



EcoRI (19)
1 **NotI (2)** **XbaI (15)** **SdaI (29)** **SpeI (36)**
CGCGCGCTATGCATCTAGAATTCTGCAGGGCCCATAGTTTCATCACCACCGCCACCCCCCGCCCCCGCCATCTGAAAGGTTCTAGGGGATTTG

101 CAACCTCTCTCGTGTGTTTCTTTCCGAGAAGCGCCGCCACACGAGAAAGCTGGCCGCGAAAGTCGTGCTGGAATCACTTCCAACGAAACCCAGGCA

NcoI (229) **BspEI (274)**
201 TAGATGGGAAAGGGTGAAGAACACGTTGCCATGGCTACCGTTTCCCGGTACGGAATAAACGCTCTCTAGGATCCGGAAGTAGTTCGCCCGACCTCT

301 **MluI (386)** **SacII (402)**
CTAAAAGGATGGATGTGTTCTCTGCTTACATTATTGGACGTTTTCCCTTAGAGGCCAAGGCCAGGCAAAGGGCGGTCCCACGCGTGAGGGGCC

BstXI (414) **BstEII (469)**
401 CGCGAGCCATTTGATTGGAGAAAAGCTGCAAACCTGACCAATCGAAAGGAGCCACGCTTCGGGCATCGGTCACCGCACCTGGACAGCTCCGATTGGTGG

501 ACTTCCGCCCCCTCACGAATCCTCATTGGGTGCCGTGGGTGCGTGGTGGCGCGATTGGTGGGTTTCATGTTTCCCGTCCCCGCCGCGAGAAGTGG

RsrII (640)
601 GGGTGAAGCGGCCGACCTGCTTGGGGTGTAGTGGCGGACCGCGGCTGGAGGTGTGAGGATCCGAACCCAGGGGTGGGGGTGGAGCGGCTCCT

PvuI (705) **BspHI (737)**
701 GCGATCGAAGGGGACTTGAGACTCACCGGCCGACGTCATGATGGAAATCAAGGTGCTGTTTGCCTCATCTGTATTGCTGTTGCTGAGGCAAAACCCAC

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

BglII (855)
801 TGAAATCAATGAAGACCTCAATATAGCTGCTGTGGCCTCCAACCTTGGCCACCACAGATCTTGAGACTGACCTGTTACCAACTGGGAGACCATGAATGTG
20 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
901 ATTAGCACTGACACAGAGCAGGTGAACACAGATGCTGACAGGGGCAAGCTGCCTGGCAAAAACTCCCCAGATGCTCTGAGGGAGCTGGAGGCCAATG
54 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
1001 CCAGAAGGGCTGGTTGCAACAAGAGGCTGCCTCATTGCTCTCCACATTAAGTGCACCCCTAAGATGAAGAAATTTATCCCTGGCAGGTGCCACACTTA
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 Y
1101 TGAAGGTGAAAAGGAGTCTGCTCAGGGAGGGATTGGAGGCAATTTGATATCCAGAGATTCTGGCTCAAGGATAAGGAGCCACTGGACCAGTTT
120 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
1201 ATTGCTCAAGTGGACCTCTGTGCTGATTGCACCACTGGCTGTCTGAAGGGCTTGCATGTCAGTGTCTGACCTCTGAAGAAGTGGCTTCCCCAGA
154 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 (1374)
1301 GGTGTACCACTTTTCCAGCAAGATTACGGGTAGGGTGGACAAAATCAAGGGTCTGGCTGGGGACAGATGATAGCTAGCTGGCCAGACATGATAAGATAC
187 R C T T F A S K I Q G R V D K I K G L A G D R •
1401 ATTGATGAGTTTGACAAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT

1501 GCAATAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATG

1601 TGGTATGGAATTAATTCTAAAATACAGCATAGCAAACTTTAACTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCA
1701 TCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTTTTCATGGAGTTTAAAGATATAGTGTATTTTCCCAAGGTTTGAACACTGCTCTTC

SspI (1853)
1801 ATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAAATTCAGAAATAATTTAAATACATCATTGCAATGAAAAAATGTTTT
1901 TTATTAGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGACTTAGGGAAACAAAGGAACCTTTAATAGAAATTGGACAGC
2001 AAGAAAGCGAGCTTCTAGCTTATCCTCAGTCTGCTCCTCTGCCACAAAGTGACGAGTTCGCGGCCGGGTGCGCAGGGGAACTCCCGCCCCACGG
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
2101 CTGCTCGCGATCTCGGTGATGGCCGGCCGGAGGCGTCCCGAAGTTCGTGGACAGACCTCCGACCACTCGGCGTACAGCTCGTCCAGGCCGCGCACCC
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 (2281)
2201 CACACCCAGGCCAGGGTGTGTCGGCACCACCTGGTCTGGACCGCGTGATGAACAGGGTACGTCGTCGGACCAACCCGCGAAGTCGTCCTCCA
66 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 V
2301 CGAAGTCCCGGAGAACCAGCGCGTGGTCCAGAACTCGACCGCTCCGGCGACGTCGCGCGCGGTGAGCACCGGAACGGCACTGGTCAACTTGGCCAT
33 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
2401 GATGGCTCCTCCTGTGAGAGAGAAAGAGAAGGTTAGTACAATTGCTATAGTGAGTTGATTATACTATGCAGATATACTATGCCAATGATTAATT

2501 GTCAAACTAGGGCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGG

2601 CTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCT

2701 CCCTCGTGCCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTTCTCCCTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAG

2801 GTATCTCAGTTCCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT

2901 GAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGA

3001 AGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATC

3101 CGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT

3201 ACGGGTCTGACGCTCAGTGAACGAAACTCACGTTAAGGGATTTGGTCATGGCTAGTTAATTAACATTTAAATCA
