



100

PvuI (7)
SgfI (6)
MfeI (82) **EcoNI (96)**

1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
 101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203)
HindIII (245) **Bsu36I (291)**

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCGCTACCTGAGGCC
 301 GCCATCCACGCGGTTGAGTCGCGTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
NgoMI (441)
NaeI (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCGTACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

KasI (535) **AgeI (552)** **BspHI (560)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCCTACCTGAGATCACCGGTCATCATGAATTCATCTAAATCATCTGAAACACAATGCACAGA
 1 M N S S K S S E T Q C T E

BsiBI (645)
BsaBI (645)
BamHI (644)

601 GAGAGGATGCTTCTCTTCCAAATGTTCTTATGGACTGTTGCTGGGATCCCCATCCTATTTCTCAGTGCTGTTTCATCACCAGATGTGTTGTGACATTT
 13 R G C F S S Q M F L W T V A G I P I L F L S A C F I T R C V V T F
 701 CGCATCTTCAAACCTGTGATGAGAAAAAGTTTCAGCTACCTGAGAATTTACAGAGCTCTCCTGCTACAATTATGGATCAGGTTTTCAGTCAAGAAATTGTT
 47 R I F Q T C D E K K F Q L P E N F T E L S C Y N Y G S G S V K N C

BstXI (802) **XmnI (814)** **PvuII (828)**
NcoI (890)

801 GTCCATTGAAGTGGGAATATTTCAATCCAGCTGCTACTTCTTTTCTACTGACACCATTTCTGGGCGTTAAGTTTAAAGAACTGCTCAGCCATGGGGGC
 80 C P L N W E Y F Q S S C Y F F S T D T I S W A L S L K N C S A M G A
 901 TCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCCTTTCTACAAGAAACCTAAAATGAGAGAGTTTTTTATGGACTGTCAGACCAGGTTGTC
 113 H L V V I N S Q E E Q E F L S Y K K P K M R E F F I G L S D Q V V

Tth111I (1035)

1001 GAGGGTCAGTGGCAATGGGTGGACGGCACACCTTTGACAAAGTCTCTGAGCTTCTGGGATGTAGGGGAGCCCAACAACATAGCTACCCTGGAGGACTGTG
 147 E G Q W Q W V D G T P L T K S L S F W D V G E P N N I A T L E D C

XcmI (1123)

1101 CCACCATGAGAGACTCTTCAAACCAAGGCAAAATTGGAATGATGTAACCTGTTTCTCAATTATTTTCGGATTTGTAAATGGTAGGAATAAATCCTTT
 180 A T M R D S S N P R Q N W N D V T C F L N Y F R I C E M V G I N P L

MscI (1257)

1201 GAACAAAGGAAAATCTCTTTAAGAACAGAAAGGCACAACCTCAAATGTGTAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCA
 213 N K G K S L •

HpaI (1389)

1301 CAACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAACAAGTTAAACAACA

MfeI (1400)

1401 CAATTGCATTTCATTTTATGTTTCAGGTTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATCTAAAATACA
 1501 GCATAGCAAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTTTGCCAATGTGCATTA
 1601 GCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGATTTTCCCAAGGTTTGAAGTCTCTTCAATTTCTTATGTTTAAATGCACTGA

SspI (1724) **SwaI (1738)**
EcoO109I

1701 CCTCCACATTCCCTTTTATGATAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATAGGCAGAATCCAGATGCTCAA
 1801 GGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTT
 1901 CCTGGTGTACTTGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATG
 139 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 Y D S I

BstXI (2028)

2001 AGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCT
 105 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 F D K Q

StuI (2163)
Eco147I (2163)

2101 GCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGT
 72 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
 2201 CTTGGTCTGATGGCCCGCCGACATGGTCTGTTGTCTCATAGAGCATGGTATCTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAG
 39 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 D Q Q S

BspHI (2313)
VspI (2371)
AseI (2371)

2301 ATGTTGAAGGCTTCATGATGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGT
 5 I N F T K M

2401 CTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTAC

2501 GACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATC

SpeI (2526) ←

SnaBI (2654)
Eco105I (2654)

2600 CACGCCCATTTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTA

NdeI (2759)

2700 CTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTAC

2800 CGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGCGC

PstI (2938)
SdaI (2937) PacI (2945) BspLU11I (2955)

2900 GTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCCTG C A G G T T A A T T A A G A A C A T G T G A G C A A A A G G C C A G A A A A G G C C A G G A A C C G T A A A A

←

2998 A G G C C G C G T T G C T G G C G T T T T T C C A T A G G C T C C G C C C C C T G A C G A G C A T C A C A A A A A T C G A C G C T C A A G T C A G A G G T G G C G A A A C C C G A C A G G A C T A T A

3098 A A G A T A C C A G G C G T T T C C C C T G G A A G C T C C C T C G T G C G C T C T C T G T T C C G A C C T G C C G C T T A C C G G A T A C C T G T C C G C T T T T C T C C C T T C G G G A A G C

ApaLI (3269)

3198 G T G G C G T T T C T C A T A G C T C A C G C T G T A G G T A T C T C A G T T C G G T G T A G G T C G T T C G T C C A A G C T G G G C T G T G T G C A C G A A C C C C C G T T C A G C C G A C C

3298 G C T G C G C C T T A T C C G G T A A C T A T C G T C T T G A G T C C A A C C G G T A A G A C A C G A C T T A T C G C C A C T G G C A G C A G C C A C T G G T A A C A G G A T T A G C A G A G C G A G

3398 G T A T G T A G G C G G T G C T A C A G A G T T C T T G A A G T G G T G G C C T A A C T A C G G C T A C T A G A A G A A C A G T A T T T G G T A T C T G C G C T C T G C T G A A G C C A G T T A C C

3498 T T C G G A A A A A G A G T T G G T A G C T C T T G A T C C G G C A A A C A A A C C C G C T G G T A G C G G T G G T T T T T T G T T T G C A A G C A G C A G A T T A C G C G C A G A A A A A A A G

3598 G A T C T C A A G A A G A T C C T T T G A T C T T T T C T A C G G G G T C T G A C G C T C A G T G G A A C G A A A A C T C A C G T T A A G G G A T T T T G G T C A T G G C T A G T T A A T T A A C A T T

PacI (3685) SwaI (3694)

EagI (3705)
NotI (3704)

3698 T A A A T C A G C G G C C G C A A T A A A A T A T C T T T A T T T T C A T T A C A T C T G T G T T G G T T T T T T G T G T A A T C G T A A C T A A C A T A C G C T C C A T C A A A A C A A A A

3798 C G A A A C A A A A C A A A C T A G C A A A A T A G G C T G T C C C C A G T G C A A G T G C A G G T G C C A G A A C A T T T C T A T C G A A