



XbaI (15) SdaI (29)

NotI (2) NsiI (14) EcoRI (19) SpeI (36)

1 **CGCGCCGCTATGCATCTAGAATTCTGCAGGGCCACTAGTCTGTAATCCCAGCATTTTGGGAGGCTGAGGCAGATGGATCACCTGAGGTCAGGAGTTCC**
101 **AGACCAGCTGGCCAACATGATGAAACCCGCTCTAGTAAAAATACAAAAATTAGCCAGGCATGGTGTATATACCTGTAGTACCAGCTACTTGGGAGA**

NcoI (239)

201 **CAGAGGTGGGAGAATTACTTGAACTGGGAGTTCAAGCCATGGGAGGTGGAAGTTGCAGTGAGCCGAGATGCCACTGCCTCCAGCCTGAGCAACAGAG**
301 **CAAGACTATCTCAAGAAAAAAGAAAGAAAGAAAGGGACTTGCCAAGGTCATGTATCAGGGCAAGGAAGCTGGGGCCAGCTGGTCTCCCTGC**
401 **TGAGCTGGGAGACCCTTGATCTGACTTCTCCATCTTCCAGCCTAAGCCAGGCCCTGGGTACGGAGGCTGGGAGGCACCGAGAACCGCCCTGC**

Acc65I (586)

501 **CATGTGCTGACAGGGAATTTTATGCTCCAGCTGGCCAGCTGGGAGGAGCCTGTGGCAGAGGCCAGAGCTGGGGCTCTGGAAGGTACTTGGGGAGG**

AvrII (680)

601 **TTGACTGTGAGAATGAGCTCAAGCTGGTGCAGAGAGCAGGGCTGACTCTGCCAGTGCCTGCATCAGCCTCATCGCTCTCTAGGCTCTGGCCTGTCTGG**
701 **ACTCTGGGCTGCAGGCTCTTCTTGAAGGCTGTGAGTAGTGAGACAAGGAGCAGGAGTGAGGGGTGGCAGGAGAGAAGATAGAGATTGAGAGAGAGAGAG**
801 **AGAGAGACAGAGAGAGAGAGAGACAGACAGACAAAAGGAGAGAGAAGCGCTTAGACAAGGAGAGAAAGATGGAAGATAAAGAGACTGGGCGCAGTGGCT**
901 **CACGCTGTAATCCCAACTTGGGAGGCAAGGTGGGAGGATGGCTGAAGGAAAGAGTCTGAGATCAACTGGCCAACATAGTGAGACCCGCTCTCT**
1001 **AAAAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGTTTTTTTTAAAGAGACAGAGAAAGAGACTCAGAGATTGAGACTGAGAGCAAGACAGAGAGA**
1101 **GACACTCACAGGGAAGGGGAGAGGAAAACGAGAAAGGGAGGAGAGTAACGGAAGAGATAAAAAAGAAAAGCAGGTGGCAGAGACACAGAGAGAGGG**

BspHI (1271)

1201 **ACCCAGAGAAAGCCAGACAGACGCGAGGTGGCTGGCAGCGGGCGCTGTGGGGTACAGTAGGGGACTGc** **M I L G P C M L L**
1301 **TGCTGCTGCTGCTGGCCTGAGGCTACAGCTCTCCCTGGGCATCATCCAGTTGAGGAGGAGAACCAGGACTTCTGGAACCGCAGGAGCCGAGGCGCCT**
10 **L L L L L G L R L Q L S L G I I P V E E E N P D F W N R E A A E A L**

BamH I (1499)

1401 **GGTGCCGCCAAGAAGCTGCAGCTGCACAGACAGCCGCAAGAACCTCATCATCTTCTGGGCGATGGGATGGGGTGTCTACGGTGACAGCTGCCAGG**
43 **G A A K K L Q P A Q T A A K N L I I F L G D G M G V S T V T A A R**
1501 **ATCCTAAAAGGGCAGAGAAGGACAAACTGGGCGCTGAGATACCCCTGGCTATGGACCGCTTCCCATATGTGGCTCTGTCCAAGACATACAATGATAGACA**
77 **I L K G Q K K D K L G P E I P L A M D R F P Y V A L S K T Y N V D**
1601 **AACATGTCCAGACAGTGGAGCCACAGCCACGGCCTACCTGTGCGGGTCAAGGGCAACTTCCAGACCATTGGCTTGTAGTGCAGCCGCCCTTTAAACA**
110 **K H V P D S G A T A T A Y L C G V K G N F Q T I G L S A A A R F N Q**
1701 **GTGCAACACGACACGGCCAGGAGTTCCTCGTGATGAATCGGGCAAGAAAGCAGGGAAGTCAAGTGGGAGTGGTAACCACCACACGAGTGCAGCAC**
143 **C N T R G N E I S V M N R A K K A G K S V G V V T T T R V Q H**
1801 **GCCTGCCAGCCGACCTACGCCACACGGTGAACCGCACTGGTACTCGGACGCCGACGTGCCTGCCTCGGCCGCCAGGAGGGTGGCAGGACATCG**
177 **A S P A G T Y A H T V N R N W Y S D A D V P A S A R Q E G C Q D I**
1901 **CTACGAGCTCATCTCCAACATGGACATTGATGTGATCTGGGTGGAGGCCGAAAGTACATGTTTCGATGGGAACCCAGACCCTGAGTACCAGATGA**
210 **A T Q L I S N M D I D V I L G G G R K Y M F R M G T P D P E Y P D D**
2001 **CTACAGCAAGTGGACACAGGCTGGACGGGAAGAATCTGTGACAGGAATGGCTGGCAGGAGCCAGGCTGCCCGTATGTGTGGAAACCCGACTGAGCTC**
243 **Y S Q G G T R L D G K N L V Q E W L A K R Q G A R Y V W N R T E L**
2101 **ATGCAGGCTTCCCTGGACCCGCTGTGACCCATCTCATGGTCTCTTTGAGCCTGGAGACATGAAATACGAGATCCACGAGACTCCACTGGACCCCT**
277 **M Q A S L D P S V T H L M G L F E P G D M K Y E I H R D S T L D P**
2201 **CCCTGATGGAGATGACAGAGGCTGCCCTGCCCTGCTGAGCAGAACCCCGCGGCTTCTCTCTCGTGGAGGGTGGTGCATCGACACGGTGCATCA**
310 **S L M E M T E A A L R L L S R N P R G F F L F V E G G R I D H G H H**
2301 **CGAAAGCAGGGCTTACCGGCACTGACTGAGACGATCATGTTGACGACGCCATTGAGAGGGCGGGCCAGCTCACCAGCGAGGAGACACGCTGAGCCTC**
343 **E S R A Y R A L T E T I M F D D A I E R A G Q L T S E E D T L S L**

BbsI (2427)

2401 **GTCAGTCCGACACTCCACGCTTCTCCTCGGAGGCTACCCCTGCGAGGGAGCTCCATCTTGGGCTGGCCCTGGCAAGGCCCGGACAGGAAAGG**
377 **V T A D H S H V F S F G G Y P L R G S S I F G L A P G K A R D R K**
2501 **CCTACACGGTCTCTATACGAAACGGTCCAGGCTATGTGCTCAAGGACGGCCCGGCGGATGTTACCGAGAGCGAGAGCGGGAGCCCGAGTATCG**
410 **A Y T V L L Y G N G P G Y V L K D G A R P D V T E S E S G S P E Y R**
2601 **GCAGCAGTGCAGCTGCCCTGGACGAAGAGACCCACGAGGCGAGGAGCTGGCGGTGTTGCGCGCGGCCCGCAGGCGCACCTGGTTCACGGCGTGCAG**
443 **Q Q S A V P L D E E T H A G E D V A V F A R G P Q A H L V H G V Q**
2701 **GAGCAGACCTTATAGCGACGCTATGGCCTCGCCGCTGCTGGAGCCCTACACCGCTGCGACCTGGCGCCCGCCCGCCGACACCGACGCGCGC**
477 **E Q T F I A H V M A F A A C L E P Y T A C D L A P P A G T T D A A**

NheI (2837)

2801 **ACCCGGGGCGGTCCCGTCCAAGCGTCTGGATTGAAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAACCACAACCTAGAATGCAGT**
510 **H P G R S R S K R L D •**
2901 **GAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAAACAAGTTAACACAACAATTGATTATT**

3001 **TATGTTTCAGGTTACAGGGGAGGTGTGGGAGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTAATTCTAAAATACAGCATAGAAAA**

3101 **CTTAAACCTCCAATCAAGCCTCTACTTGAATCCTTTCTGAGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTTCAG**
3201 **CCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGGTTTGAACCTAGCTCTTCAATTTCTTTATGTTTTAAATGCACTGACCTCCCACT**

SspI (3316)

3301 **CCCTTTTATGAAAAATATTGAGAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTATA**
3401 **ATATCCCCAGTTTGTAGTTGGACTTAGGGAACAAAGGAACCTTAAATAGAAATTGGACAGCAAGAAAGCAGGCTTCTAGCTTATCTCAGTCTGCTC**

3501 CTCTGCCACAAAGTGCACGCAGTTGCCGGCCGGTTCGCGCAGGGCGAACTCCCGCCCCACGGCTGCTCGCCGATCTCGGTTCATGGCCGGCCCGAGGCG
121 E A V F H V C N G A P D R L A F E R G W P Q E G I E T M A P G S A
3601 TCCCGGAAGTTCGTGGACACGACCTCCGACCACTCGGCGTACAGCTCGTCCAGGCCGCGCACCCACCCAGGCCAGGGTGTGTCCGGCACCACCTGGT
87 D R F N T S V V E S W E A Y L E D L G R V W V W A L T N D P V V Q D

SgrAI (3744)

3701 CCTGGACCGCGCTGATGAACAGGGTCACGTCGTCCCGGACCACCCGGCGAAGTCGTCTCCACGAAGTCCCGGAGAACCAGCCGGTCCGGTCCAGAA
54 Q V A S I F L T V D D R V V G A F D D E V F D R S F G L R D T W F
3801 CTCGACCGCTCCGGCGACGTCGCGCGCGGTGAGCACCGGAACGGCACTGGTCAACTTGGCCATGATGGCTCCTCCTGTCAGGAGAGGAAAGAGAAGAAGG
21 E V A G A V D R A T L V P V A S T L K A M
3901 TTAGTACAATTGCTATAGTGAGTTGTATTATACTATGCAGATATACTATGCCAATGATTAATTGTCAAACTAGGGCTGCAGGTTAATTAAGAACATGTGA
4001 GCAAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCT
4101 CAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGGCTCTCCTGTTCCGACCCTGCCGTTAC
4201 CGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTG
4301 GGCTGTGTGCACGAACCCCCGTTAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGG
4401 CAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGT
4501 ATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCACCGCTGGTAGCGGTGTTTTTTT
4601 GTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACACGCTT
4701 AAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCA