



PvuI (7)
SgfI (6)
1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTGCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) **PvuII (239)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCCGCTTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCAGCTTTGCTGACCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

BstEII (555)
AgeI (552) **NcoI (560)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCATGGCGTACAGTCAAGGAGCGGCAAAAAAAGTCTG

1 M A Y S Q G G G K K K V C

Tth111I (638)
601 C T A C T A C T A C G A C G G T G A T A T T G G A A A T T A T T A T T A T G G A C A G G G T C A T C C C A T G A A G C C T C A T A G A A T C C G C A T G A C C C A T A A C T T G C T G T T A A A T T A T

13 Y Y Y D G D I G N Y Y Y G Q G H P M K P H R I R M T H N L L L N Y

EcoO109I (727)
701 G G C T T A T A C A G A A A A T G G A A A T A T A T A G C C C C A T A A A G C C A C T G C C G A A G A A A T G A C A A A A T A T C A C A G T G A T G A T A T A T C A A A T T T C T A C G G T C A A

47 G L Y R K M E I Y R P H K A T A E E M T K Y H S D E Y I K F L R S

BspLU11I (812)
801 T A A G A C C A G A T A A C A T G T C T G A T A T A G T A A G C A G A T G C A G A G A T T T A A T G T T G G A G A A G A T T G T C C A G T G T T T G A T G G A C T C T T T G A G T T T T G T C A G C T

80 I R P D N M S E Y S K Q M Q R F N V G E D C P V F D G L F E F C Q L

901 C T C A A C T G G C G G T T C A G T T G C T G G A G C T G T G A A G T T A A C C G A C A C A G A C T G A T A T G G C T G T T A A T T G G G C T G G A G G A T T A C A T C A T G C T A A G A A T C A

113 S T G G S V A G A V K L N R Q Q T D M A V N W A G G L H H A K K S

BsaBI (1090)
1001 G A A G C A T C A G G A T T C T G T T A C G T T A A T G A T A T T G T G C T T G C C A T C C T T G A A T T A C T A A A G T A T C A T C A G A G A G T C T T A T A T A T T G A T A T A G A T A T T C A T C

147 E A S G F C Y V N D I V L A I L E L L K Y H Q R V L Y I D I D I H

HindIII (1118) **BstXI (1158)** **XmnI (1171)**
1101 A T G G T G A T G G T G T T G A A G A A G C T T T T A T A C A A C A G A T C G T G T A A T G A C G G T A T C A T T C C A T A A A T A T G G G A A T A C T T T C T G G C A C A G G A G A C T T G A G

180 H G D G V E E A F Y T T D R V M T V S F H K Y G E Y F P G T G D L R

1201 G G A T A T T G G T G C T G G A A A G G C A A A T A C T A T G C T G C A A T T T C C A A T G A G A G A T G G T A T A G A T A G A T G A G T C A T A T T G G C A G A T A T T T A A G C T A T T A T C

213 D I G A G K G K Y Y A V N F P M R D G I D D E S Y G Q I F K P I I

1301 T C A A A G G T G A T G G A G A T G T A C A C C T A G T G C T G T G G T A T T A C A G T G T G G T G C A G A C T C A T T A T C T G G T G A T A G A C T G G G T T G T T T C A A T C T A A C A G T C A

247 S K V M E M Y Q P S A V V L Q C G A D S L S G D R L G C F N L T V

1401 A A G G T C A T G C T A A A T G T G T A G A A G T T G T A A A A C T T T T A A C T T A C C A T T A C T G A T G C T T G G A G G A G T G G C T A C A C A A T C C G T A A T G T T G C T C G A T G T T G

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

PstI (1511)
1501 G A C A T A T G A G A C T G C A G T T G C C C T T G A T T G T G A G A T T C C C A A T G A G T T G C C A T A T A A T G A T T A C T T T G A G A T T T T G G A C C A G A C T T C A A A C T G C A T A T T

313 T Y E T A V A L D C E I P N E L P Y N D Y F E Y F G P D F K L H I

FspI (1673) **DraIII (1691)**
1601 A G T C C T T C A A A C A T G A C A A A C C A G A A C A C T C C A G A A T A T A T G G A A A G A T A A A A C A G C G T T T G T T T G A A A A T T T G C G C A T G T T A C C T C A T G C A C C T G G T G

347 S P S N M T N Q N T P E Y M E K I K Q R L F E N L R M L P H A P G

BbsI (1735)
BspHI (1731)
1701 T C C A G A T G C A A G C T A T T C C A G A A G A T G C T G T T C A T G A A G A C A G T G G A G A T G A A G A T G G A G A A G A T C C A G A C A A G A G A A T T T C A T T C G A G A T C A G A C A A

380 V Q M Q A I P E D A V H E D S G D E D G E D P D K R I S I R A S D K

EcoRI (1819)
1801 G C G G A T A G C T T G T G A T G A A G A A T T C T C A G A T T C T G A G G A T G A A G G A G A A G G A G G T C G A A G A A A T G T G G C T G A T C A T A A G A A G G A G C A A A G A A A G C T A G A

413 R I A C D E E F S D S E D E G E G G R R N V A D H K K G A K K A R

1901 A T T G A A G A A G A T A A G A A A G A A C A G A G G A C A A A A A A C A G A C G T T A A G G A A G A A T A A A T C C A A G G A C A A C A G T G G T G A A A A A C A G A T A C C A A A G G A A

447 I E E D K K E T E D K K T D V K E E D K S K D N S G E K T D T K G

NheI (2049)
XcmI (2043) **MscI (2055)**
2001 C C A A A T C A G A A C A G C T C A G A A C C C C T G A A T T T G A C A G T C T C A C C A A T T G C T A G T G G C C A G A C A T G A T A A G A T A C A T T G A T G A G T T T G G A C A A A C C A C A

480 T K S E Q L S N P •

HpaI (2187)
2101 A C T A G A A T G C A G T G A A A A A A T G C T T T A T T T G T G A A A T T T G T G A T G C T A T T G C T T T A T T T G T A A C C A T T A T A A G C T G C A A T A A C A A G T T A A C A A C A C A

EcoRI (2283)
2201 A T T G C A T T C A T T T A T G T T T C A G G T T C A G G G G A G G T G T G G G A G G T T T T T T A A A G C A A G T A A A A C C T C T A C A A A T G T G G T A T G G A A T T C T A A A A T A C A G C

2301 A T A G A A A A C T T T A A C C T C C A A A T C A A G C C T C A C T T G A A T C C T T T T C T G A G G G A T G A A T A A G G C A T A G G C A T C A G G G G C T G T T G C C A A T G T G C A T T A G C

2401 TGTTCGAGCCTCACCTCTTTCATGGAGTTAAGATATAGTGATTTTCCCAAGGTTTGAAGTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACC
SapI (2465)

2501 TCCCACATTCCTTTTTAGTAAAAATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGG
SspI (2522) **SwaI (2536)** **EcoO109I (2597)**

2601 CCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTAAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCC
141 ◀ • N R
SacI (2797)

2701 TGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAG
138 ◀ 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 L
BstXI (2826)

2801 CTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTTCTGC
105 ◀ 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 Q
StuI (2961)

2901 CCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCT
71 ◀ 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 K
3001 TGGTCTGATGGCCGCCCGACATGGTCTTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGAT
38 ◀ 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 I
BbsI (3107)
XmnI (3103) **AseI (3169)**

3101 GTTGAAGGCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCT
5 ◀ N F T K M ◀

3201 CCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGA
SacI (3226)

3301 CATTTTGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCATTGACGTCAATGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGCTATCCAC
SpeI (3324)

3401 GCCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTG
SnaBI (3452)

3501 GGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCCAAGTGGGCAGTTTACCGT

3601 AAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATTATTGACGTCAATGGGGCGGGTCTGTTGGGCGGTC

3701 AGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAAATAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCC
PstI (3736) **SdaI (3735)** **BspLU11I (3753)**
PacI (3743)

3801 GCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAGAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGAT

3901 ACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGC

4001 GCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTCCAGCCGACCGCTGC
ApaLI (4067)

4101 GCCTTATCCGGTAACTATCGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGG

4201 TAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGG

4301 AAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTTTTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCT

4401 CAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAAT
PacI (4483) **SwaI (4492)**

4501 CAGCGGCCCAATAAAATATCTTTATTTTATTACATCTGTGTGGTTTTTTGTGTGAATCGTAACATAACGCTCTCCATCAAACAAACGAAA
EagI (4503)
NotI (4502)

4601 CAAAACAAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA