



SdaI (38)

1 CCGGCCGCGTCGACGATATCTAGAATTCGGATCCTGCAGGGCCTGAAATAACCTCTGAAAGAGGAACTTGGTTAGGTACCTTCTGAGGCGAAAGAACCA
101 GCTGTGGAATGTGTGTCAGTTAGGGTGTGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGT

SpeI (275)

201 GGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCACTAGTGCCAAGAACATCTTAAGTCA
301 CAGAAACATTAGTTTTTGAAGCAGGGTTTGTGTAACATAGTAGAAATGACATTCTGATCCACTCCTAGCTTACAAGGATATCTGTGAAAGATTG
401 GGGCAAACTGTTAAGCTGTCTGAAAGTCTTTTGATAAGAAATGGGTTTTACTGCTAAAACGTGCATATTGCTGAGTTTTGAATGCCCTAATGGTAAA
501 TGATACTGGGTTGCCAAAATAACCAGATTAGTAGTTTTTTCATTCATTTGGCCGTCTCAGTAAGTCAAATATTGATACTTTCTACTAAGTCATCTTGCC
601 AACACCCATTTTGTATACTTATGCTGAATCTGTTTGCATCTCTTAAGTAAGAAAATTATTGATTATTTTGTGGGATTTAATTTAAAAAAAATGGTAA
701 TGGATACTGTAAGGAGCATTATTTGGATGGTTAAAAACATCTTCTTGATGGGAAAATCTTTTAAAGGCTTTCTAACTTGGTGAATTACTTGAATT
801 AAGGAAGTGAATGCCATTCTACTGACTTAGAACAACCTTTTTGACTTCTGCAAAGAGGACCTTACAGTATTTTGGAGAAGTTAGTAAAACCGAATC

NheI (928)

901 TGACATCATCACCTAGCAGTTTATGCAGCTAGCAAGTGGTTTGTCTTAGGGTAACAGAGGAGGAAATTTGTTCTCGTCTGATAAGACAACAGTGGAGAg
1001 tatgcatttattttactttttacatttttgattcgtttttacagagaaaaacttctacagagataacaattttttgcttttcagAAGGACGCATGCT

NcoI (1135)

1101 GTTCTTAGGGACACGGCTGACTTCCAGATATGACCATGGAATCAAGGTGCTGTTTGCCTCATCTGTATTGCTGTTGCTGAGGCAAAACCCACTGAAA
1201 TCAATGAAGACCTCAATATAGCTGTGGCCTCCAACCTTCCACCCACAGATCTTGAGACTGACCTGTTACCAACTGGGAGACCATGAATGTGATTAG
22▶ 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 I S
1301 CACTGACACAGAGCAGGTGAACACAGATGCTGACAGGGGCAAGCTGCCTGGCAAAAACTCCCCCAGATGCTCTGAGGGAGCTGGAGGCCAATGCCAGA
55▶ 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
1401 AGGGCTGGTTGCACAAGAGGCTGCTCATTGCTCTCCACATTAAGTGCACCCCTAAGATGAAGAAATTTATCCCTGGCAGGTGCCACACTTATGAAG
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
1501 GTGAAAAGGAGTCTGCTCAGGGAGGGATTGGAGAGGCAATTGTTGATATCCAGAGATTCTGGCTTCAAGGATAAGGAGCCACTGGACCAGTTTATTGC
122▶ 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 I A
1601 TCAAGTGGACCTCTGTGCTGATTGCACCACTGGCTGTCTGAAGGGCCTGCCAATGTCCAGTCTCTGACCTCCTGAAGAAGTGGCTTCCCGAGAGGTGT
155▶ 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 (1769)

1701 ACCACTTTTGCCAGCAAGATTACAGGTTAGGGTGGACAAAATCAAGGGTCTGGCTGGGGACAGATGATAAGTCTGGCCAGACATGATAAGATACATTGA
189▶ T T F A S K I Q G R V D K I K G L A G D R •
1801 TGAGTTTGACAAACCACAACCTAGAATGCAGTGAAGAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAAT
1901 AAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTA
2001 TGGAAATTAATTCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGG
▶
2101 GGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAAGATATAGTGTATTTTCCCAAGGTTTGAAGTACTGCTTTCATTTT
2201 TTTATGTTTTAAATGCACTGACCTCCCACATTCCTTTTTAGTAAAAATTCAGAAAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATT
2301 AGGCAGAAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAGGAACCTTTAATAGAAATTTGGACAGCAAGAA
2401 AGCGAGCTTCTAGCTTATCTCAGTCTCTGCTCTGCCCACAAAGTGCACGAGTTGCCGGCCGGGTGCGCAGGGCGAACTCCCGCCCCACGGTCTCT
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
2501 CGCCGATCTCGGTGATGGCCGGCCGGAGGCGTCCCGAAGTTCTGGACACGACCTCCGACCACTCGGCGTACAGCTCGTCCAGGCCGCGCACCCACAC
98▶ G I E T M A P G S A D R F N T S V V E A C S W E A Y L E D L G R V W
2601 CCAGGCCAGGGTGTGTCGGCACCACTGGTCTGGACCGCTGATGAACAGGGTCTGCTGCTCCCGACCAACCGGCGAAGTCTGCTCCACGAAAG
65▶ 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 V F
2701 TCCGGGAGAACCCGAGCCGGTCCGAGTCCAGAACTGACCGCTCCGGCAGCTGCGCGCGGTGAGCACCGAACCAGGCACTGGTCAACTTGGCCATGATGG
31▶ 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
2801 CTCTCTGTCAGGAGAGGAAAGAGAAGGTTAGTACAATGCTATAGTGAAGTTGATTATACTATGCAGATATACTATGCCAATGATTAATTGTCAA
2901 ACTAGGGCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCG
▶
3001 CCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTC
3101 GTGCGCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGATAGTATC

3201 TCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTGAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTC
3301 CAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGG
3401 TGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCA
3501 AACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGG
3601 GTCTGACGCTCAGTGAACGAAAACACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCA