



PvuI (7)
SgfI (6) **MfeI (82)**
1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)**
PvuII (239) **Bsu36I (291)**
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCGGTTGAGTCGCGTTTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

KasI (535) **NcoI (560)**
BstEII (555) **AgeI (552)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTCACCATGCGTAGGCTCTGTGCTTTCCTGATGGTCTCGCGGT
1 M A R L C A F L M V L A V

MscI (610) **Bsu36I (654)**
601 GATGAGCTACTGGCAACCTGCTCTCTAGGATGTGACCTGCCTCAGACTCATAACCTCAGGAACAAGAGAGCCTTGACACTCCTGGTACAAATGAGGAGA
13 M S Y W P T C S L G C D L P Q T H N L R N K R A L T L L V Q M R R
701 CTCTCCCCTCTCTCTGCTGAAGGACAGGAAGGACTTTGGATTCCCGCAGGAGAAGGTGGATGCCAGCAGATCAAGAAGGCTCAAGCCATCCCTGTCC
47 L S P L S C L K D R K D F G F P Q E K V D A Q Q I K K A Q A I P V
801 TGAGTGAGCTGACCCAGCAGATCCTGAACATCTTACATCAAAGGACTCATCTGCTGCTGGAATGCAACCCTCTAGACTCATTGCAATGACCTCCA
80 L S E L T Q Q I L N I F T S K D S S A A W N A T L L D S F C N D L H
901 CCAGCAGCTCAATGACCTGCAAGTTGTCTGATGCAGCAGGTGGGGGTGAGGAATTTCCCTGACCCAGGAAGATGCCCTGCTGGCTGTGAGGAAATAC
113 Q Q L N D L Q G C L M Q Q V G V Q E F P L T Q E D A L L A V R K Y

BstXI (1097)
1001 TTCCACAGGATCACTGTGTACCTGAGAGAGAAGAAACACAGCCCTGTGCTGGGAGGTGGTCAGAGCAGAAGCTGGAGAGCCCTGTCTTCTCTGCCA
147 F H R I T V Y L R E K K H S P C A W E V V R A E V W R A L S S S A

MscI (1153)
1101 ATGTGCTGGGAAGACTGAGAGAAGAAAATGAGTCTGAGCCAAAGTCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGACAAACCACAAC
180 N V L G R L R E E K

HpaI (1285) **MfeI (1296)**
1201 TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAAT

EcoRI (1381)
1301 TGCATTCATTTTATGTTTCAGGTTCAAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCAT
1401 AGCAAACTTTAACCCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTG

SapI (1563)
1501 TTTGAGCCTCACCTTCTTCATGGAGTTAAGATATAGTGTATTTCCCAAGTTTGAAGTACTGCTCTTCATTTCTTTATGTTTTAAATGCAGCTGACCTC

SspI (1620) **SwaI (1634)** **EcoO109I (1695)**
1601 CCACATTCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCC
1701 CTTATAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTTCTCG
141 N R

SacI (1895)
1801 GTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCT
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 (1924)
1901 CTCTGCATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCC
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 (2059)
2001 GTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTG
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
2101 GTCCTGATGGCCGCCCGACATGGTGTGTTGCTCATAGAGCATGGTGTCTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGT
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

AseI (2267)
2201 TGAAGTCTTCATGGTGGCCCTCTATAGTGTGATGCTATTATACTATGCGGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCC
4 F T K M

SacI (2324)
2301 AGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACA

SpeI (2422)
2401 TTTTGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGCTATCCACGC

SnaBI (2550)
2501 CCATTGATGACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCCATAAAGGTCATGACTGGG

2601 CATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAA
2701 ATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGGTCGTTGGGCGGTGAC

PacI (2841)
PstI (2834)
SdaI (2833) BspLU11I (2851)

2801 CCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGC
2901 GTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACA AAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATAC
3001 CAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTCTCCCTTCGGGAAGCGTGCCGC

ApaLI (3165)

3101 TTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCCAGCCGACCGCTGCCG
3201 CTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTA
3301 GGGCGTGCTACAGAGTTCTTGAAGTGGTGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAA
3401 AAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCA

PacI (3581) SmaI (3590)

3501 AGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC A

EagI (3601)
NotI (3600)

3601 GCGGCCGAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACA
3701 AAACAAACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGCAAGTGCCAGAACATTTCTCTATCGAA