



PvuI (7)
SgfI (6)
EcoNI (96)

1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
 101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACACGCCGCCGCCCTACCTGAGGCC
 301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
NaeI (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGTCTTTGTTTCGTTT

KasI (535)
AgeI (552)
NcoI (560)
BstEII (555)

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCCTACCTGAGATCACCGGTACCATGGAGTCAGTTTTATCCAAGTATGAAGATCAGATTAC
 601 TATTTTCACTGACTACCTAGAAGAATATCCAGATACAGATGAGCTGGTATGGATCTTAGGGAAGCAGCATCTCCTTAAAAACAGAAAAATCTAAGCTGTTG
 13▶ I F T D Y L E E Y P D T D E L V W I L G K Q H L L K T E K S K L L

Bsp120I (762)
EcoO109I (762)

701 TCTGATATAAGTGCTCGTCTATGGTTTACATACAGAAGGAAATTTTCCACAAATGGTGAACGGGCCCTTCATCAGATGCTGTTGGGATGTATGCTAC
 47▶ S D I S A R L W F T Y R R K F S P I G G T G P S S D A G W G C M L
 801 GCTGTGGACAGATGATGCTGGCTCAAGCCCTTATCTGTAGACACTTGGGAAGGACTGGAGCTGGGAGAAACAAAAAGAACAAACCCAAAGAATACCAACG
 80▶ R C G Q M M L A Q A L I C R H L G R D W S W E K Q K E Q P K E Y Q R
 901 CATCTACAGTGTCTTAGATAGAAAAAGATTGTTGCTACTCTATCCATCAAATGGCACAAATGGGTGAGGAGAAGGAAATCAATTGGAGAATGGTTT
 113▶ I L Q C F L D R K D C C Y S I H Q M A Q M G V G E G K S I G E W F
 1001 GGACCAAATACAGTTGCACAGGTGTTAAAAAACTTGTCTTATTTGACGAATGGAATTCCTTGGCTGTTTATGTTTCAATGGATAACACAGTGGTCATTG
 147▶ G P N T V A Q V L K K L A L F D E W N S L A V Y V S M D N T V V I

EcoRV (1102)
PvuII (1145)
StuI (1156)

1101 AAGATATCAAAAAATGTGCCGTGCTTCCCTTGTAGTGTGACACAGCTGGTGGACAGGCCCTCCGATCTTTAACTGCTTCAAACCAGAGTAAGGGCAC
 180▶ E D I K K M C R V L P L S A D T A G D R P P D S L T A S N Q S K G T

Ppu10I (1286)
NsiI (1286)

1201 CTCTGCCTACTGCTCAGCCTGAAACCCCTGCTGCTCATTGTGCCCTTCGCCTGGGCATAAACCAAATCAATCCTGTCTATGTTGATGCATTCAAAGAG
 213▶ S A Y C S A W K P L L L I V P L R L G I N Q I N P V Y V D A F K E

MluI (1349)

1301 TGTTTAAGATGCCACAGTCTTTAGGGGATTAGGAGGAAAACCAAATAACGCGTATTATTTTCATAGGATTCTTAGGTGACGAGCTCATCTTCTTGGACC
 247▶ C F K M P Q S L G A L G G K P N N A Y Y F I G F L G D E L I F L D

PstI (1468)

1401 CTCATAACCCAGACCTTTGTTGACACTGAAGAGAATGGAACGGTTAATGACCAGACTTTCCATTGCCTGCAGTCCCCACAGCGAATGAACATCCTAAA
 280▶ P H T T Q T F V D T E E N G T V N D Q T F H C L Q S P Q R M N I L N

BamHI (1503)

1501 CCTGGATCCTTCAGTTGCATTGGGATTTTTCTGCAAAGAAGAAAAAGACTTTGATAACTGGTGTAGCCTTGTTCAGAAGGAAATCTAAAGGAGAATTTA
 313▶ L D P S V A L G F F C K E E K D F D N W C S L V Q K E I L K E N L

XmnI (1609)
BstXI (1627)

1601 AGGATGTTTGAATTAGTTTCAAGAACATCCATCACACTGGCCTCCCTTTGTACCTCCAGCCAAGCCAGAAGTGACAACCACTGGGGCAGAATTCATTGACT
 347▶ R M F E L V Q K H P S H W P P F V P P A K P E V T T T G A E F I D

MscI (1787)
NheI (1781)

1701 CTAAGTGAACCTGGAGGAGTTTGTATCTGGAGGAAGATTTGAGATTCTGAGTGTGTAAGTCTGGGAACTCAACTTGAAGCTAGTGGCCAGACATGA
 380▶ S T E Q L E E F D L E E D F E I L S V •
 1801 TAAGATACATTGATGAGTTTGGACAAACCAACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCAT

HpaI (1919)

1901 TATAAGCTGCAATAAACAAGTTAAACAACAATTGCATTCAATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTC
 2001 TACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACTTAACTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATA
 2101 GGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTCTTTCATGGAGTTTAAAGATATAGTGATTTTCCCAAGGTTTGAAGTAGCT

SspI (2254)
SwaI (2268)

2201 CTTCAATTTCTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAAAATTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAATG

EcoO109I (2329)

2301 TTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGA
 2401 CAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCTCAATGAGC
 1414 • N R T Y K L P I L E E I T T K V L K G N M E I L

2501 ACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCC
115 V F C D P A 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
StuI (2693)

2601 TGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTC
82 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 Y A E

2701 AATGTGGACAGCAGAGATGATCTCCCAAGTCTTGGTCTGATGGCCGCCCGACATGGTGCTTGTTCCTCATAGAGCATGGTGATCTTCTCAGTGGCG
49 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 E T A

BspHI (2843)
BbsI (2839)
XmnI (2835)

2801 ACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGATGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGAT
15 V E V L E L D Q Q S I N F T K M

AseI (2901)

2901 GATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGC

SpeI (3056)

3001 CCATTTGCGTCAATGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCCTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGAC

SnaBI (3184)

3100 TTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTG

NdeI (3289)

3200 CCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATAC

3300 ACTTGATGTACTGCCAAGTGGGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTA

PstI (3468)
SdaI (3467) PacI (3475) BspLU11I (3485)

3400 TTGACGTCAATGGGCGGGGTGCTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCCTGCAGGTTAA TTAAGAACATGTGAGCAA
3498 AAGCCAGCAAAGGCCAGGAACCGTAAAAAGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAG
3598 TCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCGTTTTCCCTGGAAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGCTTACCGGA
3698 TACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCT

ApaLI (3799)

3798 GTGTGCACGAACCCCGTTCCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGC

3898 AGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTT

3998 GGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTGT

4098 GCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGG

EagI (4235)
PacI (4215) SmaI (4224) NotI (4234)

4198 GATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGAATAAAATATCTTTATTTTATTACATCTGTGTGTTGTTTTTTGTGTAATCGT

4298 AACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGAGGTGCCAGAACATTTCTCTATCG
4398 AA