



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

101 GAGAAAGTGGCGGGGTAACGGAAAGTGATGTCGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

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

301 GCCATCCACGCCGTTGAGTCGCGTTTCTGCCGCCTCCCGCTGTGGTGCCTCCTGAAGTCGCTCCGCCGTCTAGGTAAGTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

NcoI (560)
BstEII (555)
AgeI (552) 501 TCTGTTCTGGCGGTTACAGATCCAAGCTGTGACCGCGGCTACCTGAGATCACCGGTACCATTGGCGGCCCTGCTGTCTGCTGGCGTCTGCCCTCTCT
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 GTCAAGCATCCTGGCCTGCAACCTGATCTCGGAGCCCCAGATTCTCAGAACTGACCACAGTTGACATCGTACCCTGAGGGTGTGTCGGTGGAGG
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 GGTGCGATGGAGGGTGTGGCCATCCAGGACTTCAAGCCCTTTGAGAACCCTTCGCTGATGGCCCCATCTCCCTCCAAGTTGTCCACGTGGAGACCCAC
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 AGATGCAACATAAGCTGGAAATCTCCCAAGCCTCCCACTACTTTGAAAGACACCTGGAGTTCGAGGCCCGGACGCTGTCCCAAGGCCACACCTGGGAGG
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 AGGCCCCCTGCTGACTCTCAAGCAGAAGCAGGAATGGATCTGCTGGAGACGCTCACCCAGACACCCAGTATGAGTTTCAAGTGGCGGTCAAGCCTCT
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 P D T Q Y E F P D T Q Y E F P D T Q Y E F P D T Q Y E F P D T Q Y E F P L

1201 GCAAGCGAGTTCACGACCTGGAGCCCCCTGGAGCCAGCCCTGGCCTTCCAGGACAAAGCTGCAGCCCTTGGGAAGGACACATTCCGTGGCTCGGCCAC
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 CTCCTCGTGGTCTCAGCGGGGCTTTTGGCTTCATCATCTTGTGACTTGTGATCACTGCAGGAACACCGGCCATGGTGAAGAAGTCTGAAGT
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 GCATCCTTAAGCAGCAACCACTCGCTGACCAGCTGCTTACCAACCAGGGTACTTCTTCTTCCACCTCCCGGATGCCTTGGAGATAGAGGCTGCCAGG
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 GGAGGACGACGCTACTGCACCTTCCCTCCAGGGATGACCTGCTCTTCTCCCCAGTCTCCTCGTGGCCCCAGCCCCAAGCACTGCCCTGGG
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

SaII (1961)
1901 GGCAGTGGGCGGTGAAGAGAGGATGCCCCCTTTTGAAGAAAGAGTCCCAAGAGACTGGGACCCCAAGCCCTGGGGCCTCCACCCAGGAGTCC
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 GTCCAGGCTCCTGGCAGGGGAGTTCAAGGCCCTAATGCTCGCCTGCCCTGAACACTGATGCCTACTTGTCCCTCAAGAAGTCCAGGGTCAAGGAC
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 CCAACTCACTTGGTGTAGACAGATGGCCAGGGTGGGAGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAAGTGAATGCA
547▶ P T H L V •

HpaI (2376) **MfeI (2387)**
2301 GTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTGCATTCAT

EcoRI (2472)
2401 TTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCATAAATACAGCATAGCAAACT

2501 TTAACCTCAAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCC

SapI (2654)
2601 TCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCAAGGTTTGAAGTACTGCTTCTTCTTATGTTTAAATGCACTGACCTCCACATTCC

2701 **SspI (2711)** **SwaI (2725)**
 CTTTTTAGTAAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAAT
 2801 ATCCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTACTTG
 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 AGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCCGAGTCTTGGTCTGATG
 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 GCCGCCCCGACATGGTGTCTGTTGCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGGCT
 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 TCATGGTGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCT
 1 M
 3401 GACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAA
SpeI (3513)
 3501 GTCCCGTTGATTTACTAGTCAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATG
SnaBI (3641)
 3601 TACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTCCCAAGTAGGAAAGTCCCATAAAGTTCATGTACTGGGCATAATGCC
NdeI (3746)
 3701 AGGCGGGCCATTTACCGTCAATGAGCGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCAAGTGGGCGAGTTTACCGTAAATACTCCAC
 3801 CCATTGACGTCAATGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGCTGTTGGGCGGTGAGCCAGGCGGG
PaeI (3932)
SdaI (3924) **BspLU11I (3942)**
 3901 CCATTTACGTAAGTTATGTAACGCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGC
 4001 GTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTT
 4101 CCCCCTGGAAGCTCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATA
ApaLI (4256)
 4201 GCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCCTGCGCTTATCCGG
 4301 TAACTATCGTCTTGAGTCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCT
 4401 ACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTG
 4501 GTAGCTCTTGATCCGGCAAAACAAACCCTGGTAGCGGTGTTTTTTTTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCC
EagI (4692)
 4601 TTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCA
 Pacl (4672) SwaI (4681) **NotI (4691)**
 4701 ATAAAAATCTTTATTTTATTACATCTGTGTGTTGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACT
 4801 AGCAAAATAGGCTGTCCCGAGTCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA