



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
MfeI (82)
101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTGTCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGCC
PvuII (239)
Bsu36I (291)
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

BstEII (555)
AgeI (552) 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCACCATGGCTGGGGTGGGGTCCACACCTGCTGCTCCACCT
NcoI (560) 1 M A W G G V H T C C F H L

Bsu36I (619) 601 GTGCTGCTGCTCCTGGCCTCAGGGTGTGTGCCTGAAGAACTTCAAAACACCCAGGACAGACCCCTCCTCCTGCAATGCCAGTACTCACCAAGAGA
XmnI (637) 13 C C C C S W P Q G A V P E E L H K H P G Q T L L L Q C Q Y S P K R
ScaI (683)

Bsp120I (700) 701 GGGCCCTATCAGCCAAATCCTGGTGTGAGCAGACATCTCAAGTCGGTGTACCTTACTTGTACCAGCTCCAAGCCCTGGACAGCAGTTCAGAAAGTCTC
47 G P Y Q P K S W C Q Q T S P S R C T L L V T S S K P W T A V Q K S

PvuII (853)
801 ATTACACAATCTGGGACAAGCCAAATGTGGCTTCTTCAACATCACCATGATTCAGCTGACACAGAATGACTCGGGATTCTACTGGTGTGAAATCTACAA
80 H Y T I W D K P N A G F F N I T M I Q L T Q N D S G F Y W C G I Y N
901 CGTTCCGAAAACATCATCACTGTTCTTAGAAATATCAGCCTGGTGGTGTCTCCAGCCCCAACACGCTCTCCTATGTGGACTTCCCTGGCTCCCAACA
113 A S E N I I T V L R N I S L V V S P A P T T S P M W T L P W L P T
1001 AGCACAGTTCTGATCACTTCTCCAGAGGGACCTTGGCCATCCCTCCATCAATGGCTGTAGACCAGGAAATCAAGAGCCCTGCCTGCCTTGCTCAG
147 S T V L I T S P E G T S G H P S I N G S E T R K S R A P A C L G S

BstXI (1106) 1101 GTGGCCCCAGATTCTGGTCTTGGTGTATGTGGACTCCTCCTGGCCAAGGGCCTGATGTTGTGAGTCTGTTAGTGCTCCTGATCTGCAGGTGCCGCTA
180 G G P R F L V L V L C G L L L A K G L M L •
PstI (1185) 1201 GCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGC
NheI (1196)

HpaI (1334) 1301 TTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAAACAACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGGAGGTGTGGGAGGTTTTTTAA
MfeI (1345)

EcoRI (1430)
1401 AGCAAGTAAAACCTCTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACCTTAACTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGG
1501 GATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCTCACCTTCTTTCATGGAGTTAAGATATAGTATTTTCCCA

SapI (1612) 1601 AGGTTTGAAGTACTCTTCATTTCTTTATGTTTAAATGCACTGACCTCCACATTCCTTTTATGAAAATATTCAGAAATAATTTAAATACATCATTG
SspI (1669) 1701 CAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTATGAGTTGGACTTAGGGAACAAAGAACCT
SwaI (1683)
1801 TTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCA
141 • N R T Y K L P I L E E I T T K V L K G

SacI (1944) 1901 TTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCAT
120 N M E I L 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
2001 CAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAAGCAGACAGTGCACCT
87 S Y P H R 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

StuI (2108) 2101 GCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGCTTGTGCTCATAGAGCATGGTG
54 G I Y A E 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

BbsI (2254) 2201 ATCTTCTCAGTGGCGACCTCCACAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCCTATAGTGAGTCTGATTATACTATGCCG
XmnI (2250) 20 I K E T A V E V L E L D Q Q S I N F T K M
AseI (2316) 2301 ATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCATAAACGAGCTCTGCTTATATAGACCTCCACC
SacI (2373)

2401 GTACACGCTACCGCCATTTGCGTCAATGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAACAACCTCCATTGACGTC
SpeI (2471)

2501 AATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAAT
SnaBI (2599)

2601 ACGTAGATGTAAGTCCCAAGTAGGAAAGTCCATAAGGTCATGTAAGTCCGTCATTGACGTCAATAGGGGGCGTAC

2701 TTGGCATATGATACACTTGTACTGCCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGG
NdeI (2704)

2801 AACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTACGCCAGGCGGGCCATTACCCTAAGTTATGTAACGCTGCAGGTTAATTAAGA
PacI (2890)
PstI (2883)
SdaI (2882)

2901 ACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTCTGCGTTTTTCCATAGGCTCCGCCCTGACGAGCATCACA
BspLU11I (2900)

3001 TCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCTG

3101 CCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCT

3201 CCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAAGTCCAACCCGGTAAGACACGACTTATC
ApaLI (3214)

3301 GCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGA

3401 AGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTG

3501 GTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAA
EagI (3650)

3601 CTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGCGCGCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGTTTTT
PacI (3630) SwaI (3639) NotI (3649)

3701 TGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGAAGTGCAGGTGCCAGAAC

3801 ATTTCTCTATCGAA