



EcoRI (23)

1 NotI (2) **XbaI (19)** **SdaI (38)** **SpeI (45)**
CGCGCCGCTCGACGATATCTAGAATTCGGATCCTCGAGGGCCCACTAGTTCATGTCTTATATGGACTCATCTTTGCTATTGCGACACACTCAAT

101 GAACACCTACTACGCGTGTCAAAGAGCCCCGAGGCCTGAGGTGCCCCACCTCACCCTCTTCTATTGTTGTAATAATCCAGCTTCTTGTCAACAC

SphI (288)

201 CTCCAAGGAGGGGAGGAGGAGGAAGCAGGTTCTCTAGGCTGAGCCGAATGCCCTCTGTGGTCCCAGCCACTGATCGTGCATGCCACCACCTGG

301 GTACACACAGTCTGTGATTCGCGAGCAGAACCAGGCTGCCACCCGGTCTGTGTGCTACTCAGTGGACAGACCAAGGCAAGAAAGGGTACAAGGA

401 CAGGGTCTCCAGGCTGGCTTTGAGTCTAGCACCGCCCCGCCCAATCTCTGTGGCAGATGGAGTCTTGGTCCCCAGAGTCCCCAGCGGCTCC

501 AGATGGTCTGGAGGCGAGTTCAGCTGTGGTGCATAGCAGACATAACGGACGGTGGGCCAGACCAGGCTGTGTAGACCCAGCCCCGCC

BstEII (611)

601 GCAGTGCCTAGTCAACCAACGCCCCAGGCTGGTCTTGGTGGGCTGACTGTTACCCTCAAAGCAGGCTCCAGGGTAAAGGTGCCCTGCC

701 CTGTAGAGCCACCTCTCCAGGCTGGGCTGGTGGTGTGAGCTTCATCACGGGCCCTCAGCCACTGACCGTGGCCCTGCCCTGTC

801 CTGGGAGTGTGGTCTGCGACTTCTAAGTGGCCGAAGCCACTGACTCCCCAACCCACTCTACCTCTCAAGCCAGGCTCTCCCTAGTGACCC

NheI (915)

901 ACCCAGCACATTTAGCTAGCTGAGCCCCACAGCCAGAGGCTCAGGCCCTGCTTTCAGGGCAGTGTCTGAAGTCGGCAAGGGGAGTACTGCCTGG

SacI (1023)

1001 CCACTCCATGCCCTCAAAGAGCTCTTCTGAGGAGGTACAGAACCCAGGGCCCTGGCACCCGTGAGACCTGGCCACCCACCTGGGCGCTCAGTG

1101 CCCAAGAGATGTCCACACCTAGGATGTCGCGGTTGGTGGGGGCCGAGAGACGGCAGGCCGGGGCAGGCTGGCCATGCGGGGCCAACCAGGGA

1201 CTGCCAGCGTGGGCGCGGGGCCAGGCGCGCCCCAGCCCCGGGCCAGCACCCAAGGCGGCAACGCCAAACTCTCCCTCTCTCTCTCTCT

1301 CAATCTCGCTCTCGCTCTTTTTTTTTTCGAAAAGGAGGGGAGAGGGGTAATAAATGCTGCACTGTGCGGCGAAGCCGGTGAAGTGAAGCGCGGG

NotI (1446)

XhoI (1440)

1401 CCAATCAGCGTGCCTCGTTCGAAAGTTGCCTTTTATGGCTCGAGCGGCGGCCCTATAAAACCAGCGCGCGACGCGCCACCACCGCCGAG

HindIII (1556)

1501 ACCGCGTCCGCCCCGAGCAGAGCCTCGCCTTGGCGATCCGCCGCCCTCAAGTTCGAGGGCTCGCATCTCTCTTACGCGCCCCGCCCT

1601 ACCTGAGGCCCATCCAGCGGGTTGAGTCGCGTTCTGCCCTCCCCGCTGTGGTGCCTCCTGAAGTCCGTCGGCTGAGGTAAGTTAAAGCTCA

1701 GGTGAGACCGGGCTTGTCCGGCTCCCTTGGAGCCTACTAGACTCAGCCGCTCTCCACGCTTTCCTGACCTGCTTGTCAACTCTACGTCTT

NcoI (1841)

