



EcoRI (23)

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

1 CGCGCCGCGTTCAGCATATCTAGAATTCGGATCCTGCAGGGCCACTAGTCTGTAAGCTGAAGACCTGGCAGTGCTGAGCTGGTCAGCCCCAGGACCTC
101 CTTTTGTGCCACGAGTGAATCACCTTGGCATAGACATAATGGTCAGGGGTGGGCACGCAGCCTGCTTCCCCTGTGCTCCAGGCCCTCTTCGATGCTTT
201 CCGAGAAGTCTATTGAGCTGGGAGCTTGTACTGCACCCGGGGCTGACATCCTGGCATCCTGGGATAAAAAGCAGCCCACGGGGCTGCCCTTGCCATATGCC
301 TCACTGGCGGCAGAGAACAAGGCTCTATTAGCGAGTACCTGGAGTAGACACCAGAAGCCCAAGCATGGGCAGAGGAAGGCAGGGGTTGGGGGAGCAG
401 AGCTGTCTGTGTTCCAGAAGCCCAAGGACACAGATGGCTAAGGCGCTGGGAGAGGGACCTGAGTGAAGAGATAGATGGGCTGAAGTCTCAAGCAGCA
501 ACAGCCTCCTCCCCGCCATTGGTGAGGGTGGGTTTGGTTTCCGGACCTACATATCCCTCAGAGGCTGGTGTGTAGGAATTTAAGGGGGTAAATCTC

Acc65I (615)

SphI (660)

601 CTGAGAGAATGAGGGTACCCAGGAAGACGGGGTGTACAGAAAGAAAGACTCCAGCATGCACAGCCAACCTATTCAAACACTACTCTGTCAGGGGCTGCC
701 AGGGGCCAGGCTCGGGGTGGGGGTGGGGGCAACGAGAAGCTGGATCAGGGAGAAATGGCCCACTAGGCTGGATAAGAGGCCACAGAGGGGCTCAGGAA
801 TGAAGCTGCTGTCTTACCTATTAGGATCTGCGTGCATACCTTCTGCCGTGCATCTAACACACAGCCAGAGGCTCAAGTTGACCTGGAGTCACAGA
901 GAGGGCTCCAACCTTAGCCCTCCACTCTGAACCTCAGGAATGAGAAGATAGAGTTGGAGAGATTGAGGGAGAGGACTCTGTTGAGAATGGGGTCAACA
1001 GGAAACTGTAATATAGTTGATCCCGGAGGAAGGGAATAGGTTCTCAAGTTCCTAGCATCTCACAGGCCCCAGAGAAGGACAGAGTTGGGGTGTCTCT
1101 GGCTTACAGGCTCTAAGAACTGGAAGCTGATTACCCACCGAGCTGTGCACCTCTGTCTCTGTCTGTGTGCGCTCGTGCACACTTATCACACAAA
1201 TGTTTCATGTGTGTCACATACATGTGTTGAGACCAGAGGTAACCTCAGGCACTGTTGCCTTGGTTTTCTGAGAGAGCATTCTCTCTGGATCTGGAAC
1301 CGCCAATTAGTGAGAGCCAGGAAGTCTGCTGATTTTCACTGCCAGCACTGGAGTTTACAAGTATGCACTGTCAACCCAGGCTTTTGTATTCTGCTG
1401 AGCTAGAAGTGGGTGGGCTTTCATGCTTGACAGGCAAGCAATTTATGGACTAAGCTGTTCCCTCGGCCCTCTTTGACCCATTTACCAGAAAGGGGGT
1501 CTTGATCAATGGCGAAGCCAGGCTGGTGTCCCAAGAAAGCCTTGACTCTGGGTACAGTACCTCAGTGGGGTGGAGGAGTTCTCCCTAGCTGGG
1601 TGGGGCCAGCTCCACCCCTCAGGCTATTCAATGGGGGTGCTTCCAGGAAGTACAGGGCAGATTTAGTCCAACCCGTTCTCCATAAAGGCCCTGACAT

NcoI (1726)

SphI (1748)

1701 CCCAGGAGCCAGCAGAGGCGAGGCAACCATGGTTCTGGGGCCCTGCATGCTGCTGCTGCTGCTGCTGGGCTGAGGCTACAGCTCTCCCTGGGCATCA
1801 TCCCAGTTGAGGAGGAGAACCAGGACTTCTGGAACCGCAGGCGAGCCGAGGCCCTGGGTGCCCAAGAAGCTGCAGCCTGCACAGACAGCCGCAAGAA
1901 CCTCATCATCTTCTGGCGATGGGATGGGGGTGTACGGTGACAGCTGCCAGGATCTAAAAGGCAGAGAAGAAGGACAAACTGGGCGCTGAGATACCC
2001 CTGGCTATGGACCGTCCCATATGTGGCTCTGTCCAAGACATACAATGTAGACAAACATGTGCCAGACAGTGGAGCCACAGCCACGGCCTACCTGTGG
2101 GGGTCAAGGGCAACTTCCAGACCTGGCTTGTAGTGCAGCCGCGCTTTAACAGTGAACACGACACGCGGCAACGAGGTTCATCTCCGTGATGAATCG
2201 GGCCAAGAAAGCAGGGAAGTCAAGTGGGAGTGGTAACCACACAGAGTGCAGCACGCTCGCCAGCCGGCACCTACGCCACACGGTGAACCGCAACTGG
2301 TACTCGGACGCCAGCTGCCTGCCTCGGCCCGCCAGGAGGGGTGCCAGGACATCGCTACGCACTCATCTCAACATGGACATTGATGTGATCCTGGGTG
2401 YAGCCGAAAGTACATGTTTCGCATGGGAACCCAGCCTGAGTACCCAGATACAGTACAGCCAAAGGTGGGACCAGCTGGACGGGAAGAATCTGGTCA
2501 GGAATGGCTGGCGAAGCCAGGCTGCCGGTATGTGTGGAACCGCACTGAGCTCATGCAGGCTTCCCTGGACCCGCTGTGACCCATCTCATGGGTCTC
2601 TTTGAGCCTGGAGACATGAAATACGAGATCCACCGAGACTCCACTGGACCCCTCCCTGATGGAGATGACAGAGGCTGCCCTGCGCCTGCTGAGCAGGA
2701 ACCCCCGCGGTTCTTCTCTTCTGTTGAGGGTGGTGCATCGACCAGGTCATCACGAAAGCAGGGCTTACCGGGCACTGACTGAGACGATCATGTTCCA
2801 CGACGCCATTGAGAGGGCGGGCCAGCTCACCAGCGAGGAGACACGCTGAGCCTCGTCACTGCCAGCACTCCACGCTTCTCTCTCGGAGGCTACCC
2901 CTGCGAGGGAGCTCCATCTTCCGGCTGGCCCTGGCAAGGCCCGGACAGGAAGGCTACACGGTCTCTATAACGAAACGGTCCAGGCTATGTGCTCA
3001 AGGACGGCGCCCGCGGATGTTACCGAGAGCGAGAGCGGGAGCCCCGAGTATCGGCAGCAGTACAGCAGTGGCCCTGGACGAAAGAGACCCACGAGGCGA
3101 GGACGTGGCGGTGTTGCGCGCGGCCAGGCGCACTGGTTCACGGCGTGCAGGAGCAGACCTTCATAGCCAGCTGATGGCCTTCCGCGCCTGCTGAGCAGGA
3201 GAGCCCTACACCGCTGCGACCTGGCGCCCCCGCGGACACCACCGACGCGCGACCCGGGGCGGTCCCGTCCAAGCGTCTGGATTGAAAGCTAGCTGG
3301 CCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTAT

SacII (2708)

NheI (3292)

3201 GAGCCCTACACCGCTGCGACCTGGCGCCCCCGCGGACACCACCGACGCGCGACCCGGGGCGGTCCCGTCCAAGCGTCTGGATTGAAAGCTAGCTGG
3301 CCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTAT

MfeI (3441)

3401 TTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTTGGGAGGTTTTTAAAGCAA
3501 GTAAACCTCTACAAATGTGGTATGGAATTAATTCTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGG

3601 ATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAGATATAGTGATTTTCCCAA
SspI (3771)
3701 GGTTTGAAGTCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAAATTCAGAAATAATTTAAATACATCATTGC
3801 AATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAAACAAAGGAACCTT
3901 TAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTATCCTCAGTCTGCTCCTCTGCCACAAAGTGCACGCAGTTGCCGGCCGGGTGCGCGAGGGC
125 • D Q E E A V F H V C N G A P D R L A
4001 GAACTCCCGCCCCACGGCTGCTCGCCGATCTCGGTCATGGCCGGCCGGAGGCGTCCCGAAAGTTCGTGGACACGACCTCCGACCACTCGGCGTACAGC
106 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 L
SgrAI
4101 TCGTCCAGGCGCGCACCCACACCAGGCCAGGGTGTGTCGGCACCACCTGGTCTGGACCGCGCTGATGAACAGGGTACAGTCTCCGGACCACAC
72 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 V G
AatII (4275)
4201 CGGCGAAGTCGCTCCACGAAGTCCCGGAGAACCCGAGCCGGTCCGAGTCCGACCGCTCCGGCGACGTCGCGCGCGGTGAGCACCAGGACCGG
39 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 V A
MfeI (4362)
4301 ACTGGTCAACTTGGCCATGATGGCTCCTCTGTGACGAGAGGAAAGAGAAGAAGGTTAGTACAATTGCTATAGTGAGTTGTATTATACTATGCGATATA
6 S T L K A M
4401 CTATGCCAATGATTAATTGTCAAACTAGGGCTGCAGGTTAATTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGCCGCGTTG
4501 CTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAGG
4601 CGTTTCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTC
4701 TCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTAGCCCGACCGCTGCGCTTA
4801 TCCGGTAACTATCGTCTTGAAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCG
4901 GTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAG
5001 AGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAA
5101 GATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCA