



EcoRI (23) PstI (38)
NotI (2) **XbaI (19)** **BamHI (29)** SspI (51)
 1 CGGGCCGCTCGACGATATCTAGAATTCGGATCCTGCAGTTTGAGGAGAATATTTGTTATATTTGCAAATAAAATAAGTTTGAAGTTTTTTTTCTG

SacI (112)
 101 CCCCAAGAGCTCTGTGCTTGAACATAAAATACAAATAACCGCTATGCTGTTAATTATTGGCAAATGCCATTTTCAACCTAAGGAAATACCATAAA

SpeI (226)
 201 GTAAACAGATATACCAACAAAAGGTTACTAGTTAACAGGCATTGCCTGAAAAGAGTATAAAAGAATTCAGCATGATTTCCATATTGTCTCCACCACT

NcoI (311)
 301 GCCAATAACACCATGGAATCAAGGTGCTGTTTGCCTCATCTGTATTGCTGTTGCTGAGGCAAAACCCACTGAAATCAATGAAGACCTCAATATAGCTG
 1 M E I K V L F A L I C I A V A E A K P T E I N E D L N I A

BglII (426)
 401 CTGTGGCCTCCAACCTTGGCCACCACAGATCTTGAGACTGACCTGTTACCAACTGGGAGACCATGAATGTGATTAGCACTGACACAGAGCAGGTGAACAC
 30 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 T D T E Q V N T
 501 AGATGCTGACAGGGGCAAGCTGCCTGGCAAAAACTCCCCCAGATGTCTGAGGGAGCTGGAGGCCAATGCCAGAAGGGCTGGTTGCACAAGAGGCTGC
 63 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 R A G C T R G C
 601 CTCAATTTGCCTCTCCACATTAAGTGACCCCTAAGATGAAGAAATTTATCCCTGGCAGGTGCCACACTTATGAAGGTGAAAAGGAGTCTGCTCAGGGAG
 97 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 E K E S A Q G
 701 GGATTGGAGAGGCAATTGTTGATATCCAGAGATTCTGGCTCAAGGATAAGGAGCCACTGGACCAGTTATTGCTCAAGTGGACCTCTGTGCTGATTG
 130 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 Q V D L C A D C
 801 CACCACTGGCTGTCTGAAGGGCTTGCCAATGTCCAGTGTCTGACCTCCTGAAGAAAGTGCTTCCCAGAGGTGTACCACCTTTGCCAGCAAGATTGAG
 163 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 T T F A S K I Q

NheI (945)
 901 GGTAGGGTGGACAAAATCAAGGGTCTGGCTGGGACAGATGATAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTGGACAAACCACAACCTAG
 197 G R V D K I K G L A G D R •

1001 AATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAACAAACAATTCG

1101 ATTCATTTTATGTTTCAGGTTTCAGGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTAATTCTAAAATACAGCA

1201 TAGCAAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCT
 1301 GTTTGACGCCTCACCTCTTTTATGGAGTTAAGATATAGTGTATTTTCCCAAGTTTGAAGTACCTCTTCAATTTCTTTATGTTTTAAATGCACTGACCT

SspI (1424)
 1401 CCCACATCCCTTTTATGATAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGC
 1501 CCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTTGGACAGCAAGAAAGCGAGCTTCTAGCTTATCCTCAG
 125 •

1601 TCCTGCTCTCTGCCACAAAGTGACGCAGTTGCCGGCCGGGTGCGCGAGGGGCAACTCCCGCCCCACGGCTGCTCGCCGATCTCGGTCATGGCCGGCC
 123 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 G I E T M A P G
 1701 CGGAGGCGTCCCGAAGTTCGTGGACACGACCTCCGACCACTCGCGGTACAGCTGCTCAGGCGCGCACCCACACCCAGGCCAGGGTGTGTCGGGCAC
 90 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 W A L T N D P V

SgrAI (1852)
 1801 CACCTGGTCTGGACCGCTGATGAACAGGGTCACGTCGTCCCGGACCACCCGGCGAAGTCCGCGGAGAACCCGAGCCGGTCCG
 57 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 D R S F G L R D
 1901 GTCCAGAAGTCCAGCGCTCCGGCGACGTGCGCGCGGTGAGCACCGGAACGGCACTGGTCAACTTGGCCATGATGGCTCCTCTGTCTCAGGAGAGGAAAGA
 23 T W F E V A G A V D R A T L V P V A S T L K A M

PstI (2088)
 2001 GAAGAAGGTTAGTACAATTGCTATAGTGAGTTGTATTATACTATGCAGATATACTATGCCAATGATTAATTGTCAAACTAGGGCTGCAGGTTAATTAAGA

2101 ACATGTGAGCAAAAAGGCCAGCAAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAA
 ←

2201 TGCAGCTCAAGTCAAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTG

2301 CCGTTACCGGATACCTGTCCGCTTTCTCCCTCGGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCT

2401 CCAAGCTGGGCTGTGTGCACGAACCCCGTTCCAGCCGACCCTGCGCCTTATCCGTAACCTATCGTCTTGTAGTCAACCCGGTAAGACACGACTTATC

2501 GCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGTACAGAGTTCTTGAAGTGGTGGCTAACTACGGCTACACTAGA

2601 AGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAACCACCCTGGTAGCGGTG

2701 GTTTTTTTGTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGAAAA

2801 CTCACGTAAAGGATTTTGGTATGGCTAGTTAATTAACATTTAAATCA