



**XbaI (15) SdaI (29)**

**NotI (2) NsiI (14) EcoRI (19)**

1 GCGGCCGCTATGCACTAGAAATTCCTGACGGGCCACTAGTGGAGCCGAGAGTAATTCATACAAAAGGAGGGATCGCCTTCGCAAGGGGAGAGCCAGGG  
101 ACCGTCCTCTAAATTTCTCACAGACCCAAATCCCTGTAGCCGCCACGACAGCGAGGAGCATGCGCTCAGGGCTGAGCGCGGGGAGAGCAGAGCACACA  
201 AGCTCATAGACCTGGTCTGGGGGGGAGGACCGGGGAGCTGGCGCGGGGCAAACCTGGGAAAGCGGTGTCGTGTGCTGGCTCCGCCCTCTTCCGAGGGGT  
301 GGGGAGAACCGTATATAAGTGCAGCAGTCCGCTTGGACGTTCTTTTTTCGCAACGGGTTTGGCGTCAGAACGCAGGTGAGGGGGCGGTGTGGCTTCCGGC  
401 GGCCGCGAGCTGGAGTCTGCTCCGAGCGGGCCGGCCCGCTGTCGTGCGCGGGGATTAGCTGCGAGCATTCGCCCTTCGAGTTGCGGGCGGCGCGG  
501 GAGGAGAGTGCAGGCTTAGCGGCAACCCCGTAGCCTCGCCTCGTGTCCGGCTTGGGCTAGCGTGGTGTCCGCGCCGCGCGGTGCTACTCCGGC  
601 CGCACTCTGGTCTTTTTTTTTTTTGTGTGTGTGTCCTGCTGCCTTCGATTGCGGTTCCAGCAATAGGGGCTAACAAAGGGAGGGTGCGGGGCTGTGCTCGC  
701 CCGGAGCCCGGAGAGGTTCATGTTGGGGAGGAATGGAGGGACAGGATGCGCGCTGGGGCCCGCCGCTTCGGAGCACATGTCGACGCCACCTGGATG  
801 GGGGAGGCTGGGGTTTTTCCCGAAGCAACAGGCTGGGGTTAGCGTGGCGAGGCCATGTGCCCCAGCACCCGGCACGATCTGGCTTGGCGGCGCCGC  
901 GTTCCCTGCTCTCCCTAAGTGGGTGAGGCCATCCCGTCCGGCACCGTGTGCGTGGAAAGATGGCCGCTCCCGGGCCCTGTTGCAAGGAGCTCAAA  
1001 ATGGAGGACGCGCGCAGCCCGTGGAGCGGGCGGGTGAATCACCACACAAAGGAAGAGGGCCTGGTCCCTCACCGGCTGCTGCTTCCTGTGACCCCGTGG  
1101 TCCTATCGGCCGCAATAGTCACTCGGGCTTTTGTAGCACGGCTAGTCCGCGGGGGGAGGGATGTAATGCGGTTGGAGTTTGTTCACATTTGGTGGGT  
1201 GGAGACTAGTCAGGCCAGCTGGCGCTGGAAGTCATTTTTGGAATTTGTCCCTTGTAGTTTTGAGCGGAGCTAATTTCTCGGGCTTCTTAGCGTTCAAAG

**BspHI (1356)**

1301 GTATCTTTTAAACCCTTTTTAGGTGTGTGAAAACCCCGTAATTCAAAGCAATCATGATTTCTGGGGCCCTGCATGCTGCTGCTGCTGCTGCTGG  
1401 GCCTGAGGCTACAGCTCTCCCTGGGCATCATCCAGTTGAGGAGGAGAAACCGGACTTCTGGAACCGGAGGACGCGAGGCGCTGGGTGCCCAAGAA  
15 ▶ 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 G A A K K

**BamHI (1584)**

1501 GCTGCAGCCTGCACAGACAGCCGCAAGAACCTCATCATCTTCTGGGCGATGGGATGGGGGTGCTACGGTGACAGCTGCCAGGATCTTAAAGGGCAG  
48 ▶ 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 I L K G Q  
1601 AAGAAGGACAACTGGGGCTGAGATACCCCTGGCTATGGACCGCTTCCCATATGTGGCTCTGTCCAAGACATACAATGTAGACAAACATGTGCCAGACA  
82 ▶ 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 K H V P D  
1701 GTGGAGCCACAGCCACGGCTACCTGTGCGGGTCAAGGGCAAATCCAGACCATTTGGCTTGAGTGCAGCCGCGCTTTAACAGTGCACACAGACAG  
115 ▶ 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 C N T T R  
1801 CGGCAACAGGTCATCTCCGTGATGAATCGGGCAAGAAAGCAGGGAAGTCACTGGGAGTGGTAACCACACAGATGCAGCACGCTCGCCAGCCGGC  
148 ▶ G N E V I S V M N R A K K A G S V G V V T T T R V Q H A S P A G  
1901 ACCTACGCCACACCGGTGAACCGCACTGGTCTGGACCGGACGTGCTGCTCGGCCGCCAGGAGGGTGCAGGACATCGCTACGCACTCATCT  
182 ▶ 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 A T Q L I  
2001 CCAACATGGACATTTGATGTGATCCTGGGTGGAGGCGAAAGTACATGTTTTGCGATGGGAACCCAGACCTGAGTACCCAGATGACTACAGCCAAGGTGG  
215 ▶ 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 Y S Q G G  
2101 GACCAGGCTGGACGGGAAGAACTGGTGCAGGAATGGCTGGCGAAGCGCCAGGGTGCCTGGTATGTTGGAAACCGCACTGAGCTCATGCAGGCTTCCCTG  
248 ▶ T R L D G K N L Q E W L A K R Q G A R Y V W N R T E L M Q A S L  
2201 GACCCGTCTGTGACCCATCTCATGGTCTCTTTGAGCTGGAGACATGAAATACGAGATCCACCGAGACTCCACACTGGACCCCTCCCTGATGGAGATGA  
282 ▶ 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 S L M E M  
2301 CAGAGGCTGCCCTGCGCTGCTGAGCAGGAACCCCGGGCTTCTTCTCTTGTGGAGGGTGGTGCATCGACACCGTTCATCAGAAAGCAGGGCTTA  
315 ▶ 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 E S R A Y  
2401 CCGGGCACTGACTGAGAGCATGTTTCGACGAGCCATTGAGAGGGCGGGCCAGCTCACAGCGAGGAGACAGCTGAGCCTCGTCACTGCCGACCCAC  
348 ▶ 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 V T A D H

**BbsI (2512)**

2501 TCCCACGTCTTCTCCTTCGGAGGCTACCCCTGCGAGGGAGCTCCATCTTCGGGCTGGCCCTGGCAAGGCCCGGGACAGGAAGGCCTACACGGTCTCTCC  
382 ▶ 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 A Y T V L  
2601 TATACGGAAACCGTCCAGGCTATGTGCTCAAGGACGGCGCCCGCGGATGTTACCGAGAGCGAGAGCGGGAGCCCGAGTATCGGCAGCAGTCAGCAGT  
415 ▶ 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 Q Q S A V  
2701 GCCCCGAGCAAGAGAGACCCACGAGGGCAGGACGTGGCGGTGTTGCGCGCGGGCCCGAGGCGACCTGGTTCACGGCGTGCAGGAGCAGACCTTCATA  
448 ▶ 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 E Q T F I  
2801 GCGCAGTCATGGCCTTCGCGCCTGCTGGAGCCCTACACCGCTGCGACCTGGCGCCCCCGCGGACCAACCGAGCCCGGCAACCCGGGGCGGTCCC  
482 ▶ 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 H P G R S

**NheI (2922)**

2901 GGTCCAAGCGTCTGGATTGAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTTA  
515 ▶ R S K R L D •  
3001 TTTGTGAAATTTGTGATGCTATTTGCTTTATTTGTAACCATTTATAAGCTGCAATAAAACAAGTTAAACAACAACATTTGCATTTATTTATGTTTCAGGTTCA  
3101 GGGGGAGGTGTGGAGGTTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTAATTTCAAATACAGCATAGCAAACTTTAACCTCCAAT

3201 CAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGCTGTGCGCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTTCA  
3301 TGGAGTTTAAAGATATAGTGTATTTTCCCAAGGTTTGAAGTACTGCTTTCATTTCTTTATGTTTAAATGCAGTACCTCCACATTCCTCTTTTAGTAAAA  
3401 TATTCAGAAATAATTTAAATACATCATTTGCAATGAAAATAAATGTTTTTTATTAGGCAGAAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTA  
3501 GTAGTTGGACTTAGGGAAACAAAGAACCTTTAATAGAAATTTGACAGCAAGAAAGCGAGCTTCTAGCTTATCCCTCAGTCTGCTCTGCCACAAAGTG

**SspI (**

3601 CACGCAGTTGCCGCGGGTCCGCGCAGGGCGAACTCCGCCCCACGGCTGCTGCGGATCTCGGTTCATGGCCGCGGAGGCGTCCCGGAAGTTCGTG  
116 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 D R F N T  
3701 GACACGACCTCCGACCACTCGGCGTACAGCTCGTCCAGGCCGCGCACCCACACCCAGGCCAGGGTGTGTCCGGCACCACCTGGTCTGGACCGCGTGA  
82 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 Q V A S I  
**SgrAI (3829)**  
3801 TGAAACAGGGTCACGTCTCCCGGACCACCCGGCGAAGTCTCTCCACGAAGTCCCGGGAGAACCAGGCGGTCCGACTCGACCGCTCCGCGC  
49 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 E V A G A  
3901 GACGTCGCGCGCGGTGAGCACCGGAACGGCACTGGTCAAATGGCCATGATGGCTCCTCCTGTCAGGAGAGGAAAGAGAAGAAGGTTAGTACAATTGCTA  
16 V D R A T L V P V A S T L K A M  
4001 TAGTGAGTTGTATTATACTATGCAGATATACTATGCCAATGATTAATTGTCAAAGTAGGGCTGCAGGTTAATTAAGAACAATGTGAGCAAAGGCCAGCAA  
4101 AAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGC  
4201 GAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCTGCCGCTTACCGGATACCTGTCCGC  
4301 CTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAA  
4401 CCCCCGTTTCAGCCGACCGCTGCGCTTATCCGTAAGTATCGTCTTGGTCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTA  
4501 ACAGGATTAGCAGAGCGAGGTAAGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGC  
4601 TCTGCTGAAGCCAGTTACCTTCGGAAGAGTGGTAGCTCTTGATCCGGCAAAACAAACCACCGCTGGTAGCGGTGGTTTTTTGTTTGAAGCAGCAG  
4701 ATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCA  
4801 TGGCTAGTTAATTAACATTTAAATCA