



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
MfeI (82)
101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTTCGAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACCGCGCCCGCCCTACCTGAGGCC
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

BstEII (555) **AgeI (552)** **SfiI (576)**
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCATTGGGCGTCCCACGGCCCTGGAGGCCGGCAGCTGGCG
1 M G V P T A L E A G S W R

SapI (612) **BamHI (604)** **AvrII (639)**
601 CTGGGATCCCTGCTCTTCGCTCTTCTGGTGGTCCCTAGTCCGGTGGCAGCCTTCAAGGTCGCCACGCCGATTCCCTGTATGTCTGTCCCAG
13 W G S L L F A L F L A A S L G P V A A F K V A T P Y S L Y V C P E
701 GGCAGAACGTCACCCTACCTGCAGGCTCTTGGCCCTGTGGACAAAGGGCAGCATGTGACCTTCTACAAGACGTGGTACCAGCTCGAGGGCGAGG
47 G Q N V T L T C R L L G P V D K G H D V T F Y K T W Y R S S R G E
801 TGCAGACCTGCTCAGAGCGCCGCCATCCGCAACCTCACGTTCCAGGACCTCACCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCAGCAGCT
80 V Q T C S E R R P I R N L T F Q D L H L H H G G H Q A A N T S H D L

XcmI (887) **FspI (959)**
901 GGCTCAGCGCCACGGGCTGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCCTGCTGGATAGCGGCCCTCTACTGCTGC
113 A Q R H G L E S A S D H H G N F S I T M R N L T L L D S G L Y C C
1001 CTGGTGGTGGAGATCAGGCACCACCTCGGAGCACAGGGTCCATGGTGCATGGAGTGCAGGTGCAGACAGGCAAAGATGCACCATCCAACCTGTGTGG
147 L V V E I R H H H S E H R V H G A M E L Q V Q T G K D A P S N C V
1101 TGTACCCATCCTCCTCCAGGAGAGTAAAACATCACGGTGCAGCCCTGGTACGGGTGCATCGTAGGAATCCTCTGCCTCCCCCTCATCCTGCT
180 V Y P S S S Q E S E N I T A A A L A T G A C I V G I L C L P L I L L
1201 CCTGGTCTACAAGCAAAGGCAGGACCTCCAACCGCGTGCAGGAGCTGGTGGGATGGACAGCAACATTCAAGGGATTGAAAACCCCGCTTTGAA
213 L V Y K Q R Q A A S N R R A Q E L V R M D S N I Q G I E N P G F E
1301 GCCTCACACCTGCCAGGGGATACCGAGGCCAAAGTCAGGCACCCCTGTCTATGTGGCCAGCGGCAGCCTTCTGAGTCTGGCGGCATCTGCTTT
247 A S P P A Q G I P E A K V R H P L S Y V A Q R Q P S E S G R H L L

BbsI (1441) **Tth111I (1459)**
1401 CGGAGCCAGCACCCCTGTCTCCTCCAGGCCCGGAGAGCTTCTTCCATCCCTGGACCCTGCTCCTGACTCTCAAACCTTTGAGGTACATAGCC
280 S E P S T P L S P P G P G D V F F P S L D P V P D S P N F E V I •

MscI (1512) **NheI (1506)**
1501 CAGCTGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTAAAAAATGCTTTATTTGTGAAATTTGTG

HpaI (1644) **MfeI (1655)**
1601 ATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAAACAACAACAAATGCATTCAATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGA

EcoRI (1740)
1701 GGTTTTTTAAAGCAAGTAAAACCTTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAAACCTTAACTCCAAATCAAGCCTCTACTGATCC
1801 TTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTG

SapI (1922) **SspI (1979)** **Swal (1993)**
1901 TATTTTCCAAGGTTTGAAGTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTAGTAAAATATTCAGAAAATAATTTAAA
2001 TACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAAC
2101 AAAGAACCTTTAATAGAAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGAC
141 • N R T Y K L P I L E E I T T K V

SacI (2254)
2201 CAGCTTGCCATTCATCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTG
124 L K G 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
2301 TCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGA
90 D V E D 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

StuI (2418)
2401 CAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCACTTGGTCTGATGGCCGCCCCGACATGGTGCTTGTGCTCCTACA
57 T V R 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

BbsI (2564)
XmnI (2560)

2501 GAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCCTATAGTGAGTCGTATTA
24 L M T I K E T A V E V L E L D Q Q S I N F T K M ←

AseI (2626) SacI (2683)

2601 TACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGATGGCGTCTCCAGCTTATCTGACGGTTCATAAACGAGCTCTGCTTATATAG
←

SpeI (2781)

2701 ACCTCCCACCGTACACGCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTACGACATTTTGAAAGTCCC GTT GATTTACTAGICAAAACAACTCC
←

2801 CATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGC
←

SnaBI (2909)

2901 GATGACTAATACGTAGATGTA CTGCAAGTAGGAAAAGTCCATAAGGTCATGTA CTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATA
←

NdeI (3014)

3001 GGGGGCGTACTTGGCATATGATACACTTGATGTA CTGCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCG
←

SdaI (3192)

3101 TTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTACGCCAGGCGGGCCATTTACCCTAAGTTATGTAACGCCTGCAGG
←

PacI (3200) **BspLU11I (3210)**

3201 TTAATTAAAGACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTCCATAGGCTCCGCCCCCTGACGAGC
←

3301 ATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGT
←

3401 TCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAG
←

ApaLI (3524)

3501 GTCGTTCCGCTCCAAGCTGGGCTGTGTCACGAACCCCGTTCAGCCCGACCCTGCGCCTTATCCGGTAACTATCGTCTTGTAGTCCAACCCGGTAAGAC
←

3601 ACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGTACAGAGTTCTTGAAGTGGTGCCTAACTACGG
←

3701 CTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCT
←

3801 GGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTCTACGGGTCTGACGCTCAGT
←

EagI (3960)

PacI (3940) SwaI (3949) **NotI (3959)**

3901 GGAACGAAAACCTACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTTCATTACATCTGTGT
←

4001 GTTGGTTTTTTGTGTGAATCGTAACATAACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGAAGTGACG
4101 GTGCCAGAACATTTCTCTATCGAA