



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

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCGCCCTACCTGAGGGC
PvuII (239)
Bsu36I (291)
301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCAGCTTTGCCTGACCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

AgeI (552) **BspHI (560)**
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCTACCTGAGATCACCGGTCATCATGACTTTTGTGACCTAAAGATCCAGACTGTGAAGGA
1 M T F D D L K I Q T V K D

BbsI (638) **NcoI (658)** **EcoO109I (689)**
601 CCAGCCTGATGAGAAGTCAAATGAAAAAAGCTAAAGGTCTTCACTTCTTACTCTCCATGGTGGTGCCTGGCTGCTGCGACTCTAGGGGTCTTTGC
13 Q P D E K S N G K K A K G L Q F L Y S P W W C L A A A T L G V L C

SphI (731)
701 CTGGGATTAGTAGTACCATTATGGTGTGGGCATGCAATTATCCCAGGTGTCTGACCTCCTAACACAAGAGCAAGCAAACCTAACTACCAGAAAAAGA
47 L G L V V T I M V L G M Q L S Q V S D L L T Q E Q A N L T H Q K K

BglIII (812) **HindIII (839)**
801 AACTGGAGGGACAGATCTCAGCCCGGCAACAAGCAGAAGAAGCTTACAGGAGTCAGAAAACGAAGTCAAGGAAATGATAGAAACCTTGTCTCGGAAGCT
80 K L E G Q I S A R Q Q A E E A S Q E S E N E L K E M I E T L A R K L
901 GAATGAGAAATCAAAGAGCAAATGAACTTACCACCAAGAAATCTGAATCTCCAAGAAACACTGAAGAGAGTAGCAAATTTGTCAGCTCCTTGTCCGCAA
113 N E K S K E Q M E L H H Q N L N L Q E T L K R V A N C S A P C P Q
1001 GACTGGATCTGGCATGGAGAAAAGTGTACCTATTTTCTCGGGCTCATTTAACTGGGAAAAGAGCCAAGAGAAGTGTCTTTGGATGCCAAGTTGC
147 D W I W H G E N C Y L F S S G S F N W E K S Q E K C L S L D A K L

AseI (1105) **PvuII (1115)**
1101 TGAATAATAGCACAGCTGATCTGGACTTATCCAGCAAGCAATTTCTATTCCAGTTTTCCATTCTGGATGGGGTGTCTCGGAGGAACCCAGCTA
180 L K I N S T A D L D F I Q Q A I S Y S S F P F W M G L S R R N P S Y

NcoI (1201) **BstXI (1201)** **Acc65I (1282)**
1201 CCCATGGCTCTGGGAGGACGGTTCTCCTTTGATGCCCCACTTATTTAGAGTCCGAGGCGCTGTCTCCAGACATACCTTACAGTACCTGTGCATATATA
213 P W L W E D G S P L M P H L F R V R G A V S Q T Y P S G T C A Y I
1301 CAACGAGGAGCTGTTTATGCGGAAAAGTGCATTTTAGCTGCCTTCAATATATGTCAGAAAGGCAACCTAAGAGCAGAGTGAATTTGAAGGCTCTGGA
247 Q R G A V Y A E N C I L A A F S I C Q K K A N L R A Q •

MscI (1411) **NheI (1405)**
1401 AGAAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGACAAACCACAACCTAGAATGCAGTGAAGAAAAATGCTTTATTTGTGAATTTGTGA

HpaI (1543) **MfeI (1554)**
1501 TGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACATTCATTCTTTATGTTTCAGGTTACAGGGGAGGTGTGGGAG

EcoRI (1639)
1601 GTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTTCAAATACAGCATAGCAAACCTTAACTCCAATCAAGCCTCTACTTGAATCCT
1701 TTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGT

SapI (1821) **SspI (1878)** **Swal (1892)**
1801 ATTTTCCAAGTTTGAAGTACTGCTCTTCAATTTCTTTATGTTTTAAATGCACTGACCTCCCACATTCCTTTTTAGTAAATATTCAGAAATAATTTAAAT

EcoO109I (1953)
1901 ACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACA
2001 AAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTGTAGTTCCTGGTACTTGGAGGGGATGAGTTCCTCAATGGTGGTTTTGACC
141 • N R T Y K L P I L E E I T T K V

SacI (2153) **BstXI (2182)**
2101 AGCTTGCCATTCTCAATGAGCACAAGCAGTCAAGGAGCATAGTCAAGATGAGCTCTGACATGCCACAGGGGCTGACCACCTGATGGATCTGT
123 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 R I S R D
2201 CCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAAATGGCAATGGCTTCAAGCAGAC
90 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 (2317)
2301 AGTGACCCTGCCAATGTAGGCCCTCAATGTGGACAGCAGAGATGATCTCCCGTCTTGGTCTGATGGCCGCCCGACATGGTGTCTTGTCTCATAG
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 (2463)
XmnI (2459)

2401 AGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTAT
23 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 (2525) SacI (2582)

2501 ACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCCTAAACGAGCTCTGCTTATATAGA

SpeI (2680)

2601 CCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCC
2701 ATTGACGTCAATGGGGTGAGACTTGAAATCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCAAAACCGCATCATCATGGTAATAGCG

SnaBI (2808)

2801 ATGACTAATACGTAGATGTAAGTCCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGGCGGCCATTTACCGTCATTGACGTCAATAG

NdeI (2913)

2901 GGGGCGTACTTGGCATATGATACTTGTACTGCAAGTGGGCGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGT

PacI (3099)

PstI (3092)
SdaI (3091)

3001 TACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAACGCCTGCAGGT

BspLU11I (3109)

3101 TAAATAAGAACATGTGAGCAAAAGGCCAGAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCTGACGAGCA
3201 TCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGGCTCTCCTGTT
3301 CCGACCCTGCCGTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGG

ApaLI (3423)

3401 TCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCCAGCCGACCGTGGCGCTTATCCGGTAACTATCGTCTTGAAGTCCAACCCGTAAGACA
3501 CGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGC
3601 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAACCACCGCTG
3701 GTAGCGGTGGTTTTTTTGTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTG

EagI (3859)
PacI (3839) SwaI (3848) NotI (3858)

3801 GAACGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTG
3901 TTGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGG
4001 TGCCAGAACATTTCTCTATCGAA