



PvuI (7)
SgfI (6) 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA **MfeI (82)**
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCGCTACCTGAGGCC **PvuII (239)** **Bsu36I (291)**
301 GCCATCCACGCGGTTGAGTGCAGTTCGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCGGCTCTCCACGCTTGGCTGACCCTGCTTGTCTAACTCTACGCTTTGTTTCGTTT

SphI (560)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCGCTACCTGAGATCACCGGTGACGATGCAGATCCACAGGCGCCCTGGCCAGTGCCTGGGC **AgeI (552)** **XcmI (571)**
1 M Q I P Q A P W P V V W A
601 GGTGTACAACCTGGGCTGGCGCCAGGATGTTTCTTAGACTCCCGAGACAGCCCTGGAACCCCCCACCTTCTCCAGCCCTGCTCGTGGTGACCGAA **XcmI (643)** **BstEII (690)**
13 V L Q L G W R P G W F L D S P D R P W N P P T F S P A L L V V T E

Acc65I (761)
701 GGGACAACGCCACCTTACCTGCAGCTTCTCAACACATCGGAGAGCTTCGTGCTAAACTGGTACCGCATGAGCCCCAGCAACCAGACGGACAAGCTGG **Bsp120I (896)**
47 G D N A T F T C S F S N T S E S F V L N W Y R M S P S N Q T D K L
801 CCGCCTTCCCGAGGACCGCAGCCAGCCCGCCAGGACTGCCGCTTCCGTGTACACAACCTGCCAACGGGCGTACTCCACATGAGCGTGGTCAGGGC
80 A A F P E D R S Q P G Q D C R F R V T Q L P N G R D F H M S V V R A
901 CCGGCGCAATGACAGCGGCACCTACCTGTGGGGCCATCTCCCTGGCCCCAAGGCGCAGATCAAAGAGAGCTGCGGGCAGAGCTCAGGTTGACAGAG
113 R R N D S G T Y L C G A I S L A P K A Q I K E S L R A E L R V T E

NgoMIV (1048)
1001 AGAAGGGCAGAAGTGCCACAGCCACCCAGCCCTCACCCAGGCCAGCGGCGCAGTCCAAACCTGGTGGTGGTGTCTGGGCGGCGCTGCTGGGCA
147 R R A E V P T A H P S P S P R P A G Q F Q T L V V G V V G G L L G

XmaI (1139)
1101 GCCTGGTGTCTAGTCTGGTCTGGCGTCTGCTCCCGGCGCCAGCAGGAGGACAATAGGAGCCAGGCGCACCGGCCAGCCCTGAAGGAGGACCC
180 S L V L L V W V L A V I C S R A A R G T I G A R R T G Q P L K E D P

BbsI (1257)
1201 CTCAGCCGTGCCTGTGTTCTGTGGACTATGGGAGCTGGATTTCCAGTGGCAGAGAGAACCCCGGAGCCCCCGTGCCTGTGCTCCTGAGCAGACG
213 S A V P V F S V D Y G E L D F Q W R E K T P E P P V P C V P E Q T

Bsu36I (1396)
StuI (1393)
1301 GAGTATGCCACCATTGTCTTTCCTAGCGGAATGGGCACCTCATCCCCGCCCGCAGGGGCTCAGCCGACGGCCCTCGGAGTGCCAGCCACTGAGGCCTG
247 E Y A T I V F P S G M G T S S P A R R G S A D G P R S A Q P L R P

NheI (1465)
1401 AGGATGGACTGCTCTTGGCCCTCTGACCGGCTTCTTGGCCACCAGTGTCTGCAGACCTCGCTAGCTGGCCAGACATGATAAGATACATTGATGA
280 E D G H C S W P L •

1501 GTTTGGACAAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAA

HpaI (1603) **MfeI (1614)** 1601 CAAGTAAACAACAACAATTGCATTCAATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGG **EcoRI**
1701 AATTCTAAAATACAGCATAGCAAACTTAACTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTT

SapI (1881)
1801 GCCAATGTGATTAGCTGTTTGCAGCCTCACCTCTTTTCATGGAGTTAAGATATAGTGTATTTCCCAAGGTTTGAAGTACTAGCTCTTCATTTCTTTATGT

SspI (1938) **SwaI (1952)**
1901 TTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGA
2001 ATCCAGATGCTCAAGGCCCTTATAATATCCCCAGTTTGTAGTGTGGACTTAGGGAACAAGGAACCTTAAATAGAAATTGGACAGCAAGAAAGCGAGC

2101 TTCTAGCTTTAGTTCCTGGTGTACTTGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAGCAGTCAGGAG
141 • N 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
2201 CATAGTCAGAGATGAGCTCTGTCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGT
110 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 V A V I T

StuI (2377)
2301 GTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCCAGCAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAG
77 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 I H V A S
2401 ATGATCTCCCGAGTCTGGTCTGATGGCCGCCCGACATGGTCTTGTGCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCA
43 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 V E V L E L

BbsI (2523)
XmnI (2519) 2501 GATCTGCTGAGAGATGTTGAAGGCTTTCATGGTGGCCCTCTATAGTGAAGTATTATACTATGCCGATATACTATGCCGATGATTAATTGCAAAAC
104 D Q Q S I N F T K M

AseI (2585)

2601 AGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCATAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTGCGTCAATGG

2701 GCGGGAGTTGTTACGACATTTTGGAAAGTCCCCTTGATTTACTAGTCAAAAACAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAG

SpeI (2740) ←

2801 TCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCC

SnaBI (2868)

2901 ATAAGTCATGTACTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGCGTACTTGGCATATGATACACTTGTACTGCCAA

NdeI (2973)

3001 GTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGG

3101 GGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCCTGCAGGTTAAATAAGAACTGTGAGCAAAAGGCCAGCAAAAGGCCAG

SdaI (3151) PacI (3159) BspLU11I (3169) ←

3201 GAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG

3301 ACAGGACTATAAAGATACCAGGCGTTTTCCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCGGACCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCC

3401 CTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGCT

ApaLI (3483)

3501 TCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT

3601 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGA

3701 AGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCG

3801 CAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGT

PacI (3899)

EagI (3919)

Swal (3908) NotI (3918)

3901 TAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTGGTTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCA

4001 TCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA