



EcoRI (23)
NotI (2) **XbaI (19)** **SdaI (38)** **SpeI (45)**

1 GCGGCCGCGTCGACGATATCTAGAAATTCGGATCCTGCAGGGCCCACTAGTAAACCGAGGGTTGTGAGGAGAGTGAGAGGTGGACAGAGGGCACCGACGAT

101 TTAGCATCTCTTCTCTCTCGGGGTCGAGGATGAGAGACAAAAAGAAAGCTGCCAGGAAACATAAAAATTCAGAGGGCTCAGCTGCAGGGCTGAGGTCTG

BsrGI (211)

201 CAAGCATGCTGTGTACTTGTGCATGTTGTGCCCTGCACAAGGGCATCTCTGAAGGGGCTGCACTGGACCCAGGGGCAGGGGCAGAAAGGTGAGTTTAT

301 ATCAGTTCTGAGCACTGTGGCTCCATCCAGCACTCTGAGGACAGGCAGGATACAGCTGGAGGACTGAGGGCTCCCCACACCAGCTCTCTGTTCCTCTGC

401 CCAAGACCCCTGGACCTGCAGACAACAATTCAACGCCTCAGAGTCCCAGTTAAGAACTCCCTGAAGAAGCCCCAGTGGCTGCGTGGTGGATTTTTC

501 GCAAAGCTGTCTCCACTACATCCACCTGTTTGGCAGCCCTACATACTCTTTCACAGCATGAGGAAGGGAGGCTCTCACCAGACCTGGACTGAATC

601 TTCTCCAGTGGCTGCCACCTGACCTGCTCTTGTCTCCAGAACCTCTGTGGCTCCATCCTCCACAGGGTCAACTTCCAACATGGCTGCTGCACTCCA

701 GCCAAGAGGCTCTGCTCTGGGCCCTCCAGATGCCTGACCTGGTCTGTGGCTGCCCTGTCCTTCTCAGTGTCTCTTCCCGCTGGGTGAGGAATAGT

801 TCAGGACAGAGGAGCTAAGTTACAGTTCAATTCATAGGACAGGTGCCTATTTTCGCTCACGGCCAGGAATAGAGACTTCCCGGGCTCGGCCCTTCGGGGAG

AgeI (945)
SgrAI (945)

901 TTGGCAGACGGCAGAGGGGAGGCTGGCTGGCCAGGGGATGACCACCGGTGGGGTAAGCACAGACAGAGGGGAGCACAGGCTTCCCCAGAAAGACTGAGA

1001 GGCCCCCAGAGGCATCCACAGAGGACCCAGCTGTGCTGCCAAGCTGGGGCAGCCGCAAACTTAGCGGCCAGCTGACAAAAGCTGCCCTCCCCCA

1101 GGGTCCCCGGAGAGCTGGTGCCTCCCTGGGTCCCAATTTGCATGGCAGGAAGGGGCTGGTGGAGGAAGGGCGGGGAGGGACAGGCTGCAGCCGCTGC

NcoI (1269)

1201 AGTTACACGTTTCTCCAAAGGACCTCGACGTTGTACCGGGTTGGGGTCGGGGACAGAGCGGTGACCATGGTTCTGGGGCCCTGCATGCTGTGCTG

1301 CTGCTGTGCTGGCCCTGAGGCTACAGCTCTCCCTGGGCATCATCCAGTTGAGGAGGAGAAACCGGACTTCTGGAACCGCGAGGCAGCCGAGGCCTGG

11▶ 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

1401 GTGCCCGCAAGAAGCTGCAGCCTGCACAGACAGCCGCAAGAACCTCATCATCTTCTGGCGATGGGATGGGGTGTCTACGGTGACAGCTGCCAGGAT

44▶ 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 I

NdeI (1564)

1501 CCTAAAAGGGCAGAAGAAGGACAAACTGGGGCCTGAGATACCCCTGGCTATGAGACCGCTTCCCATATGTGGCTCTGTCCAAGACATACAATGTAGACAAA

77▶ 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 K

1601 CATGTGCCAGACAGTGGAGCCACAGCCACGGCCTACCTGTGCGGGTCAAGGGCAACTTCCAGACCATTTGGCTTGAGTGCAGCCGCGCCGCTTAAACAGT

111▶ 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 GCAACACGACACGCGCAACGAGGTCATCTCCGTGATGAATCGGGCCAAGAAAGCAGGGAAAGTCAAGTGGAGTGGTAAACACACAGAGTGCAGCAGCC

144▶ C N T T R G N E V I S V M N R A K K A G K S V G V V T T T R V Q H A

1801 CTGCCAGCCGACCTACGCCACACGGTGAACCGCACTGGTACTCGGACGCGGAGCTGCTGCTCGGCCCGCAGGAGGGGTGCCAGGACATCGCT

177▶ 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 A

1901 ACGCAGCTCATCTCCAACATGGACATGTATGTGATCCTGGTGGAGGCCGAAAGTACATGTTTCGCATGGGAAACCCAGACCCCTGAGTACCCAGATGACT

211▶ 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 ACAGCCAAGGTGGACAGGCTGGACGGGAAGAACTGTGGTGCAGGAATGGCTGGCGAAGCGCCAGGGTCCCGGTATGTGTGGAAACCGCACTGAGTCCAT

244▶ 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 M

2101 GCAGGCTTCCCTGGACCCGCTGTGACCCATCTCATGGTCTCTTTGAGCCTGGAGACATGAAATACGAGATCCACCGAGACTCCACACTGGACCCCTCC

277▶ 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 S

SacII (2251)

2201 CTGATGGAGATGACAGAGGCTGCCCTGCGCCTGCTGAGCAGGAAACCCCGGCTTCTTCTCTTCTGAGGGTGGTGCATCGACCAAGGTCATCAG

311▶ 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 AAAGCAGGGCTTACCGGCACTGACTGAGACGATCATGTTTCGACGACGCCAATTGAGAGGGCGGGCAGCTCACCAGCGAGGAGACAGCTGAGCCTCGT

344▶ 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 V

2401 CACTGCCGACCACTCCACAGTCTTCTCCTTCCGAGGCTACCCCTGCGAGGGAGCTCCATCTTCCGGCTGGCCCTGGCAAGGCCCGGGACAGGAAGGCC

377▶ 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 A

2501 TACACGTCCTCTATACGGAACCGTCCAGGCTATGTGCTCAAGGACGCGCGCCCGGATGTTACCGAGAGCGAGAGCGGGAGCCCGAGTATCGGC

411▶ Y T V L 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 AGCAGTCAGCAGTCCCTGGACCAAGAGACCCACGCAGGCGAGGACGTGGCGGTGTTTCGCGCGCGCCCGCAGGCGCACCTGGTTACAGGCGTGCAGGA

444▶ 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 E

2701 GCAGACCTTATAGCGCAGTCAATGCGCTTCCGCGCCTGCTGGAGCCCTACACCCGCTGCGACCTGGCGCCCGCCCGCCGACCAAGCGCCGCGCAC

477▶ 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 H

NheI (2835)

2801 CCGGGCGGTCCTCCGCTCAAGCTCTGGATTGAAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAAACCAACTAGAAATGCAGTGA

511▶ P G R S R S K R L D •

MfeI (2984)

2901 AAAAAATGCTTTATTTTGGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTAAGCTGCAATAAACAAAGTTAACAAACAACAATTCATTTCAITTTA

3001 TGTTTCAGGTTTCAGGGGAGGTTGGGGAGGTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTAATTCTAAAATACAGCATAGCAAAACT

3101 TTAACCTCCAATCAAGCCTCTACTTGAATCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCC

3201 TCACCTTCTTTTCAGGAGTTTAAAGATATAGTGTATTTTCCCAAGGTTTGAAGTACTGCTTCTCATTTCTTTATGTTTTAAATGCAGTCACTCCACATTTCC

3301 CTTTTTAGTAAATATTCAGAAATATTTAAATACATCATTGCAATGAAATAAATGTTTTTTATTTAGGCAGAAATCCAGATGCTCAAGGCCCTTCATAAT

3401 ATCCCCAGTTTGTAGTTGACTTAGGGAAACAAAGAACCTTTAATAGAAATTTGGACAGCAAGAAAGCGAGCTTCTAGCTTTATCTCAGTCTGCTGCTCT

3501 CTGCCACAAAGTGCACGCAGTTGCCGGCCGGGTCGCGCAGGGCGAACTCCCGCCCCACGGCTGCTCGCCGATCTCGGTCAATGGCCGGCCGGAGGCGTC
120 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 D
3601 CCGGAAGTTCGTGGACACGACCTCCGACCCTCGGCGTACAGCTCGTCCAGGCCGCGCACCCACACCCAGGCCAGGGTGTGTCCGGCACCACTGGTCC
87 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 (3742)
3701 TGGACCGCGCTGATGAACAGGGTCACGTCGTCCCGGACCACACCGCGAAGTCTCTCCACGAAAGTCCCGGGAGAACCCGAGCCGGTCCGATCCAGAACT
53 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 E
3801 CGACCGCTCCGGCGACGTCGCGCGCGGTGAGCACCGGAAACGGCACTGGTCAACTTGGCCATGATGGCTCCTCCTGTCAGGAGAGGAAAGAGAAGAGGTT
20 V A G A V D R A T L V P V A S T L K A M
MfeI (3905)
3901 AGTACAATTGCTATAGTGTGATTGTATTATACTATGCAGATATACTATGCCAATGATTAATTGTCAA ACTAGGGCTGCAGGTTAATTAAGAACATGTGAGC
4001 AAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCGTGTCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCA
4101 AGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCCCTGGAAGCTCCCTCGTGGCTCTCCTGTTCCGACCCCTGCCGTTACCG
4201 GATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCGCTCCAAGCTGGG
4301 CTGTGTGCACGAACCCCGGTTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCA
4401 GCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTAT
4501 TTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCCCGCTGGTAGCGGTGTTTTTTGT
4601 TTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAA
4701 GGGATTTTGGTCATGGCTAGTTAAITTAACAITTTAAATCA