



EcoRI (23)

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

1 CGGCCCGCGTCGACGATATCTAGAAATTCGGATCCTGCAGGGCCCACTAGTTCCCCACTTCCCGCCTCTCAGCCTTTGAAAGAAAGAAAGGGGAGGGGG

NruI (117)

101 CAGGCCCGGTGACGTGCGAGCGGTGCTGGGCTCCGGTCCAATTCATCTCAGTCGCTCCAAAGTCTTCTGTTTCATCCAAGCGTGAAGGTCC

201 CCGTCCTTGACTCCCTAGTGTCTGCTGCCACAGTCCAGTCTGGGAACAGCACCGATCACCTCCATCGGGCCAATCTCAGTCCCTTCCCCCTACG

301 TCGGGGCCACACGCTCGGTGCTGCCAGTTGAACAGGCGGTGCGGAAAAAAGCGGGGAGAAAGTAGGGCCGGCTACTAGCGGTTTTACGGG

401 CGCAGTAGCTCAGGCTCAAGACCTTGGGCTGGGACTGGCTGAGCCTGGCGGGAGGCGGGTCCGAGTACCGCTGCCCGCGCCCCGGTTTTCTAT

501 AAATTGAGCCCGACGCTCCCGCTTCTGCTCTCTCTCTGCTCTCTCTGTTGACAGTCAGCCGCATCTTTTTCGCTCGCCAGgtgaagacgggaggagagaaa

SfiI (674)

601 cccgggaggctaggacggcctgaaggcggcagggcgggcgaggccggtggttcgcccgtgccccgggcccggcctccgattgcagg

701 ggccgggaggagcgtgatgcggcgggcgtggcatggaggcctggtgggggaggggagggcggtggtcgccgggcccactaggcgctcact

NotI (841)

801 gttctctccctccgcgagCCGAGCCACATCGCTGAGACCAATGAAATCAAGGTGCTGTTGCCCTCATCTGTATTGCTGTTGCTGAGGCAAAACCCA

1 M E I K V L F A L I C I A V A E A K P

BglII (956)

901 CTGAAATCAATGAAGACCTCAATATAGCTGCTGTGGCTCCAACCTTTCACCACAGATCTTGAGACTGACCTGTTCACTGAGGAGCCATGAATGT

20 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 T N W E T M N V

1001 GATTAGCACTGACACAGAGCAGGTGAACACAGATGCTGACAGGGCAAGCTGCCTGGCAAAAACTCCCCCAGATGCTCTGAGGGAGCTGGAGGCCAAT

53 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 L R E L E A N

1101 GCCAGAAGGGCTGGTTGCACAAGAGGCTGCCTCATTTGCCTCTCCACATTAAGTGCACCCTAAGATGAAGAAATTTATCCCTGGCAGGTGCCACACTT

87 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 I P G R C H T

1201 ATGAAGGTGAAAAGGAGTCTGCTCAGGGAGGGATTGGAGAGGCAATGTTGATATCCAGAGATTCTGGCTCAAGGATAAGGAGCCACTGGACCAGT

120 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 D K E P L D Q F

1301 TATTGCTCAAGTGGACCTCTGTGCTGATTGACCACTGGCTGTGAAGGGCCTTGCCTGCAAGTGTCCAGTGTCTGACCTCTGAAGAAAGTGGCTCCCCAG

153 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 L K K W L P Q

NheI (1475)

1401 AGGTGTACCACTTTTCCAGCAAGATTGAGGTAGGGTGGACAAAATCAAGGGTCTGGCTGGGGACAGATGATAGCTAGCTGGCCAGACATGATAAGATA

187 R C T T F A S K I Q G R V D K I K G L A G D R •

1501 CATTGATGAGTTTGGCAAAACCACAACCTAGAATGCAAGTGAAGAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTGTAACATTATAAGC

1601 TGCAATAACAAGTTAACAACAACAATTGCATTCAATTTATGTTTCAGGTTTCAGGGGAGGTGTTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAAT

1701 GTGGTATGGAATTAATCTAAATACAGCATAGCAAACTTAACTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGC

1801 ATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGTTTGAAGTCTCTT

SspI (1954)

1901 CATTCTTTATGTTTAAATGCACTGACCTCCACATTCCTTTTATGTAATAATTCAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTT

2001 TTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTTGGACAG

2101 CAAGAAAGCGAGCTTCTAGCTTATCCTCAGTCTGCTCTCTGCCACAAAGTGCACGAGTTGCCGGCCGGTCCGCGAGGGCGAACTCCCGCCCCACG

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

2201 GCTGCTCGCGATCTCGGTGATGGCCGGCCGGAGGCGTCCCGAAGTTCGTGGACACGACCTCCGACCACTCGGCGTACAGCTCGTCCAGGCCGCGCAC

100 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 E D L G R V

SgrAI (2382)

2301 CCACCCAGCCAGGGTGTGTCCGGACCACCTGGTCTGGACCGCGCTGATGAACAGGGTACGTCGTCGGGACCACCCGGCGAAGTGTCTCTCC

67 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 A F D D E

2401 ACGAAGTCCCGGAGAACCAGCGGTGCGTCCAGAACTCGACCGCTCCGGCGAGTCCGCGCGGTGAGCACCGAAGCGACTGGTCAACTTGGCCA

33 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 S T L K A M

2501 TGATGGCTCCTCTGTCAGGAGAGAAAGAGAAGGTTAGTACAATTGCTATAGTGTGATTATACTATGAGATATACTATGCAATGATTAAT

2601 TGTCAAAGTGGGCTGAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGTTGCTGGCGTTTTTCCATAG

2701 GCTCCGCCCCCTGACGAGCATCAGAAATCGACGCTCAAGTCAAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCCCTGGAAGC

2801 TCCCTCGTGGCTCTCTGTTCCGACCTGCCGCTTACCGGATACCTGTCGCTTTCTCCCTTCGGGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTA

2901 GGTATCTCAGTTCGGTGTAGGCTGTTCCGCTCCAAGCTGGGCTGTGTGCAGAACCCCCGTTTCAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCT

3001 TGAGTCCAACCCGGTAAGACAGCACTTATGCCACTGGCAGCAGCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTG

3101 AAGTGGTGGCCTAACTACGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGAT

3201 CCGGCAACAACCCAGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTT

3301 TACGGGGTCTGACGCTCAGTGAACGAAAACACGTTAAGGGATTTGGTCATGGCTAGTTAATTAACATTTAAATCA

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