A C C H R

DraIII (1749) XcmI (1785)
1701 TCAGACCCCGCCACAGCTCCCACAGCCTCAGCAGGATGACCACAGGACGACCCCTGTGTGATGTGGGCTCCCTGGGCAGCTGGGTCCACCCCTGGTGG

380 L R P R H S S H S L S R M T T G S T L C D V G S L G S W V H P L A G

MscI (1869)
NheI (1863)
1801 GAACGATGGCCAGAGGCGCAGCAAGAGACCGATCCATCCTGAGTGGAGCCTTAAAGTGGCTTGTAGCTGGCCAGACATGATAAGATACATTGATGAT

413 N D G P E A Q Q E T D P S •

1901 TTGGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACA

HpaI (2001) EcoRI (2097)
2001 AGTTAAACAACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAA

2101 TTCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGC

SapI (2279)
2201 CAATGTGCATTAGCTGTTTGAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGATTTTCCCAAGGTTTGAAGTACTGCTTTCATTTCTTTATGTTT

SspI (2336) SwaI (2350)
2301 TAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAATGTTTTTATTAGGCAGAAT

2401 CCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTGTAGTGTGGACTTAGGGAACAAGGAACCTTAAATAGAAATTGGACAGCAAGAAAGCGAGCTT

2501 CTAGCTTTAGTTCCTGGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCA
 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

BstXI (2640)

2601 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 (2775)

2701 CAAAGTCCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTACGACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGAT
 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

2801 GATCTCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGTGTTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGTCCAGA
 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 (2921)

XmnI (2917) AseI (2983)

2901 TCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAG
 9 D Q Q S I N F T K M

3001 CGTGGATGGCGTCTCCAGCTTATCTGACGGTCTACTAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCCTACCGCCATTTGCGTCAATGGGG

SpeI (3138)

3101 CGGAGTTGTTACGACATTTTGGAAAGTCCCCTTGATTTACTAGTCAAAAACAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTC

SnaBI (3266)

3201 AAACCGCTATCCACGCCATTGATGTACTGCCAAAACGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCAT

NdeI (3371)

3301 AAGGTCATGTAAGTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCCAAGT

3401 GGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGG

SdaI (3549) PacI (3557) BspLU11I (3567)

3501 GTCGTTGGGCGGTACGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATTAAAGAACATGTGAGCAAAAGGCCAGCAAAGGCCAGGA
 CCTGCAGGTTAATTAAAGAACATGTGAGCAAAAGGCCAGCAAAGGCCAGGA

3601 ACCGTA AAAAGGCCGCTTGGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGAC

3701 AGGACTATAAAGATACCAGGCTTTCCCCCTGGAAGTCCCTCGTGGCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCT

3801 TCGGGAAGCGTGGCGTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTC

3901 AGCCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAG

4001 CAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAG

4101 CCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCAGCTGGTAGCGGTGGTTTTTTTTGTTTGCAAGCAGCAGATTACGCGCA

PacI (4297)

4201 GAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTA

EagI (4317)

SwaI (4306) NotI (4316)

4301 ATTAACATTTAATCAGCGGCCGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATC

4401 AAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA