



EcoRI (23) SdaI (38)
XbaI (19) BamHI (29)

1 GCGGCCGCGTCGACGATATCTAGAATTCGGATCCTGCAGGTGAAGACGTTACACAAGTAACATGAGAAAGCAGAAAATGCAGGTCATCCACGCACCCCTG
101 ACCCAGGCCAGCAGGGCGGGCTGCAGCATCAGTACACAGGAGAAAGATCCTTATTCTAAGAATGAGAAAGCAAAGCGCCCGATAGAATAAATTAGCA
201 TAGAAGGGGCTTTCCAGGAGTTAAACTTTCTTCTGAGCGATTACCTACTAAAACCAGGGCTTTTGCCCACTACCATTACCTAGGATCTTGGCTTGC
301 ACGGATTCATAGGGGCATATCCCTCCCCCTCTTCTTAGAGTCGTTCTTAAAAGATCGCTCTCCACGCCCTAGGCAGGGAAAACGACAAAATCTGGCTCA
401 ATTCAGGCTAGAACCCTACAAATTCACAGGGATATCGAAGGATACTGGGGCATAACCCACAGGGAGTCCAAGAATGTGAGGTGGGGTGGCGAAGGT
501 AATGTCTTTGGTGTGGGAAAAGCAGCAGCCATCTGAGATAGGAACTGGAAAACCAGAGGAGAGGCGTTTCAGGAAGATTATGGAGGGGAGGACTGGCCCC
601 CACGAGCGACCAGAGTTGTCACAAGGCCGAAGAACAGGGGAGGTGGGGGCTCAGGGACAGAAAAAAGTATGTGTATTTTGGAGCAGGGTTGGAG
701 GCCTCTCTGAAAAGGTATAAAGCTGGAGTAGGCAATACCCAGGCAAAAAGGGGAGACCAGAGTAGGGGAGGGGAAGAGTCTGACCCAGGGAAGACA
801 TTA AAAAGGTAGTGGGGTCTGACTAGATGAAGGAGAGCCTTCTCTCTGGGCAAGAGCGGTGCAATGGTGTGTAAGGTAGCTGAGAAGACGAAAAGGCA
901 AGCATCTTCTGCTACCAGGCTGGGAGGCCAGGCCACGCCCCAGGAGAGGGAACGCAGGGAGACTGAGGTGACCCCTCTTTCCCCGGGGCCCGG
1001 TCGTGTGGTTCGGTGTCTTTTTCTGTTGGACCCTTACCTTGACCCAGGCGCTGCCGGGCTGGGCCGGGTGCGGCGCACGGCACTCCCGGGAGGCA
1101 GCGAGACTCGAGTTAGGCCAACCGCGCCACGGCGTTTCTTGCCGGGAATGGCCGTACCCGTGAGGTGGGGTGGGGGCAGAAAAGCGGAGCGA
1201 GCCCGAGGCGGGGAGGGGAGGGCCAGGGCGGAGGGGCGGCACTACTGTGTTGGCGGACTGGCGGACTAGGGCTGCGTGAGTCTCTGAGCGCAGGC
1301 GGGCGGCGGCCGCCCTCCCCGGCGGCGCAGCGGCGGAGCTCACTCAGCCCGCTGCCGAGCGGAAACGCCACTGACCGCACGGGGAT
1401 TCCAGTGCCGGCGCCAGGGCAGCGGACACGCCCTCCCGCCGCCATTGGCCTCTCCGCCACCGCCACACTTATTGGCCGGTGCGCCGCA
1501 ATCAGCGGAGGCTGCCGGGCGCCCTAAAGAAGAGGCTGTGCTTTGGGGCTCCGGCTCCTCAGAGAGCCTCGGCTAGttaggggatcgggactctgycgg
1601 gagggcggcttggtgctttgccccgatggcgccgccccgagcgttggtgagccgttctgtgagacagccgggtacgagtcgtgacgct
1701 ggaaggggcaagcgggtggtggcgaggaatgcggtccgccctcgaccaaccggaggggggagaggggagcggaaaagtctccaccggacgcgccat
1801 ggctcggggggggggggcagcggaggagcgttccggccgacgtctcgtcgtgattggcttctttctcccgccgtgtgtgaaaacacaattgtact

Agel (1947)

1901 aaccttcttctcttctctcctgacagGTGTGAAACAGGAAGAGAACCGGTAGGAGGGCCATCATGGAATCAAGGTGCTGTTGCCCTCATCTGTATT
2001 GCTGTTGCTGAGGCAAAACCACTGAAATCAATGAAGACCTCAATATAGTGTGCTGTCCTCAACTTTGCCACCACAGATCTTGAGACTGACCTGTTC
13▶ A V A E A K P T E I N E D L N I A A V A S N F A T T D L E T D L F
2101 CCAACTGGGAGACCATGAATGTGATTAGCACTGACACAGAGCAGGTGAACACAGATGCTGACAGGGGCAAGCTGCCTGGCAAAAACCTCCCCAGATGT
46▶ T N W E T M N V I S T D T E Q V N T D A D R G K L P G K K L P P D V
2201 CCTGAGGGAGCTGGAGGCCAATGCCAGAAGGGCTGGTGCACAAGAGGCTGCCTCATTGGCTCTCCACATTAAGTGACCCCTAAGATGAAGAAATTT
79▶ L R E L E A N A R R A G C T R G C L I C L S H I K C T P K M K K F
2301 ATCCCTGGCAGGTGCCACACTTATGAAGGTGAAAAGGAGTCTGCTCAGGGAGGGATTGGAGAGGCAATTGTTGATATCCAGAGATTCTGGCTTCAAGG
113▶ I P G R C H T Y E G E K E S A Q G G I G E A I V D I P E I P G F K
2401 ATAAGGAGCCACTGGACCAGTTTATTGCTCAAGTGACCTCTGTGCTGATTGCACCACTGGCTGTCTGAAGGGCCTTGCCAATGTCCAGTGCTCTGACCT
146▶ D K E P L D Q F I A Q V D L C A D C T T G C L K G L A N V Q C S D L
2501 CCTGAAGAAGTGGCTTCCCCAGAGGTGTACCACTTTTGCCAGCAAGATTACAGGGTAGGGTGGACAAAATCAAGGGTCTGGCTGGGACAGATGATAGCTA
179▶ L K K W L P Q R C T T F A S K I Q G R V D K I K G L A G D R •
2601 GCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGA AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGC
2701 TTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAACAAACAATTGCATTATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTTAA
2801 AGCAAGTAAAACCTCTACAAATGTGGTATGGAATTAATTCTAAAATACAGCATAGCAAACTTAACTCCAATCAAGCCTCTACTTGAATCCTTTTCT
2901 GAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTTATGGAGTTAAGATATAGTGTATTTT
3001 CCCAAGTTTGAAGTCTCTTCTTTTATGTTTAAATGCACTGACCTCCACATTTCTTTTATGTA AAAATATTGAGAAATAATTTAAATACATC
3101 ATTGCAATGAAAATAAATGTTTTTATTAGGCAAGATCCAGATGCTCAAGGCCCTTATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGA
3201 ACCTTTAATAGAAATTTGGACAGCAAGAAAGCGAGCTTCTAGCTTATCTCAGTCTGCTCCTGCCACAAAGTGCACGCAGTTGCCGGCGGGTCCGCG

NheI (2597)

3301 AGGGGGAAGTCCCGCCCCACGGCTGCTCGCCGATCTCGGTATGGCCGGCCGGAGGCGTCCCGGAAGTTCGTGGACACGACCTCCGACCACTGGGCGT
107 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 E A Y
3401 ACAGCTCGTCCAGGCCGCGCACCCACCCAGGCCAGGGTGTGTCCGGCACCACCTGGTCTTGACCCGCGCTGATGAACAGGGTCACGTCGTCCCGGAC
74 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 D R V
3501 CACACCGCGAAGTCGTCTCCACGAAGTCCCGGGAGAACCCGAGCCGGTCCGTCAGAACTCGACCGCTCCGGCGACGTCCGCGCGGTGAGCACCGGA
41 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 L V P
3601 ACGGCACTGGTCAACTTGGCCATGATGGCTCTCTGTGAGGAGAGAAAGAGAAGAAGGTTAGTACAATTGCTATAGTGAGTTGATTATACTATGCAG
7 V A S T L K A M
3701 ATATACTATGCCAATGATTAATTGTCAAAGTAGGGCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCG
CGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATA
3801
3901 CCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCGACCTGCCGTTACCGGATACCTGTCCGCCTTCTCCCTTCGGAAGCGTGGCG
4001 CTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTACGCCGACCGCTGCG
4101 CCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGT
4201 AGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGA
4301 AAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCCGCTGGTAGCGGTGGTTTTTTTGGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTC
4401 AAGAAGATCCTTTGATCTTTTACGGGGTCTGACGCTCAGTGAACGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC
4501 A