



PvuI (7)
SgfI (6) 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA **MfeI (82)**
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

Psp1406I (203) 201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACGCGCCCGCCGCTACCTGAGGCC
HindIII (245)
301 GCCATCCACGCGCGTTGAGTCGCGTTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAAGTCGCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT
NgoMIV (441)

501 TCTGTTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTGAGTGCCTTCTCAGGGCCCTGAAGGACCTCAGCTTCAG
KasI (535) **AgeI (552)** **SphI (560)** **Bsp120I (575)**
1 M P S S G A L K D L S F S
BspLU11I (677)
601 TCAGCACTCAGGATGATGGTGATTTGCATAGTGTCTCTGCAGGTGCTCCTGCAGGCTGTGTCTGTGGCTGTGACTTACATGACTTCACCAACGAGATG
13 Q H F R M M V I C I V L L Q V L L Q A V S V A V T Y M Y F T N E M
BglIII (785)
701 AAGCAGCTGCAGGACAATTACTCCAAAATTGGACTAGCTTGTCTCTCAAAGACGGATGAGGATTTCTGGGACTCCACTGATGGAGAGATCTTGAACAGAC
47 K Q L Q D N Y S K I G L A C F S K T D E D F W D S T D G E I L N R
ScaI (898)
801 CCTGCTTGCAGGTTAAGAGGCAACTGTATCAGCTCATTGAAGAGGTGACTTTGAGAACCCTTTCAGGACACCATTCTACAGTTCCAGAAAAGCAGCTAAG
80 P C L Q V K R Q L Y Q L I E E V T L R T F Q D T I S T V P E K Q L S
901 TACTCCTCCCTTGCCAGAGGTGAAGACCTCAGAAAAGTGGCAGCTCACATTACTGGGATCACTCGGAGAAGCAACTCAGCTTAAATCCAATCTCCAAG
113 T P P L P R G G R P Q K V A A H I T G I T R R S N S A L I P I S K
BbrPI (1069)
1001 GATGGAAAGACCTTAGGCCAGAAGATTGAATCCTGGGAGTCTCTCGGAAAGGCATTATTTCTCAACCAGTGCTCTTTAGGAATGGAGAGCTGGTCA
147 D G K T L G Q K I E S W E S S R K G H S F L N H V L F R N G E L V
BstXI (1199)
1101 TCGAGCAGGAGGGCCTGTATTACATCTATTCCAAACATACTTCCGATTTTCAGGAAGCTGAAGACGCTTCCAAGATGGTCTCAAAGGACAAGGTGAGAAC
180 I E Q E G L Y Y I Y S Q T Y F R F Q E A E D A S K M V S K D K V R T

1201 CAACAGCTGGTGCAGTACATCTACAAGTACACCAGCTATCCGGATCCCATAGTGTCTATGAAGAGCGCCAGAAAACAGCTGTTGGTCCAGAGATGCCGAG
213 K Q L V Q Y I Y K Y T S Y P D P I V L M K S A R N S C W S R D A E
1301 TACGGACTGACTCCATCTATCAGGGAGGATTGTTGAGCTAAAAAAAATGACAGGATTTTGTTCGTGACAAAATGAACATTTGATGGACCTGGATC
247 Y G L Y S I Y Q G G L F E L K K N D R I F V S V T N E H L M D L D
MscI (1471)
1401 AAGAACCCAGCTTCTTTGGAGCCTTTTTAATTAATACTAAATGACCAGTAAAGATCAAACACAGCCCGCTAGCTGGCCAGACATGATAAGATACATTGATGA
280 Q E A S F F G A F L I N •
1501 GTTTGGACAAACCACAACATAAGATGCAAGTGAAGGATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAA

1601 CAAGTTAAACAACAACAAATTGCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGTTTTTAAAGCAAGTAAAACCTCTACAAATGGGTATGG **EcoRI**
1701 AATTCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTT

1801 GCCAATGTGCATTAGCTGTTTGAGCCTCACCTTCTTTCATGGAGTTTAAAGATATAGTGTATTTTCCCAAGGTTTGAAGTACTGCTCTTCATTTCTTTATGT
SapI (1881)

1901 TTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAAATATTCAGAAAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGA
SspI (1938) **SwaI (1952)**
2001 ATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTAAATAGAAAATTGGACAGCAAGAAAGCGAGC
2101 TTCTAGCTTTAGTCTCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCTCAATGAGCACAAAGCAGTCAGGAG
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
SacI (2213) **BstXI (2242)**
2201 CATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGT
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 GTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCCAGCACAGACAGTACCCTGCCAATGTAGGCCCTCAATGTGACAGCAGAG
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 ATGATCTCCCGAGTCTGGTCTGATGGCCGCCCGACATGGTCTTGTGCTCCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCA
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
XmnI (2519) **AseI (2585)**
2501 GATCCTGCTGAGAGATGTTGAAGGCTTTCATGGTGGCCCTCTATAGTGAGTCTATTATACTATGCCGATATACTATGCCGATGATTAATTGCAAAAC
10 D Q Q S I N F T K M

2601 AGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCCACGTACACGCCTACCGCCATTTCGCTCAATGG

SacI (2642)

2701 GGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAG

SpeI (2740)

2801 TCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCC

SnaBI (2868)

2901 ATAAGTTCATGTACTGGCATAATGCCAGGCGGGCCATTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGTACTGCCAA

NdeI (2973)

3001 GTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGG

3101 GGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTACCGTAAGTTATGTAACGCCTGCAGGTTAAATAAGAACTGTGAGCAAAGGCCAGCAAAGGCCAG

BspLU11I (3169)

3201 GAACCGTAAAAAGCCGCGTTGTGCGCTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCAAACCCG

3301 ACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCGGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCC

3401 CTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGT

ApaLI (3483)

3501 TCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT

3601 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGA

3701 AGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTGCAAGCAGCAGATTACGCG

3801 CAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGT

EagI (3919)

Swal (3908) NotI (3918)

3901 TAATTAACATTTAAATCAGCGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCA

4001 TCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAAGTGCCAGAACATTTCTCTATCGAA