1801 TGTTCGTTTTCTGTTCTGCGCCGTACAGATC**CAAGCCACC**ATGGAAATCAAGGTGCTGTTGCCCTCATCTGTATTGCTGTTGCTGAGGCAAAACCA

BglII (1956)

1901 CTGAAATCAATGAAGACCTCAATATAGCTGTGCGCTCCAATTTGCCACCACAGATCTTGAGACTGACCTGTTACCAACTGGGAGACCATGAATGT
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

2001 GATTAGCACTGACACAGCAGGTGAACACAGATGCTGACAGGGCAAGTCTGCTGGCAAAAACCTCCCCAGATGCTCTGAGGGAGCTGGAGGCCAAT
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

2101 GCCAGAAGGCTGGTTGCACAAAGAGGCTGCCTCATTGCTCTCCACATTAAGTGCACCCCTAAGTGAAGAAATTTATCCCTGGCAGGTGCCACACTT
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

2201 ATGAAGTGAAAAGGAGTCTGCTCAGGAGGGATTGGAGGCAATTTGATATCCAGAGATTCTGGCTTCAAGGATAAGGAGCCACTGGACAGTT
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

2301 TATTGCTCAAGTGGACCTCTGTGCTGATTGCACACTGGCTGTCTGAAGGCTTCCCAATGTCAGTGTCTGACCTCTGAAGAAGTGGCTTCCCGAG
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 (2475)

2401 AGGTGTACACTTTTGCCAGCAAGATTCAAGGTAGGGTGACAAAATCAAGGTCTGGCTGGGACAGATGATAGCTAGCTGGCCAGACATGATAAGATA
187▶ R C T T F A S K I Q G R V D K I K G L A G D R •

2501 CATTGATGAGTTTGGACAAACCACTAGAATGCAAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTGTAACCATTATAAGC

2601 TGCAATAAACAGTTAAACAACAACAAATTCATTCATTTATGTTTCAGGTTCAAGGGGAGGTGTTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAT

2701 GTGGTATGGAAATTAATCTAAAAACAGCATAGCAAACTTAACTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGC

2801 ATCAGGGCTGTTGCAATGTGCATTAGCTGTTGCGCCTCACCTCTTTTATGAGTAAAGATATAGTATTTTCCAAGGTTTGAAGTACTGCTCTT

2901 CATTCTTTATGTTTTAAATGCACTGACCTCCACATCCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTT

3001 TTTATTAGGAGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAAGGAACCTTAAATAGAAAATGGACAG

3101 CAAGAAAGCGAGCTTCTAGCTTATCCTCAGTCTGCTCTGCCACAAGTGCACGAGTTGCCGCGGGTGGCGAGGCGCAACTCCGCCCCCAGC

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

3201 GCTGCTCGCCGATCTCGGTCATGGCCGGCCGGAGGCGTCCCGAAGTTCTGGACACGACCTCCGACCACTCGGCGTACAGCTCGTCCAGGCCGCGCAC
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 (3382)
3301 CCACACCCAGGCCAGGGTGTGTCCGGCACCACCTGGTCCTGGACCGCGCTGATGAACAGGGTCACGTCGTCCCGACCACACCGCGAAGTCGTCTCC
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
3401 ACGAAGTCCCGGGAGAACCAGCGGTCCGAGTCCAGAACTCGACCGCTCCGGCGACGTCGCGCGGGTGAGCACCGGAACGGCACTGGTCAACTGGCCA
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
3501 TGATGGCTCCTCCTGTCAGGAGAGAAAGAGAAGGTTAGTACAATTGCTATAGTGAGTTGTATTATACTATGCAGATATACTATGCCAATGATTAAT
0
3601 TGTCAA ACTAGGGCTGCAGGTTAATTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGCTGGCGTTTTCCATAG
3701 GCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGCGTTTTCCCTGGAAGC
3801 TCCCTCGTGCCTCTCCTGTCCGACCCTGCCGTTACCGGATACCTGTCGCTTTCTCCCTTCGGGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTA
3901 GGTATCTCAGTTCGGTGTAGGTCTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCTTATCCGGTAACTATCGTCT
4001 TGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTTCTTG
4101 AAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGAT
4201 CCGGCAAACAACCCAGCGTGGTAGCGGTGGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTC
4301 TACGGGGTCTGACGCTCAGTGAACGAAAACACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCA