



PvuI (7)  
SgfI (6) EcoNI (96)  
1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

HindIII (245) Bsu36I (291)  
Psp1406I (203) PvuII (239) EcoNI (287)  
201 GTGAACGTTCTTTTTCGCAACGGGTTTCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACCGCCGCCCGCCCTACCTGAGGCC  
301 GCCATCCACGCGGTTGAGTGCCTTCTGCCGCTCCCGCCTGTGGTGCCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)  
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

NcoI (560)  
BstEII (555)  
AgeI (552)  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCCCTACCTGAGATCACCGGTCCACCATGGCTGAAGACAGTGGCAAAAAAAAAAGGCCTAAGAA  
601 TTTTGAAGCCATGTTCAAAGGTATCCTTTCAGAGTGGATTGGATAACTTCGTGATAAACACCATGCTAAAGAACAACGTGGCTGGACAAACATCTATCCAG  
13▶ F E A M F K G I L Q S G L D N F V I N H M L K N N V A G Q T S I Q  
1▶ M A E D S G K K K R R K N

SalI (726)  
701 ACCCTAGTACCTAATACGGATCAAAAGTCGACCAAGTGTAAAAAAGACAACCAAAAAAAAAACAGTTAAGATGTTGGAATACCTGGGCAAAGATGTTCT  
47▶ T L V P N T D Q K S T S V K K D N H K K K T V K M L E Y L G K D V

EcoO109I (893)  
801 TTCATGGTGTTTTAAATTTTGGCAAAACACGATGTTCTGACATTGAAGGAAGAGGAAAAGAAAAAATATTATGATACAAAATTTGAAGACAAGGCCCT  
80▶ L H G V F N Y L A K H D V L T L K E E E K K K Y Y D T K I E D K A L  
901 GATCTTGGTAGACTCTTTGCGAAAGAATCGCGTGGCTCATCAATGTTTACCCAAACACTTCTCAATATGGACCAAAAGATCACCAGTGTAAACCTCTT  
113▶ I L V D S L R K N R V A H Q M F T Q T L L N M D Q K I T S V K P L

EcoRI (1069) BspHI (1095)  
1001 CTGCAAAATCGAGGCTGGACCACCTGAGTCAGCAGAATCTACAAATATACTCAAACCTTTGCTCCTGTAAGAATTCCTGAGACTGTGTAAAAAAAAAATCATG  
147▶ L Q I E A G P P E S A E S T N I L K L C P R E E F L R L C K K N H

BglIII (1103) NdeI (1152)  
1101 ATGAGATCTATCCAATAAAAAAGAGAGAGACCGCAGACGCCTGGCTCTCATCATGCAATACAAAGATTTGATCACCTGCCTGCAAGGAATGGGGCTCA  
180▶ D E I Y P I K K R E D R R R L A L I I C N T K F D H L P A R N G A H

BstXI (1274)  
1201 CTATGACATCGTGGGGATGAAAAGGCTGTTCAAGGCCTGGGCTACACTGTGGTTGACGAAAAGAAATCTCACAGCCAGGGATATGGAGTCAGTGTGAGG  
213▶ Y D I V G M K R L L Q G L G Y T V V D E K N L T A R D M E S V L R

BstAPI (1300) FspI (1389)  
1301 GCATTTGCTGCCAGACCAGAGCACAAGTCTCTGACAGCAGTTCCTGGTACTCATGTCTCATGGCATCTAGAGGGAATCTGCGGAATGCGCATAAAA  
247▶ A F A A R P E H K S S D S T F L V L M S H G I L E G I C G T A H K  
1401 AGAAAAAACCGGATGTGCTGTTTATGACACCATCTCCAGATATTCAACAACCGCAACTGCCTCAGTCTAAAGGACAAACCAAGGTATCATTGTCCA  
280▶ K K K P D V L L Y D T I F Q I F N N R N C L S L K D K P K V I I V Q

PstI (1503)  
1501 GGCCTGCAGAGGTGAAAAACATGGGGAACCTCTGGGTCAGAGACTCTCCAGCATCCTTGGCACTCATCTCTTACAGTCATCTGAGAACCTGGAGGCAGAT  
313▶ A C R G E K H G E L W V R D S P A S L A L I S S Q S S E N L E A D  
1601 TCTGTTTCAAGATCCACGAGGAGAAAGACTTCATTGCTTTCTGTTTCAACACCACATAACGTGCTCTGGAGAGACCGCACAAGGGGCTCCATCTTCA  
347▶ S V C K I H E E K D F I A F C S S T P H N V S W R D R T R G S I F  
1701 TTACGGAACCTCATCACATGCTTCCAGAAATATTCTTGTGCTGCCACCTAATGAAATATTTGCGAAGGTACAGAAATCATTGAAAGTCCACAGGCTAA  
380▶ I T E L I T C F Q K Y S C C C H L M E I F R K V Q K S F E V P Q A K

MscI (1881) NheI (1875)  
1801 AGCCAGATGCCACCATAGAACGAGCAACCTTGACAAGAGATTTCTACCTCTTCTGGCAATTGAAAATGAAAAGCTAGCTGGCCAGACATGATAAGAT  
413▶ A Q M P T I E R A T L T R D F Y L F P G N •  
1901 ACATTGATGAGTTTGACAAACCAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAG

HpaI (2013)  
2001 CTGCAATAAAACAGTTAAACAACAACAAATTCATTCTATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAACCTCTACAAA

EcoRI (2109)  
2101 TGTGGTATGGAATTCTAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATC

SapI (2291)  
2201 AGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAAGATATAGTGTATTTTCCCAAGGTTTGAAC TAGCTTTCAT

Swal (2362)  
2301 TTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTT

EcoO109I (2423)  
2401 ATTAGGCAGAATCCAGATGCTCAAGGCCCTTATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAATTTGGACAGCAA

2501 GAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAG  
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

2601 CAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGTGCCTGACAG  
 113 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 A  
 2701 CCACAATGGTGTCAAAGTCCTTCTGCCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTG  
 80 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  
 2801 GACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGTGTTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCC  
 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

SacI (2623) BstXI (2652)

2901 ACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCTATAGTGAGTCTATTATACTATGCCGATATACTATGCCGATGATTA  
 13 V L E L D Q Q S I N F T K M

AseI (2995)

3001 TTGTCAAACAGCGTGGATGGCGTCTCCAGCTIATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCATT  
 T T G T C A A A C A G C G T G G A T G G C G T C T C C A G C T I A T C T G A C G G T C A C T A A A C G A G C T C T G C T T A T A T A G A C C T C C C A C C G T A C A C G C C T A C C G C C A T T T

SacI (3052)

3101 GCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAAA  
 G C G T C A A T G G G G C G G A G T T G T T A C G A C A T T T T G A A A G T C C C G T T G A T T T A C T A G T C A A A A C A A A C T C C A T T G A C G T C A A T G G G G T G G A G A C T T G G A A A

SpeI (3150)

3201 TCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTA  
 T C C C C G T G A G T C A A A C C G T A T C C A C G C C A T T G A T G T A C T G C C A A A A C C G C A T C A T C A T G G T A A T A G C G A T G A C T A A T A C G T A G A T G T A C T G C C A A G T A

SnaBI (3278)

3301 GGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGAT  
 G G A A A G T C C C A T A A G G T C A T G T A C T G G G C A T A A T G C C A G G C G G G C C A T T T A C C G T C A T T G A C G T C A A T A G G G G G C G T A C T T G G C A T A T G A T A C A C T T G A T

NdeI (3383)

3401 GTACTGCCAAGTGGGCGAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGT  
 G T A C T G C C A A G T G G G C A G T T T A C C G T A A A T A C T C C A C C A T T G A C G T C A A T G G A A A G T C C C T A T T G G C G T T A C T A T G G G A A C A T A C G T C A A T T A T T G A C G T

PacI (3569)

3501 CAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATAAGAACATGTGAGCAAAAGGCCAGC  
 C A A T G G G C G G G G T C G T T G G G C G G T C A G C C A G G C G G G C C A T T T A C C G T A A G T T A T G T A A C G C T G C A G G T T A A T A A G A A C A T G T G A G C A A A A G G C C A G C

PstI (3562) SdaI (3561) BspLU11I (3579)

3601 AAAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTTCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTG  
 A A A A G G C C A G G A A C C G T A A A A A G C C G G T T G C T G G C G T T T T T C A T A G G C T C C G C C C C T G A C G A G C A T C A C A A A A T C G A C G C T C A A G T C A G A G G T G

3701 GCGAAACCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCC  
 G C G A A A C C G A C A G G A C T A T A A A G A T A C C A G G C G T T T C C C C T G G A A G C T C C C T C G T G C G C T C T C T G T T C C G A C C T G C C G T T A C C G G A T A C C T G T C C

ApaLI (3893)

3801 GCCTTTCTCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCAG  
 G C C T T T C T C C T T C G G G A A G C G T G G C G C T T T C T C A T A G C T C A C G C T G T A G G T A T C T C A G T T C G G T G T A G G T C G T T C G C T C C A A G C T G G G C T G T G T G C A G

3901 AACCCCCGTTGAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGG  
 A A C C C C C G T T G A G C C C G A C C G C T G C G C C T T A T C C G G T A A C T A T C G T C T T G A G T C C A A C C C G T A A G A C A C G A C T T A T C G C C A C T G G C A G C A G C C A C T G G

4001 TAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGC  
 T A A C A G G A T T A G C A G A G C G A G G T A T G T A G G C G G T G C T A C A G A G T C T T G A A G T G G T G G C C T A A C T A C G G C T A C A C T A G A A G A A C A G T A T T T G G T A T C T G C

4101 GCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGC  
 G C T C T G C T G A A G C C A G T T A C C T T C G A A A A A G A G T T G G T A G C T C T T G A T C C G G C A A A C A A A C C A C C G C T G G T A G C G G T G G T T T T T T G T T T G C A A G C A G C

4201 AGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGT  
 A G A T T A C G C G C A G A A A A A A G G A T C T C A A G A A G A T C C T T T G A T C T T T T C T A C G G G T C T G A C G C T C A G T G A A C G A A A A C C T A C G T T A A G G G A T T T T G G T

EagI (4329)

4301 CATGGCTAGTTAATTAACATTTAAATC AGCGGCCCAATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACAT  
 C A T G G C T A G T T A A T T A A C A T T T A A A T C A G C G G C C A A T A A A A T A T C T T T A T T T T C A T T A C A T C T G T G T G T T G G T T T T T T G T G T G A A T C G T A A C T A A C A T

PacI (4309) SmaI (4318) NotI (4328)

4401 ACGCTCTCCATCAAACAAAACGAAACAAAACAAACTAGCAAATAGGCTGTCCCCAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA  
 A C G C T C T C C A T C A A A C A A A A C G A A A C A A A A C A A A C T A G C A A A T A G G C T G T C C C C A G T G A A G T G C A G G T G C C A G A A C A T T T C T C T A T C G A A