



PvuI (7)
SgfI (6)
1 GGATCTGCATCGCTCCGGTGCCTGCAGTGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA **EcoNI (96)**

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCTCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCCGCGCCCTACCTGAGGCC **EcoNI (287)**

301 GCCATCCACGCGGTTGAGTGCCTCTCCGCTCCCGCTGTGGTGCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTGAGACC

NgoMIV (441)
401 GGGCTTTGTCCGGCGCTCCTTGGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

NcoI (560)
BstEII (555)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCCCTACCTGAGATCACCGGTCACCATGGCCCCAGAGATTCACATGCCAGAACCTTGTGCCT

601 CATTGGGAGCAGGGACACCTAGTAACTAACCAAGAGCCCTGAAGATTCTGTCTGCCATCACACAGCCAGTGGTGGTGGTAGCCATTGTGGGCTT
13> I G S T E G H L V T N Q E A L K I L S A I T Q P V V V V A I V G L

BsrGI (771)
701 TATCGCACAGGCAATCCTACCTGATGAACAAGCTGGCTGGGAAGGAGAAGGGCTTTCTGTTGGATCCACTGTACAGTCTCACACCAAGGGGATCTGGA
47> Y R T G K S Y L M N K L A G K E K G F S V G S T V Q S H T K G I W

BamHI (763)
801 TGTGGTGTGTGCCTACCCCCAAAAGCCAGACCACACTTTGGTTCTGCTTGCACCTGAAGGCTGGGAGATGTGGAGAAGGATGATAAAAAGAAATGATAC
80> M W C V P H P Q K P D H T L V L D T E G L G D V E K D D K N D T

StuI (858)
BglII (902) **Bst1107I (940)** **DraIII (988)**
901 TCAGATCTTGCAGTACCACTCCTCCTCAGTACACCTTTGTATAACAACACTATGAACAAAATTGACCAGGGGCTATCGACCTATTGCACAATGTGACA
113> Q I F A L A I L L S S T F V Y N T M N K I D Q G A I D L L H N V T

BspEI (1016) **BsaBI (1036)** **XcmI (1084)**
1001 GAACTGACAGACTTGCTCCGACAAAGAACTCCTGATTCTAATCAAAGTGAAGGGTGGGACCTGCTGACATGAGCTTCTTCCAGACTTGGTGTGGA
147> E L T D L L R T R N S S D S N Q T E G E G P A D M S F F P D L V W

SphI (1137) **BsaBI (1153)**
1101 CTCTGAGAGATTTCTTCTGGACCTGCAAGCCAATGGGCATGCCATCACATCAGATGAATATCTGGAGAATTCACTGAAGCTGAAGCAAGGTAGCGATGA
180> T L R D F F L D L Q A N G H A I T S D E Y L E N S L K L K Q G S D E

SacII (1222) **XmnI (1239)** **HindIII (1294)**
1201 AAGAACTCAAACATTCACTACCGCGGCTGTGCATACAGAAGTTCTTCCAGTAAAGAAATGCTTTGTTTTGACGCTCCTGCGCTTGAAGTAAAGCTT
213> R T Q T F N L P R L C I Q K F F P V K K C F V F D A P A L G S K L

1301 TCCAGCTTCAAACACTCAGCAACGAGGAGCTGAAGTCTAGATTTTGTGCAAGGACCTTTCAGAATTCTGTTACACATCTTACCCAATCTAAGACCAAGA
247> S Q L P T L S N E E L N S D F V Q D L S E F C S H I F T Q S K T K

XbaI (1434)
1401 CTCTCCAGGAGGATCCAGGTCAACGGACCTCGTCTAGAAAGCCTGGTGTGACTTATGTGCATGCCATCAACAGCGGGGCTTGCCTTCCATAGAGAA
280> T L P G G I Q V N G P R L E S L V L T Y V D A I N S G A L P S I E N

1501 CACAGTAGTAACCTTGGCCCGAGGGAGAAGTCTGCAGCTTCAAAGGCCATTGGTCACTACGATCAGTGTAGAGGAGAAGGTGCAGCTGCCACAC
313> T V V T L A R R E N S A A V Q K A I G H Y D Q L M S E K V Q L P T

1601 GAGACCCTCCAGGAGCTGCTGGACCTGCACCGACCTGTGAGCGAGAGCCATAGAAATCTTCAGGAAGCATTCTGTTCAAGGATGAGGGTGAATTTTCC
347> E T L Q E L L D L H R T C E R E A I E I F R K H S F K D E G E F F

1701 AGAAAGAATTGGAGAGCTACTAAGTGAAGCAGGATGAGATTTGTAAGAAGAAGCAGGATGCTTCTGCAGCCCTCTGCTCAACCTACTTGGGAGTAT
380> Q K E L E S L K A K Q D E I C K K N A D A S A A L C S T L L G S I

1801 TTTAAGCCTCTGGAACAAGAAGTGGCGCAGGATTTCTATCATAAAACAGGAGCCACAAGCTTCTTCTCAGAGGATGGAACAGCTGAAGGCAAATTAC
413> F K P L E Q E V A Q E F Y H K P G G H K L F L Q R M E Q L K A N Y

1901 CGTCAGCAGCCAGGAAAGGAAACACAGGCTGAGGAAAGTCTGACAGACCTATTTGAACGCCAAAGAAACAGTGAAGCGTACAATTCTACAAACAGACCAGG
447> R Q Q P G K G T Q A E E V L Q T Y L N A K E T V S R T I L Q T D Q

BstAPI (2044)
2001 TTCTCACAGACAAGGAGATCCAGAGTAAAGCGGAACAAGAAAGAGCAGAGGCTGCCGCGCTCGAAGCACAGAGGTTGGAGGCTATTCCGATCCAGGAAGA
480> V L T D K E I Q S K A E Q E R A E A A R L E A Q R L E A I R I Q E E

BstAPI (2164) **BamHI (2189)**
2101 GCAAAGGAAAGCAGAGATGGAGAGACAGCATCAAGAGCAATTGAGGCAATAGCATTGGAGAAGGCAAGGTTGCACAAGAGCAACAGTGGATCCTGAAG
513> Q R K A E M E R Q H Q E Q L R Q I A L E K A R V A Q E Q Q W I L K

2201 CAGAGAGCCAGGAAAGGCTGATAGAATCAAGGCAGAGCAGGAAAGCTCAACTCAGAGCACTTCAACAGCAGCTCCAACACATGAGGAAATGAACACC
547> Q R A Q E E A D R I K A E Q E A Q L R A L Q Q Q L Q H M R E M N H

MscI (2356)
2301 ACCGTAGACATCATCATGACTGTGTTATAAGCTAATACGCCAAAACCTGAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGCAAACCC
580> H R R H H H D C V I S •

BspHI (2313) **NheI (2350)**
2401 AACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAGTTAACAAACAAC **HpaI (2488)**

2501 AATTGCATTCATTTTATGTTTCAGGTTCCAGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTTCTAAAATACAG

2601 CATAGCAAACCTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTCATTAG
2701 CTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCAAGGTTTGAAGTCTCTTCATTTCTTTATGTTTTAAATGCACTGAC

SspI (2823) **SwaI (2837)**
2801 CTCCCACATTCCTTTTTAGTAAATATTCAGAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAG
2901 GCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTC
141 • N **SacI (3098)**

3001 CTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGA
138 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 C D P A Y D S I L
BstXI (3127)
3101 GCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTG
105 E 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
StuI (3262)
3201 CCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTC
72 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 V A S I I E G T
3301 TTGGTCTGATGGCCGCCCGACATGGTCTTGTGTCTCATAGAGCATGGTATCTTCTCAGTGGCAGCTCCACCAGCTCCAGATCTGCTGAGAGA
38 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 V L E L D Q Q S I
BbsI (3408)
3401 TGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTC
5 N F T K M **XmnI (3404)** **AseI (3470)**

SacI (3527)
3501 TCCAGCTTATCTGACGGTTCATAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACG

SpeI (3625)
3601 ACATTTTGAAAGTCCCCTGTTGATTTACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCA

SnaBI (3753)
3701 CGCCATTGATGACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTCATGACT

NdeI (3858)
3801 GGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGACTGCCAAGTGGGCAGTTTACCG
3901 TAAATACTCCACCATTGACGTCAATGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGGGGGGTCTTGGGGCGT

PacI (4044) **SdaI (4036)** **BspLU11I (4054)**
4001 CAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCCTGCAGGTTAAATAAGAACATGTGAGCAAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGC
4101 CGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGA
4201 TACCAGGCGTTTTCCCTGGAAGTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCTTCGGGAAGCGTGG

ApaLI (4368)
4301 CGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCCGTTCCAGCCGACCGCTG
4401 CGCCTTATCCGGTAACTATCGTCTTGTGCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTAT
4501 GTAGCGGGTCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCCTCTGCTGAAGCCAGTTACCTTCG
4601 GAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATC
4701 TCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTTCATGGCTAGTTAATTAACATTTAAA
PacI (4784) SwaI (4793)

EagI (4804) **NotI (4803)**
4801 TCAGCGGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAA
4901 ACAAAAACAACTAGCAAAATAGGCTGTCCCAAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA