



PvuI (7)
SgfI (6) 1 GGATCTGGATCGTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
 MfeI (82)

101 GAGAAAGTGGCGGGGTAACGGAAAGTGTGCTGTACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

201 GTGAACGTTCTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCCGCCCTACCTGAGGCC

301 GCCATCCACGCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTCGCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

NcoI (560)

BstEII (555)

AgeI (552)

501 TCTGTTCTGGCGGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTACCATTGGCGGCCCTGCTGTCTGCTGGCGTCTGCCCTCCT
 1▶ M A A P A L S W R L P L L

XhoI (678)

601 CATCTCCTCCTGCCCTGGCTACCTCTTGGGCATCTGCAGCGGTGAATGGCACTTCCAGTTTACATGCTTACAACCTCGAGAGCCAAACATCTCCTGT
 13▶ I L L L P L A T S W A S A A V N G T S Q F T C F Y N S R A N I S C

701 GTCTGGAGCAAGATGGGCTCTGCAGGACACTTCTGCAAGTCCATGCCTGGCCGGACAGACGGCGGTGGAACCAACCTGTGAGCTGCTCCCGTGA
 47▶ V W S Q D G A L Q D T S C Q V H A W P D R R R W N Q T C E L L P V

Th111I (865)
Bsu36I (876)

801 GTCAAGCATCCTGGGCTGCAACCTGATCTCGGAGCCCCAGATTCTCAGAACTGACCACAGTTGACATCGTACCCTGAGGGTGTGTGCCGTGAGGG
 80▶ S Q A S W A C N L I L G A P D S Q K L T T V D I V T L R V L C R E G

BsaBI (915)
BbrPI (985)

901 GGTGCGATGGAGGGTGTGGCCATCCAGGACTTCAAGCCCTTTGAGAACCCTCGCCTGATGGCCCCATCTCCCTCCAAGTTGTCCACGTGGAGACCCAC
 113▶ V R W R V M A I Q D F K P F E N L R L M A P I S L Q V V H V E T H

Th111I (1071)
XcmI (1081)

1001 AGATGCAACATAAGCTGGGAAATCTCCCAAGCCTCCCACTACTTTGAAAGACACCTGGAGTTCGAGGCCCGGACGCTGTCCCAAGGCCACACCTGGGAGG
 147▶ R C N I S W E I S Q A S H Y F E R H L E F E A R T L S P G H T W E

1101 AGGCCCCCTGCTGACTCTAAGCAGAAGCAGGAATGGATCTGCTGGAGACGCTCACCCAGACACCCAGTATGAGTTTCAAGTGGCGGTCAAGCCTCT
 180▶ E A P L L T L K Q K Q E W I C L E T L T P D T Q Y E F V R V K P L

1201 GCAAGCGAGTTCACGACCTGGAGCCCTGGAGCCAGCCCTGGCCTTCCAGGACAAAGCTGCAGCCCTTGGGAAAGACACATTCCGTGGCTCGGCCAC
 213▶ Q G E F T T W S P W S Q P L A F R T K P A A L G K D T I P W L G H

NcoI (1375)

1301 CTCCTCGTGGTCTCAGCGGGGCTTTTGGCTTCATCATCTTGTGTACTTGTGTATCACTGCAGGAACACCGGCCATGGTGAAGAAGTCTGAAGT
 247▶ L L V G L S G A F G F I I L V Y L L I N C R N T G G P W L K K V L K

1401 GTAACACCCAGACCCCTCGAAGTTCTTTTCCAGCTGAGCTCAGAGCATGGAGGAGAGCTCCAGAAGTGGCTCTCTTCCGCTTCCCTCATCGTCTT
 280▶ C N T P D P S K F F S Q L S S E H G G D V Q K W L S S P F P S S S F

BglIII (1523)

1501 CAGCCTGGCGGCTGGCACCTGAGACTCGCCACTAGAAGTGTGGAGAGGGACAAGGTGACGAGCTGCTCCTGCAGCAGGACAAGTGCCTGAGCCC
 313▶ S P G G L A P E I S P L E V L E R D K V T Q L L L Q Q D K V P E P

1601 GCATCCTTAAGCAGCAACCACTCGCTGACCAGCTGCTTACCAACCAGGGTACTTCTTCTTCCACCTCCCGGATGCCTTGGAGATAGAGGCCTGCCAGG
 347▶ A S L S S N H S L T S C F T N Q G Y F F F H L P D A L E I E A C Q

1701 TGTACTTTACTTACGACCCTACTCAGAGGAAGACCCTGATGAGGGTGTGGCGGGGACCCACAGGGTCTTCCCCCAACCCCTGCAGCCTCTGTGAGG
 380▶ V Y F T Y D P Y S E E D P D E G V A G A P T G S S P Q P L Q P L S G

SapI (1845)

1801 GGAGGACGACGCTACTGCACCTTCCCTCCAGGGATGACCTGCTGCTTCTCCCCAGTCTCCTCGTGGCCCCAGCCCCAAGCACTGCCCTGGG
 413▶ E D D A Y C T F P S R D D L L L F S P S L L G G P S P P S T A P G

SmaI (1961)

1901 GGCAGTGGGCGGTGAAGAGAGGATGCCCCCTTTTGAAGAAAGAGTCCCCAGAGACTGGGACCCCAAGCCCTGGGGCCTCCACCCAGGAGTCC
 447▶ G S G A G E E R M P P S L Q E R V P R D W D P Q P L G P P T P G V

2001 CAGACCTGGTGGATTTTACGCCACCCCTGAGCTGGTGTGCGAGAGGCTGGGAGGAGTCCCTGACGCTGGCCCCAGGGAGGAGTCAAGTTCCCTG
 480▶ P D L V D F Q P P P E L V L R E A G E E V P D A G P R E G V S F P W

Bsp120I (2129)

2101 GTCCAGGCTCCTGGGACGGGGAGTTCAAGGCCCTAATGCTCGCCTGCCCTGAACACTGATGCCTACTTGTCCCTCAAGAAGTCCAGGGTCAAGGAC
 513▶ S R P P G Q G E F R A L N A R L P L N T D A Y L S L Q E L Q G Q D

DraIII (2206)
NheI (2238)

2201 CCAACTCACTTGGTGTAGACAGATGGCCAGGGTGGGAGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCA
 547▶ P T H L V •

HpaI (2376)
MfeI (2387)

2301 GTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCAT

EcoRI (2472)

2401 TTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCATAAATACAGCATAGCAAACT

2501 TTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCC

SapI (2654)

2601 TCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTCCCAAGGTTTGAACCTAGCTTCTTCTTATGTTTTAAATGACTGACCTCCACATTCC

2701 **SspI (2711)** **SwaI (2725)**
CTTTTTAGTAAAAATATTCAGAAATAATTTAAATACATCATTGGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAAT

2801 ATCCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTACTTG
141 • N R T Y K

2901 AGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACA
134 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 E R C M

BstXI (3015)
3001 TGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCAC
101 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 G N S V

3101 AGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATG
68 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 T R I

XmnI (3292)
3201 GCCGCCCCGACATGGTGCTTGTGTCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGGCT
34 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 N F T K

AseI (3358)
3301 TCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCT
1 M

3401 GACGGTTCATAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAA

SpeI (3513)
3501 GTCCCGTTGATTTACTAGTCAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATG

SnaBI (3641)
3601 TACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTCCCAAGTAGGAAAGTCCCATAAAGTTCATGTAAGTGGCATAATGCC

NdeI (3746)
3701 AGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCAAGTGGGCGAGTTTACCGTAAATACTCCAC

3801 CCATTGACGTCAATGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGCTGTTGGGCGGTGAGCCAGGCGGG

PaeI (3932)
SdaI (3924) **BspLU11I (3942)**
3901 CCATTTACGTAAGTTATGTAACGCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGC
4001 GTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTT
4101 CCCCCTGGAAGCTCCTCGTGCGCTCTCTGTCCGACCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATA

ApaLI (4256)
4201 GCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCTTATCCGG
4301 TAACTATCGTCTTGAGTCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCT
4401 ACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTG
4501 GTAGCTCTTGATCCGGCAAAACAAACCCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCC

EagI (4692)
PaeI (4672) **SwaI (4681)** **NotI (4691)**
4601 TTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCA

4701 ATAAAAATCTTTATTTTATTACATCTGTGTGTTGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACT
4801 AGCAAAATAGGCTGTCCCGAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA