



EcoRI (23)

NotI (2) **XbaI (19)** **SdaI (38)** **Acc65I (75)**
1 CCGGCCGCGTCGACGATATCTAGAATTCCGGATCCTGCAGGGCCTGAAATAACCTCTGAAAGAGGAACCTTGGTTAGGTACCTTCTGAGGCTGAAAGAACCA
101 GCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCAGGCTCCCAGCAGGCAGAGATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGT

SpeI (275)

201 GGAAAGTCCCAGGCTCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCACAGTTCAGATGGTAAATATACAC
301 AAGGGATTTAGTCAACAATTTTTTTGGCAAGAATATTATGAATTTTGTAAATCGGTTGGCAGCCAATGAAATACAAAGATGAGTCTAGTTAATAATCTACA

NcoI (487)

401 ATTATTGGTTAAAGAAGTATATTAGTGCTAATTTCCCTCCGTTTGTCTAGCTTTTCTTCTGTCAACCCACACGCCTTTGGCACATGGTTCTGGGG
501 CCCTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGGCCTGAGGCTACAGCTCTCCCTGGGCATCATCCCAGTTGAGGAGGAGAACCCGGACTTCTGGAACCGG
5 P C M L L L L L L L L L 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
601 AGGCAGCCGAGGCCCTGGGTGCCGCAAGAAGCTGCAGCCTGCACAGACAGCCGCAAGAACCTCATCATTTCTGGCGATGGATGGGGGTGTCTAC
38 E A A E A L 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

NdeI (782)

701 GGTGACAGCTGCCAGGATCTAAAAGGGCAGAAGAAGGACAAACTGGGGCCTGAGATACCCCTGGCTATGGACCGCTTCCATATGTGGCTCTGTCCAAG
71 V T A A R 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
801 ACATACAATGTAGACAAACATGTGCCAGACAGTGGAGCCACAGCCACGGCCTACCTGTGCGGGGTCAAGGGCACTTCCAGACCATGGCTTGGATGCAG
105 T Y N V D K H V P D S G A T A T A Y L C D G V K G N F Q T I G L S A
901 CCGCCGCTTTAACCAGTGCACACGACACGCGCAACGAGGTCTATCCTGGTGAATCGGGCAAGAAAGCAGGGAAAGTCAAGTGGAGTGGTAACCAC
138 A A R F N Q 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
1001 CACACGAGTGCAGCAGCCTCGCCAGCCGACCTACGCCACACGGTGAACCGCAACTGGTACTCGGACCGCAGGTGCCCTGCCTCGGCCCGCAGGAG
171 T R V Q H 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
1101 GGGTGCAGGATCGCTACGCAGTCTCAACATGGACATTGATGTGATCCTGGGTGGAGCCGAAAGTACATGTTTCGCATGGGAACCCAGCACC
205 G C Q D I 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
1201 CTGAGTACCCAGATGACTACAGCCAAGTGGGACAGGCTGGACGGGAAGATCTGGTGCAGGAATGGCTGGCGAAGCGCCAGGTTGCCGGTATGTGTG
238 P E Y P D D 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
1301 GAACCGCACTGAGCTCATGCAGGCTTCCCTGGACCGCTGTGACCCATCTCATGGGTCTCTTTGAGCCTGGAGACATGAAATACGAGATCCACCGAGAC
271 N R T E L 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

SacII (1469)

1401 TCCCACTGGACCCCTCCCTGATGGAGATGACAGAGGCTGCCCTGCGCTGCTGAGCAGGAACCCCGGGCTTCTTCTCTTCTGAGGGGTGGTCGCA
305 S T L D P 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
1501 TCGACCAGGTCATCAGGAAAGCAGGGCTTACCGGCACTGACTGAGACGATCATGTTGACGACGCCATTGAGAGGGCCAGCTCACCAGCGAGGA
338 I D H G H H 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
1601 GGACACGCTGAGCCTCGTCACTGCCAGCACTCCACGCTTCTCTTCTTGGAGGTACCCCTGCGAGGGAGCTCCATCTTGGGCTGGCCCTGGCAAG
371 D T L S L 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
1701 GCCCGGACAGGAAGGCCTACACGGTCTCCTATACGGAACGGTCCAGGCTATGTGCTCAAGGACGGCGCCCGCCGGATGTTACCAGAGCGAGAGCG
405 A R D R K 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
1801 GGAGCCCCGAGTATCGGCAGCAGTCCAGTCCCTGGACGAAGACCCAGCAGGACGGAGGAGCTGGCGGTGTTTCGCGCCGGCCGAGCGCACCT
438 G S P E Y R 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
1901 GGTTCAGCGCTGCAGGACGACCTTTCATAGCGACGTGATGCCCTTCCCGCTGCTGGAGCCCTACCCGCTGCGACTGGCCCGCCCGCCGGC
471 V H G V Q 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

NheI (2053)

2001 ACCACCGACGCCGCGACCCGGGCGGTCCCGGTCCAAGCGTCTGGATTGAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTGGACAAAC
505 T T D A A H P G R S R S K R L D •
2101 ACAACTAGAATGCAGTGAIAAAAATGCTTTATTTGTGAAATTTGTGATGTATTGCTTTTATTGTAAACCATTATAAGCTGCAATAAACAAAGTTAAACAAC

MfeI (2202)

2201 ACAATTGCATTCAATTTATGTTTTCAGGTTCCAGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTAATTCTAAA

2301 ATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTG
2401 CATTAGCTGTTTGCAGCCTCACCTTCTTTTCATGGAGTTTAAAGATATAGTGTATTTTCCCAAGTTTGAAGTACTTCTTATTCTTTATGTTTAAATGC
2501 ACTGACCTCCACATTCCCTTTTTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTTATTAGGCAGAAATCCAGATG
2601 CTCAGGCCCTTCAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTT
2701 ATCCTCAGTCTGCTCTCTGCCCACAAAGTGCACGAGTGGCCGGCGGGTGGCGAGGGCAACTCCGCCCCACGGCTGCTCGCCGATCTCGGTCA
125 • D Q E 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
2801 GGCCGGCCGGAGGCGTCCCGGAAGTTCGTGGACACGACCTCCGACCACTCGCGCTACAGCTCGTCCAGGCCCGCACCCACCCAGGCCAGGTTGT
93 A P G S A 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

SgrAI (2960)

2901 TCCGGACCACCTGGTCTGGACCGCTGATGAACAGGTCACGTCTCCCGACACACCCGGGAAGTCTGCTCCACGAAGTCCCGGGAGAACCCGA
59 D P V V Q D 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
3001 GCCGGTCCGTCAGAACTCGACCGCTCCGGCGACGTGCGCGCGGTGAGCACCAGGCAACTGGTCAACTGGCCATGATGGCTCCTCTGTACAGGAG
26 R D T W F E V A G A V D R A T L V P V A S T L K A M

MfeI (3123)

3101 AGGAAAGAGAAGAAGTTAGTACAATTGCTATAGTGAGTTGATTATACTATGCAGATATACTATGCCAATGATTAATTGTCAAAGTGGGCTCGAGGTT
3201 AATTAAGAATGTGAGCAAAAAGCCAGCAAAAAGCCAGGAACCGTAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCAT
3301 CACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTGTCGCTCTCTGTTC
3401 CGACCCTGCGCTTACCGGATACCTGTCCGCCCTTCTCCCTTCCGGAAAGCGTGGCGCTTTTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGT
3501 CGTTCGCTCAAGCTGGGCTGTGTGCAGAACCCCGCTTACGCCGACCGCTGCGCTTATCCGGTAACATCGCTTGTAGTCCAACCCGGAAGACAC

3601 GACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCT
3701 AACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGG
3801 TAGCGGTGGTTTTTTTGTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGG
3901 AACGAAAACACGTTAAGGGATTTGGTCATGGCTAGTTAATTAACATTAAATCA