



EcoRI (23)

EcoRV (17)

NotI (2) SalI (9) XbaI (19) SdaI (38) SpeI (45)

1 GCGGCCGCGTCCACGATATCTAGAATTCGGATCCTGCAGGGCCCACTAGTACATTGTTTGTGCACGTTGGATTTTAAATGCTAGGAACTTTGGGAGA

BglII (136)

101 CTCATATTTCTGGGCTAGAGGATCTGTGGACCACAAGATCTTTTTATGATGACAGTAGCAATGTATCTGTGGAGCTGGATTCTGGTTGGGAGTGAAGG

201 AAAAGAATGTACTAAATGCCAAGACATCTATTTACAGGAGCATGAGGAATAAAAGTTCTAGTTTCTGGTCTCAGAGTGGTGCAGGGATCAGGGAGTCTCAC

301 AATCTCTGAGTGTGGTGTCTTAGGGCACACTGGGTCTTGGAGTCAAAGATCTAGGCACGTGAGGCTTTGTATGAAGAATCGGGATCGTACCCACC

401 CCCTGTTTCTGTTTCATCTCTGGCGTGTCTCTCTGCCTTTGTCCCCTAGATGAAGTCTCCATGAGCTACAGGGCCTGGTGCATCCAGGGTGTCTAGTA

NheI (518)

501 ATTGAGAACAGCAAGTGTAGCTCTCCCTCCCCTTCCACAGCTCTGGGTGTGGGAGGGGTTGTCCAGCCTCCAGCAGCATGGGAGGGCCTTGGTCAG

HindIII (682)

601 CCTCTGGGTGCCAGCAGGGCAGGGCGGAGTCTGGGGAATGAAGTTTTATAGGCTCTCTGGGGAGGCTCCCCAGCCCCAAGCTTACCACCTGCACCC

NcoI (715)

701 GGAGAGCTGTGCACCATGGTTCTGGGCCCTGCATGCTGCTGCTGCTGCTGCTGGCCTGAGGCTACAGCTCTCCTGGGCATCATCCAGTTGAG

801 GAGGAGAACCCGACTTCTGGAACCGGAGGCAGCCGAGGCCCTGGTGCCGCAAGAAGCTGCAGCCTGCACAGACAGCCGCAAGAACCTCATCATCT

901 TCCTGGGCGATGGATGGGGGTGTCTACGGTGACAGCTGCCAGGATCCTAAAAGGGCAGAAGAAGGACAACTGGGGCCTGAGATACCCCTGGCTATGGA

1001 CCGCTTCCCATATGTGGCTCTGTCCAAGACATACAATGTAGACAAACATGTGCCAGACAGTGGAGCCACAGCCACGGCTACCTGTGCGGGTCAAGGGC

1101 AACTTCCAGACCATTGGCTTGTGAGTGCAGCCGCCGCTTAAACAGTGAACACGACGACCGGCAACGAGGTCTCTCGTGTGAATCGGGCCAAGAAAG

1201 CAGGGAAGTCAAGTGGAGTGGTAAACCACACAGTGCAGCAGCCTGCCAGCCGACCTACGCCACAGCCTGGAACCCGCAACTGGTACTCGGACGC

1301 CGAGTGCCTGCCTCGCCGCCAGGAGGGTGCAGGACATCGTACGACGCTCATCTCCAACATGGACATTGATGTATCTGGTGGAGGCCGAAAG

1401 TACATGTTTGCATGGGAACCCAGACCTGAGTACCCAGATGACTACAGCAAGTGGGACCAGGCTGGACGGGAAGAATCTGGTGCAGGAATGGCTGG

1501 CGAAGCGCCAGGGTGCCTGGTATGTGTGGAACCGCACTGAGCTCATGCAGGCTTCCCTGGACCCGCTGTGACCCATCTCATGGGTCTTTGAGCCTGG

1601 AGACATGAAATACGAGATCCACCGAGACTCCACACTGGACCCTCCCTGATGGAGATGACAGAGGCTGCCCTGCGCCTGCTGAGCAGGAACCCCGCGG

1701 TTCTTCTTCTCGTGGAGGGTGGTGCATCGACCAGGTGCATCACGAAAGCAGGGCTTACCGGGCACTGACTGAGACGATCATGTTGACGACGCCATTG

1801 AGAGGGCGGGCAGCTCACCAGCGAGGAGGACAGCCTGAGCCTCGTCACTGCCGACCACTCCACGCTTCTCCTTCCGGAGGCTACCCCTGCGAGGGAG

1901 CTCCATCTTCCGGCTGGCCCTGGCAAGGCCCGGACAGGAAGGCCATACAGGCTCCTATACGGAACGGTCCAGGCTATGTGCTCAAGGACGGCGCC

2001 CGCCGGATGTTACCGAGAGCGAGAGCGGAGCCCGAGTATCGGCAGCAGTGCAGAGTCCCTGGACGAAGAGACCCACGAGGCAGGACGTGGCGG

2101 TGTTCCGCGCGGGCCGAGGCGCACCTGGTTCACGGCGTGCAGGAGCAGACCTTATAGCGCAGTGCATGGCCTTCCGCGCTGCCTGGAGCCCTACAC

2201 CGCCTGCGACCTGGCGCCCCCGCCGCGCACACCACGCGCCGCGCACCCGGGGCGGTCCCGGTCCAAGCGTCTGGATTGAACTAGCTGGCCAGACATGAT

2301 AAGATACATTGATGAGTTTGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATT

NheI (2281)

2401 ATAAGCTGCAATAAAACAAGTAAACAACAACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCT

2501 ACAAATGTGGTATGGAATTAATTCTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGC

MfeI (2430)

2601 ATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGGTTTGAAC

2701 GCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTATGATAAATATTTCAGAAATAATTTAAATACATCATTGCAATGAAAATAA

2801 ATGTTTTTATTAGGCAGAAATCCAGATGCTCAAGCCCTTCAATATCCCCAGTTTGTAGTTGGACTTAGGGAACAAGGAACCTTTAATAGAATTT

2901 GGACAGCAAGAAAGCGAGCTTCTAGCTTATCCTCAGTCTCTCCAGTCCGCAAAAGTGCACGCAGTTGCGGGCGGGTCCGCGAGGCGAECTCCGCC

SgrAI (3188)

3001 CCCACGGCTGCTCGCGATCTCGGTGATGGCCGGCCGGAGGCGTCCCGAAGTTCGTGGACACGACCTCCGACCACTCGGCGTACAGCTCGTCCAGGCC

3101 GCGCACCCACACCCAGGCCAGGTTGTGTCGGCACCACTGGTCTGGACCGCGTGTGAACAGGGTACGCTCGTCCCGACCAACCGGCAAGTCCG

3201 TCCTCCACGAAGTCCCGGAGAACCAGCGGCTGGTCCAGAACTGCAGCCTCCGGCGACGTCGCGCGGGTGGACCCGGAACGGCACTGGTCAACT

3301 TGGCCATGATGGCTCCTCTGTGAGGAGGAAAGAGAAGGTTAGTACAATGCTATAGTGAAGTGTATTATACTATGCAGATATACTATGCCAATG

MfeI (3351)

3401 A M

3401 ATTAATTGTCAAACTAGGGCTGCAGGTTAATTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTT
3501 CCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCT
3601 GGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCAC
3701 GCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTA
3801 TCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAG
3901 TTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAAGAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCT
4001 CTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCCGAGAAAAAAGGATCTCAAGAAGATCCTTTGAT
4101 CTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCA