



PvuI (7)
SgfI (6)
1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

MfeI (82)
101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGACTGGCTCCGCCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) **PvuII (239)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCCTCCCGCCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCTGACCTGCTTGTCTCAACTCTACGCTTTGTTCGTTT

AgeI (552) **BspHI (560)** **NcoI (572)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTATCATGAGTGACTCCATGGAATCAAAGACACAGCAAGTGGT
1 M S D S M E S K T Q Q V V

EcoRV (646) **Bst1107I (696)**
601 CATTCCAGAGGATGAAGAGTGTGATGAGTGGCACCAGGTATTCTGATATCAGCTCCCGATTACAACAAAATTTGGAATCAAGAGTTTGGCAGAGTAT
13 I P E D E E C L M S G T R Y S D I S S R L Q T K F G I K S L A E Y

PvuII (730)
701 ACGAAGCAGAGCCGCAACCCCTTGTCCTGCAGCTGCTTTCCTTCTGTTCTTGGCTGGGCTTCTGCTGATCATTCTGATCCTAGTGTCAAAGTCCCCA
47 T K Q S R N P L V L Q L L S F L F L A G L L I I L I L V S K V P

BspHI (855)
801 GCTCAGAGTTTGAACAAAATCTACCAGGAGCTCATGCAACTGAAGGCTGAAGTTTATGATGGCTTGTGCCAACCTGCGCCAGGGACTGGACATTCTT
80 S S E V Q N K I Y Q E L M Q L K A E V H D G L C Q P C A R D W T F F

Bsp120I (974)
901 CAATGGAAGCTGTTACTTCTTCTCCAAGTCCAAAGAAATTGGCAACTCCACCCTGCCTGCCAGGAAGTGGGGCCCACTGGTTCATCATAGAGACT
113 N G S C Y F F S K S Q R N W H N S T T A C Q E L G A Q L V I I E T

NsiI (1069) **DraIII (1090)**
1001 GATGAGGAGCAGACTTCTGTCAGCAGACTTCTAAGGCTAGAGGACCAACCTGGATGGGTCTCTCAGACATGCATAATGAAGCCATGGCACTGGGTGG
147 D E E Q T F L Q Q T S K A R G P T W M G L S D M H N E A T W H W V

1101 ATGGCTCACTCTGTCAACCAGCTTTACACGCTATTGGAATAGAGGGAGCCCAACAATGTGGTGATGAAGATTGTGCAGAGTTCTCTGGGGATGGCTG
180 D G S P L S P S F T R Y W N R G E P N N V G D E D C A E F S G D G W

MscI (1282)
NheI (1276)
1201 GAATGATCTCAGTTGTGATAAACTACTTTTCTGGATCTGTAAGAAAGTTTCAACCTCATCATGCACCACCAAATAGGCTAGCTGGCCAGACATGATAAGA
213 N D L S C D K L L F W I C K K V S T S S C T T K •

1301 TACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATA

HpaI (1414) **MfeI (1425)**
1401 GCTGCAATAAACAAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTTGGAGGTTTTTTAAAGCAAGTAAACCTCTACAA

EcoRI (1510)
1501 ATGTGGTATGGAATCTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCAT

SapI (1692)
1601 CAGGGGCTGTGCCAATGTGCATTAGCTGTTGCAGCCTCACCTTCTTCATGGAGTTAAGATATAGTATTTTTCCAAGTTTGAACCTAGCTCTTCA

SspI (1749) **Swal (1763)**
1701 TTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAAATATTCAGAAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTT

1801 TATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCA

1901 AGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTTCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAA
141 • N R T Y K L P I L E E I T T K V L K G N M E I L V F

BstXI (2053)
2001 GCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACA
114 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 S Y P H R V

StuI (2188)
2101 GCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGT
80 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 G I Y A E I H

2201 GGACAGCAGAGATGATCTCCCAGCTTGGTCTGATGGCCGCCCGACATGGTGCTTGTGTCTCATAGCATGGTGTCTTCTCAGTGGCGACCTC
47 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 I K E T A V E

BbsI (2334) **XmnI (2330)** **AseI (2396)**
2301 CACCAGCTCCAGATCCTGCTGAGAGATGTTGAAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTA
14 V L E L D Q Q S I N F T K M

2401 **ATTGTCAA**AACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCATAAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCATT
←

2501 TCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCCTTGATTT**ACTAGT**CAAAACAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAA
SpeI (2551) ←

2601 ATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTA**CTG**CCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTA**CTG**CCAAGT
SnaBI (2679)

2701 AGGAAAGTCCCATAAGGTCATGTA**CTG**GGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGA
NdeI (2784)

2801 TGTA**CTG**CCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCA**TTATT**GACG
←

2901 TCAATGGGCGGGGTCGTTGGGCGGT**CAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAA**TTAAGAA**CA**TGTGAGCAAAAGGCCAG
PacI (2970) SdaI (2962) BspLU11I (2980) ←

3001 CAAAAGCCAGGAACCGTAAAAAGCCCGT**TGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATC**AAAAATCGACGCTCAAGT**CAGAGT**
←

3101 GGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCC**CCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCTGCCGCTTACCGGATACCTGC**
←

3201 CGCCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTG**TAGGTATCTCAGTTCGGTGTAGGTCGTT**CGCTCCAAGCTGGGCTGTGTGCAC
ApaLI (3294)

3301 GAACCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT**GAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTG**
←

3401 GTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTG
←

3501 CGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTT**GATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTT**GTTTGAAGCAG
←

3601 CAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAAACTCACGTTAAGGGATTTTGG
←

EagI (3730)
PacI (3710) SwaI (3719) NotI (3729)

3701 TCATGGCTAGTTAATTAACATTTAAATCAGCGCGCGCAATAAAATATCTTTATTTT**CATTACATCTGTGTGGTTTTTT**GTGTGAATCGTAACTAACA
←

3801 TACGCTCTCCATCAAACAAACGAAACAAACAAACTAGCAAATAGGCTGTCCCAGTGAAGTG**CAGGTGCCAGAACATTTCTCTATCGAA**