



PvuI (7)
SgfI (6) 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGCGCAATTGAACGGGTGCCTA

101 GAGAAGGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGACTGGCTCCGCCTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

AgeI (552) **SphI (560)** **XbaI (573)**
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCAGCATGCCAGGGGTCTAGAAGCCCTCAGAGCCCTGCCTCT
1 M P G G L E A L R A L P L

SandI (627)
601 CCTCTCTTCTTGTACATACGCTGTTTGGTCCCGGATGCCAGGCCCTGCGGGTAGAAGGGGTCCACCATCCTGACGGTGAACCTGGGCGAGGAGGCC
13 L L F L S Y A C L G P G C Q A L R V E G G P P S L T V N L G E E A

DraIII (738) **MscI (795)**
701 CGCTCACCTGTGAAAACAATGGCAGGAACCTAATATCACATGGTGGTTCAGCCTTCAGTCTAACATCACATGGCCCCAGTGCCACTGGGTCTGGCC
47 R L T C E N N G R N P N I T W W F S L Q S N I T W P P V P L G P G

801 AGGGTACCACAGGCCAGCTGTTCTTCCCGAAGTAAACAAGAACACAGGGGCTTGTACTGGTCCAAAGTATAGAAAACAACATATTAACGCTCCTG
80 Q G T T G Q L F F P E V N K N H R G L Y W C Q V I E N N I L K R S C

FspI (917) **AvrII (931)**
901 TGGTACTTACCTCCGCGTGGCAATCCAGTCCCTAGGCCCTTCTGGACATGGGGGAAGGTACCAAGAACCGCATCATCACAGCAGAAGGGATCATCTTG
113 G T Y L R V R N P V P R P F L D M G E G T K N R I I T A E G I I L

BsaBI (1093)
1001 CTGTTCTGTGCGAGTGGTCCAGGACGCTGCTGCTATTAGGAAACGGTGGCAAAATGAGAAGTTGGGGTGGACATGCCAGATGACTATGAAGATGAAA
147 L F C A V V P G T L L L F R K R W Q N E K F G V D M P D D Y E D E

1101 ATCTCTATGAGGGCTGAACCTTGATGACTGTTCTATGTATGAGGACATCTCCAGGGGACTCCAGGGCACCTACCAGGATGTGGCAACCTCCACATTGG
180 N L Y E G L N L D D C S M Y E D I S R G L Q G T Y Q D V G N L H I G

MscI (1253)
1201 AGATGCCAGCTGGAAAAGCCATGACTGACATGTCCACCCTTCCCTGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAAC
213 D A Q L E K P •

BspLU11I (1228) **NheI (1247)**
1301 TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAACAAGTTAACAACAACAAT

EcoRI (1481)
1401 TGCATTATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAATACAGCAT
1501 AGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTG

SapI (1663)
1601 TTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGTTTGAAGTACTCTTCATTCTTTATGTTTAAATGCACTGACCTC

SspI (1720) **SwaI (1734)**
1701 CCACATCCCTTTTATGATAAAATATTAGAAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAAATCCAGATGCTCAAGGCC

1801 CTTATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTAAATAGAAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTCTCTG
141 • N R

SacI (1995)
1901 GTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCT
137 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 Y D S I L E

BstXI (2024)
2001 CTCTGCACATGCCACAGGGGCTGACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCC
104 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 D F D K Q G

StuI (2159)
2101 GTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTG
71 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 I I E G T K

2201 GTCCTGATGGCCGCCGACATGGTGTCTGTTGCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGT
37 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 D Q Q S I N

BbsI (2305) **XmnI (2301)** **AseI (2367)**
2301 TGAAGTCTTCATGGTGGCCCTCTATAGTGTGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCC
4 F T K M

2401 **SacI (2424)**
AGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACGCCCATTTGCGTCAATGGGGCGGAGTTGTTACGACA

2501 **SpeI (2522)**
TTTTGAAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAAATCCCCGTGAGTCAAACCGCTATCCACGC

2601 **SnaBI (2650)**
CCATTGATGTA CTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAGGTCATGTACTGGG

2701 **NdeI (2755)**
CATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCGAGTTACCGTAA

2801 ATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGAAACATACGTCATTATTGACGTCAATGGGCGGGGGTCTGTTGGGCGGTCA

2901 **PacI (2941)**
PstI (2934)
SdaI (2933) **BspLU11I (2951)**
CCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATTAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGC

3001 GTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATAC

3101 CAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCTGCCGTTACCGGATACCTGTCCGCCTTCTCCCTTCGGGAAGCGTGGCGC

3201 **ApaLI (3265)**
TTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCCAGCCGACCGCTGCGC

3301 CTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTA

3401 GCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAA

3501 AAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCA

3601 **PacI (3681)** **SwaI (3690)**
AGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCA

EagI (3701)
NotI (3700)
3701 GCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACA

3801 AAACAAACTAGCAAAATAGGCTGTCCCAAGTCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA