



EcoRI (23)
NotI (2) **XbaI (19)** **SdaI (38)** **SpeI (45)**
1 CCGGCCGCTGACGATATCTAGAAATTCGGATCCTGCAGGGCCACTAGTGCCAAGAACATCTTAAGTCACAGAAACATTAGTTTTGGAAGCAGGTTT

101 GCTGTAACATAGTAGAAATGACATCTGATTCCTACTCTAGCTTACAAGGATATCTGTAAAGATTTGGGGCAAACTGTTAAGCTGTCTGAAAGTGC

201 TTTTGATAAAGAAATGGGTTTTACTGCTAAAAGTGCATATTGCTGAGTTTTGAATGCCCTAATGGTAAATGATACTGGTTGCCAAAAATAACAGATT

SspI (341)
301 AGTAGTTTTTTCATTCATTTGGCCGCTCTCAGTAAGTCAATATTGATACTTTCTACTAAGTCATCTTGCCAACACCCATTTTGTATACTATGCTGAAT

401 CTGTTTGTCTCTTAAGTAAGAAAATTATTGATTATTTTGGGGATTTAATTTAAAAAAAATGGTAAATGGTACTGTAAGGAGCATTATTTGGATG

501 GTTTAAAAACATCTTCTTGATGGGAAAATCTTTTAAAGGCTTCTAACTTGGTGAATTACTTGAATTAAGGAAGTCAATGCCATTCTACTGACTTA

601 GAACAACTTTTTGAATCTCTGCAAGAGGACCTTACAGTATTTTTGGAGAAGTTAGTAAAACCGAATCTGACATCATCACCTAGCAGTTCATGCAGCT **NheI (69)**

Ppu10I (771)
NsiI (776)
701 AGCAAGTGGTTGTTCTTAGGGTAACAGAGGAGGAAATTTGTTCTCGTCTGATAAGACAACAGTGGAGAgatgcatattattttacttttacat

SphI (868)
801 tgattcgtttttacagagaaaaacttctacagagataacaattatgtttcagAAGGACGCATGCTGTTTCTTAGGGACACGGCTGACTTCCAGAT

NcoI (905)
901 ATGACCATGGAAATCAAGGTGCTGTTTGCCTCATCTGATTGCTGTTGCTGAGGCAAAACCCACTGAAATCAATGAAGACCTCAATATAGCTGCTGTGG
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 A V

BglII (1020)
1001 CCTCCAACCTTTGCCACCACAGATCTTGAGACTGACCTGTTCCACCAACTGGGAGACCATGAATGTGATTAGCACTGACACAGCAGGTAACACAGATGC
32 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 D A
1101 TGACAGGGGCAAGCTGCTGGCAAAAACCTCCCCAGATGCTCTGAGGGAGCTGGAGGCCAATGCCAGAAGGGCTGGTTGCACAAGAGGCTGCCTCATT
65 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 L I
1201 TGCCTCTCCACATTAAGTGCACCCTAAGATGAAGAAATTTATCCCTGGCAGTGCCACACTTATGAAGGTGAAAAGGAGTCTGCTCAGGGAGGATTG
99 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 G I
1301 GAGAGGCAATGTTGATATCCAGAGATCTGGCTTCAAGGATAAAGGAGCCACTGGACCAGTTTATTGCTCAAGTGGACCTCTGTGCTGATTGCACCAC
132 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 T T
1401 TGGCTGTCTGAAGGGCTTGCATGCTCCAGTCTGACCTCTGAAGAAGTGGCTCCCCAGAGGTGATCCACTTTTGCACGCAAGATTCCAGGGTAGG
165 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 G R

NheI (1539)
1501 GTGGACAAAATCAAGGGTCTGGCTGGGACAGATGATAAGTCTGACGACAGATGATAAGATACATTGATGAGTTGGACAAAACCAACTAGAAATGCA
199 V D K I K G L A G D R •

1601 GTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACATTATAAGCTGCAATAAACAAGTTAACAACAACAAATGCAATTCAT

1701 TTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGTTTTTAAAGCAAGTAAAACCTCTACAATGTGGTATGGAATTAATTCTAAAATACAGCATAGCAA

1801 AACTTTAACCTCAAATCAAGCCTCTACTTGAATCTTTTCTGAGGATGAATAAGGCATAGGCATCAGGGGCTTTGCCAATGTGCATTAGCTGTTTGC
1901 AGCCTCACCTCTTTTCATGGAGTTTAAAGATAGTGATTTTTCCCAAGGTTTGAAGTCTTCTTATGTTTTAAATGCACTGACCTCCCA

SspI (2018)
2001 TTCCCTTTTATGATAAATATTCAGAAATAATTAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAAATCCAGATGCTCAAGGCCCTTCA
2101 TAATATCCCCAGTTTATGATGTTGACTTAGGGAACAAGGAACCTTAAATGAAATTTGGACAGCAAGAAAGCGAGCTTCTAGCTTATCTCAGTCTGCG
125 • D Q

2201 TCCTCTGCCAAAAGTGCACGAGTTGCCGGCCGGTCCGCGAGGGCAACTCCCGCCCCACGGCTGCTCGCCGATCTCGGTGATGGCCGGCCGGGAGG
121 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 S A
2301 CGTCCCGGAAGTCTGGGACACGACTCCGACCACTCGCGCTACAGCTGCTCCAGGCCGCGCACCCACCCAGGCCAGGGTGTGTCCGGCACCACCTG
88 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 V Q

SgrAI (2446)
2401 GTCCTGGACCGCGTGATGAACAGGGTACGCTGCTCCCGACCAACCGCGAAGTCTGCTCCACGAAGTCCCGGAGAACCCGAGCCGGTCCGTCCAG
55 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 T W
2501 AACTCGACCGCTCCGGCAGCTGCGCGCGGTGAGCACCAGGCAACGGCACTGGTCAACTGGCCATGATGGCTCCTCTGTCAGGAGAGGAAAGAGAAGAA
21 F E V A G A V D R A T L V P V A S T L K A M
2601 GGTAGTACAATGCTATAGTGAGTTGATTATACTATGCAGATATACTATGCCAATGATTAATTGTCAAAGTGGCTGAGGTTAATTAAGAACATGT
2701 GAGCAAAAGGCCAGAAAAGGCCAGGAACCGTAAAAGGCCGCTGTGCTGGCTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAAATCGAGC

2801 CTCAAGTCAGAGTGGCGAAAACCCGACAGGACTATAAAGATACAGGCGTTTTCCCTGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCTGCCGCTT

2901 ACCGGATACCTGTCCGCTTTCTCCCTCGGGAAGCGTGGCGTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCCGGTGTAGGCTGTTCCGCTCAAGC

3001 TGGGCTGTGTGCACGAACCCCGTTCAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGTGAGTCAACCCGGTAAGACACGACTTATCGCCACT

3101 GGCAGCAGCCACTGGTAACAGGATTAGCAGAGCAGGATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACA

3201 GTATTTGGTATCTCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTTTGATCCGGCAACAACACCAGCTGGTAGCGGTGTTTTT

3301 TTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACTCACG

3401 TTAAGGATTTTTGGTCATGGCTAGTTAATTAACATTTAATCA