



EcoRI (23)

NotI (2) XbaI (19) SdaI (38) SpeI (45)

1 CGGGCCGCGTCGACGATATCTAGAATTCGGATCCTGCAGGGCCACTAGTTCCAGAGCTTTCGAGGAAGGTTTCTCAACTCAAATTCATCCGCTGAT
101 AATTTTCTTATATTTTCTAAAGAAGGAAGAGAAGCGCATAGAGGAGAAGGAAATAATTTTTTAGGAGCCTTTCTTACGGCTATGAGGAATTTGGGGCT

Tth111I (271)

201 CAGTTGAAAAGCCTAAACTGCCTCTCGGGAGGTTGGGCGGGCGAACTACTTTCAGCGGCGCACGGAGACGGCGTCTACGTGAGGGGTGATAAGTGACGC
301 AACACTCGTTGCATAAATTTGCGCTCCGCCAGCCCGAGCATTAGGGGCGGTTGGCTTTGTTGGGTGAGCTTGTGTGTCCCTGTGGGTGACGTGGT
401 TGGTGATTGGCAGGATCCTGGTATCCGCTAACAGtactggcccacagccgtaaaagacctgcggggcgtagaggggggaatgggtgaggtcaagctgg
501 aggccttctggggtgggtgggcccgtgaggggaggggagggcgaggtgacgcgacacccggccttctgggagagtgggccttgttgacctaaagggggg
601 cgagggcagttggcacgcgacgcgcccacagaaactaacagacattaaccaacagcgattccgctcgcgtttacttgggaggaaggcggaaaagaggtag

NruI (786)

701 tttgtgtggcttctgaaacccctaatttgaatcccagtatgagaatggtgtcccttctgtgtttcaatgggatttttacttctcgagtcctgtgggt

BspEI (877)

801 ttggttttgtttcagtttgctaacaccgtgcttaggtttgaggcagattggagttcggtcggggagtttgaatatccggaacagtttagtgggaaag
901 ctgtggacgcttgtaagagagcgctctggattttccgctgttgacgttgaaccttgaatgacgaatttcgtattaagtgacttagccttgtaaaattg
1001 aggggaggttgcggaatattaacgtatattaaggcattttgaaggaatagttgctaattttgaagaatattaggtgtaaaagcaagaatacaatgatcc

NeoI (1140)

SphI (1162)

1101 tgaggtgacacgcttatgttttacttttaactagGTCACCATGGTTCTGGGGCCCTGCATGCTGCTGCTGCTGCTGGCCTGAGGCTACAGCT
1201 CTCCTGGGCATCATCCCAGTTGAGGAGGAGAACCCGACTTCTGGAACCGCAGGACCGAGGCCCTGGGTGCCCAAGAAGCTGCAGCCTGCACAG
201 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 L Q P A Q
1301 ACAGCCCAAGAACCTCATCTTCTGGCGATGGGTTGTCTACGGTGACAGTCCAGGATCCTAAAAGGCGAGAAGGACAACTGG
541 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 K K D K L
1401 GGCCTGAGATAACCCCTGGCTATGGACCGCTTCCATATGTGGCTCTGTCCAAGACATAAATGTAGACAAACATGTGCCAGACAGTGGGCCACAGCCAC
871 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 S G A T A T
1501 GGCCTACCTGTGCGGGTCAAGGGCAACTCCAGACCATTGGCTTGTAGTGCAGCCGCCGCTTAAACAGTGAACACGACACCGGGCAACGAGGTCATC
1201 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 R G N E V I
1601 TCCGTGATGAATCGGGCCAAAGAAAGCAGGGAAGTCACTGGGAGTGGTAACACCACACAGAGTGCAGCAGCCTCGCCAGCCGGCACCTACGCCACACGG
1541 S V M N R A K K A G K S V G V V T T T R V Q H A S P A G T Y A H T
1701 TGAACCGCAACTGGTACTCGGACCGCAGCTGCCTGCCTCGGCCCGCAGGAGGGGTGCCAGGACATCGTACGACGCTCATCTCCAACATGGACATTGA
1871 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 S N M D I D
1801 TGTGATCCTGGTGGAGCCGAAAGTACATGTTTCGCATGGGAACCCAGACCCCTGAGTACCAGATGACTACAGCAAGGTGGACCAGGCTGGACGGG
2201 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 T R L D G
1901 AAGAATCTGGTGCAGGAATGGCTGGCGAAGCGCCAGGTTGCCGGTATGTGTGGAACCGCACTGAGCTCATGCAGGCTTCCCTGGACCCGTCTGTGACC
2541 K N L V Q E W L A K R Q G A R Y V W N R T E L M Q A S L D P S V T
2001 ATCTCATGGTCTCTTTGAGCCTGGAGACATGAAATACGAGATCCACCGAGACTCCACACTGGACCCCTCCCTGATGGAGATGACAGAGGCTGCCCTGGC
2871 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 T E A A L R

SacII (2122)

2101 CCTGCTGAGCAGGAACCCCGGGCTTCTCTCTCTCGTGGAGGGTGGTGCATCGACCAGGTCATCACGAAAGCAGGGCTTACCGGGCACTGACTGAG
3201 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 R A L T E
2201 ACGTATGTTTCGACGACGCCATTGAGAGGGCGGGCCAGCTCACCAGCGAGGAGGACAGCTGAGCCTCGTCACTCGCCGACCCTCCACGTTCTTCTCT
3541 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 S H V F S
2301 TCGGAGGCTACCCCTGCGAGGGAGCTCCATCTTCCGGCTGGCCCTGGCAAGGCCGGGACAGGAAGGCCACACGGTCTCTTATACGAAACGGTCC
3871 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 L Y G N G P
2401 AGGCTATGTGCTCAAGGACGGCGCCCGCCGGATGTTACCAGAGCGAGAGCGGGAGCCCGAGTATCGGACGAGTCAAGAGTGCACAGTGCACAGTGCACAG
4201 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 P L D E E
2501 ACCACGCGAGGCGAGGACGTGGCGGTGTTCCGCGCCGGCCGAGGCGACCTGGTTCACGGCGTCAAGGACAGACCTTCAATGCGACGCTATGGCCT
4541 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 A H V M A
2601 TCGCCGCTGCTGGAGCCCTACACCGCTGCGACCTGGCGCCCGCCGGCACCACCGACGCCCGCACCAGGGGCGTCCGGTCCAGCGTCTGGA
4871 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 R S K R L D

NheI (2706)

2701 TTGAAGCTAGCTGGCAGACATGATAAGATACATTGATGAGTTTGGACAAACCAACTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGA
5201 •

MfeI (2855)

2801 TGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTACAGGGGAGGTGGGGAG
2901 GTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTAATTCTAAAATACAGCATAGCAAACTTAACTCCAATCAAGCCTCTACTTGAA

3001 TCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTCAGCCCTCACCTTCTTTCATGGAGTTTAAAGATATA
3101 GTGTATTTTCCCAAGGTTTGAACACTGCTTTCATTTTATGTTTAAATGCACTGACCTCCACATTCCCTTTTATAGTAAATATTCAGAAATAATTT
3201 AAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAAATCCAGATGCTCAAGGCCCTTCAATAATCCCCAGTTTAGTAGTTGGACTTAGGG
3301 AACAAAGGAACCTTAAATAGAAATTTGACAGCAAGAAAGCGAGCTTCTAGCTTATCCTCAGTCTGCTCCTGCCCACAAAGTGCACGAGTTGCCGGCC
1251 • D Q E E A V F H V C N G A
3401 GGGTCGCGCAGGGCGAACTCCCGCCCCACGGCTGCTCGCGATCTCGGTTCATGGCCGGCCGGAGGCGTCCCGGAAGTTCGTGGACACGACCTCCGACC
1101 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 S V V E S W
3501 ACTCGCGTACAGCTCGTCCAGGCCGCGACCCACACCCAGGCGCAGGGTGTGTCCGGCACCACCTGGTCTGACCGCGCTGATGAACAGGGTACAGTC
771 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 F L T V D

SgrAI (3613)

AatII (3689)

3601 GTCCCGGACCACACCGGCGAAGTCGTCCTCCACGAAGTCCCGGGAGAACCCGAGCCGGTCCGGTCCAGAACTCGACCGCTCCGGCGACGTCGCGCGCGGGTG
44 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 V D R A T
3701 AGCACGGAAACGGCACTGGTCAACTTGGCCATGATGGCTCCTCCTGTCAGGAGAGGAAAGAGAAGAAGGTTAGTACAATTGCTATAGTGAGTTGTATTAT
10 L V P V A S T L K A M
3801 ACTATGCAGATATACTATGCCAATGATTAATTGTCAACTAGGGCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTA
3901 AAAAGGCCGCGTTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT
4001 ATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTCTCCCTTCGGGA
4101 AGCGTGGCGCTTTTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTTCAGCCCG
4201 ACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGC
4301 GAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTT
4401 ACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGCAAGCAGCAGATTACGCGCAGAAAAA
4501 AAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGCTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAAC
4601 ATTTAAATCA