



EcoRI (23)

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

1 GCGGCCGCGTCGACGATATCTAGAATTCGGATCCTGCAGGGCCGCTGCTCGGGAGGCTGAGGCAGGAGAATCACTTGAACCAGGGAGGCAGAGTTGTGG
101 TGAGCAGAGATCGGCCATTGCTCTCCAGCTGGGCAACAAGAGCAAAGTTCGTTTAAAAAAAAAAAAAAGTCTTTTCGATGTGACTGTCTCTCCCAA
201 ATTTGTAGACCCTCTTAAGATCATGCTTTTCAGATACTTCAAAGATTCAGAAGATATGCCCCGGGGTCTCTGGAAGCCACAAGGTAACACAACACATC
301 CCCCTCTTGACTATCAATTTTACTAGAGGATGTGGTGGGAAAACCATTTATTTGATATTAACAACAAATAGGCTTGGGATGGAGTAGGATGCAAGCTCCCC

AvrII (452)

401 AGGAAAGTTTAAGATAAAACCTGAGACTTAAAAGGTGTTAAGAGTGGCAGCCTAGGGAATTTATCCCGACTCCGGGGAGGGGGCAGAGTCACCAGCC
501 TCTGCATTTAGGGATTCTCCGAGGAAAAGTGTGAGAACGGCTGCAGGCAACCCAGGCGTCCCGGCGCTAGGAGGGACGCACCCAGGCTGCAGGAAAGAGA
601 GGGAGAAAGTGAAGCTGGGAGTTGCCACTCCAGACTTGTGGAATGCAGTTGGAGGGGGCAGCTGGGAGCGCGTTGCTCCAATCACAGGAGAAGGA
701 GGAGGTGGAGGAGGGCTGCTTGGAGGATATAAGAATGAAGTTGTGAAGCTGAGATTCCTCCATTGGGACCGGAGAAACAGGGGAGCCCCCGG
801 GCAGCCGCGCCCTTCCACGGGGCCCTTACTGCGCCGCGCCCGGCCACCCTCGCAGCACCCGCGCCCGCCCTCCAGCCGGGTCCA

NcoI (934)

901 GCCGGAGCCGTGGGGCCGAGCCGAGTGCAGCACCATGGAAATCAAGGTGCTGTTGCCCTCATCTGTATTGCTGTTGCTGAGGCAAAACCCACTGAAAT
M E I K V L F A L I C I A V A E A K P T E I

BglIII (1049)

1001 CAATGAAGACCTCAATATAGCTGCTGTGGCCTCCAACCTTGGCCACCACAGATCTTGAGACTGACCTGTTCCACCACTGGGAGACCATGAATGTGATTAGC
22 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 I S
1101 ACTGACACAGAGCAGGTGAACACAGATGCTGACAGGGGCAAGCTGCCTGGCAAAAACTCCCCCAGATGTCTGAGGGAGCTGGAGCCAATGCCAGAA
56 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 A R
1201 GGGCTGGTTGCACAAGAGGCTGCCTCATTGCTCTCCACATTAAGTGCACCCCTAAGTGAAGAAATTTATCCCTGGCAGGTGCCACACTTATGAAGG
89 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 Y E G
1301 TGAAAAGGAGTCTGCTCAGGGAGGGATTGGAGAGGCAATTGTTGATATCCAGAGATTCTGGCTTCAAGGATAAGGAGCCACTGGACCAGTTTATTGCT
122 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 I A
1401 CAAGTGGACCTCTGTGCTGATTGCACCACTGGCTGTCTGAAGGGCCTTGCAATGTCCAGTGTCTGACCTCTGAAGAAGTGGCTTCCCCAGAGGTGTA
156 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 R C

NheI (1568)

1501 CCACTTTTGGCAGCAAGATTGAGGGTGGGCAAAAATCAAGGGTCTGGCTGGGACAGATGATAGCTAGCTGGCCAGACATGATAAGATACATTGAT
189 T T F A S K I Q G R V D K I K G L A G D R
1601 GAGTTTGGACAAACCACAACCTAGAATGCAGTGAAGAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATA
1701 AACAAAGTTAACAAACAACAAATTGCATTCATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTAT
1801 GGAATTAATTCTAAAATACAGCATAGCAAACTTAACTCCAAATCAAGCCTCTACTTGAAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGG
1901 GCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAAGATATAGTGTATTTTCCCAAGGTTTGAAGTACTCTTCATTCT

SspI (2047)

2001 TTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAAATATTAGAAATAATTTAAATACATCATTGCAATGAAAATAATGTTTTTTATTA
2101 GGCAGAAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAGGAACCTTTAATAGAAATTGGACAGCAAGAAA
2201 GCGAGCTTCTAGCTTATCCTCAGTCTGCTCCTCTGCCACAAAGTGCACGAGTTGCCGGCCGGTCCGCGAGGGCGAACTCCCGCCCCACGGTGTCT
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
2301 GCCGATCTCGGTGATGGCCGGCCGAGGCGTCCCGAAGTCTGGACACGACTCCGACCCTCGGCGTACAGCTCGTCCAGGCCGCGCACCCACACC
98 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 W V

SgrAI (2475)

2401 CAGGCCAGGGTGTGTCGGCACCACCTGGTCTGGACCGCGTGTGAACAGGGTACGTCGTCCCGACCACACCGGCAAGTGTCTCCACGAAGT
64 W A L T N D P V V Q D Q V A S I F L T V D B R V V G A F D D E V F D
2501 CCCGGGAGAACCAGCCGTCGGTCCAGAACTCGACCGCTCCGGCAGCTCGCCGCGGTGAGCACCAGGAAACGGCACTGGTCAACTTGGCCATGATGGC
31 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
2601 TCCTCTGTGAGGAGGAAAGAGAAGGTTAGTACAATTGCTATAGTGTGATTATACTATGCAGATATACTATGCCAATGATTAATTGTCAA
2701 CTAGGGCTGACGGTTAATTAAGAACATGTGAGCAAAAAGGCCAGAAAAGGCCAGAACCTGAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCG
2801 CCCCCTGACGAGCATCACAATAATCGACGCTCAAGTCAAGGTTGGCGAAACCCGACAGACTATAAGATACCAGGCGTTTTCCCCTGGAAGCTCCCTCG
2901 TCGCTCTCTGTTCCGACCCTGCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCT
3001 CAGTTCGGTGTAGTTCGCTCCTCAAGCTGGGCTGTGTGACGAACCCCGTTCAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGTAGTCC
3101 AACCCGGTAAGACACGACTTATCGCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGT

3201 GGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAA
3301 ACAACCACCGCTGGTAGCGGTGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGG
3401 TCTGACGCTCAGTGAACGAAAACACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCA