



EcoRI (23)

NotI (2) XbaI (19) SdaI (38) SpeI (45) HindIII (55)

1 CGCGCCGCGTCGACGATATCTAGAATTCGGATCCTGCAGGGCCACTAGTGGCCAAGCTTAGAAACATGACAGGTCCTCTTGGGAGGGCTGACCGCAGGG
101 AGCGTTGGGTTTCAGGCTGTGGCGTCGGCTTCTGTGGTGCCTTTCTGTGGCTATGAGAGTCCAGACAGTGCCCAACCTCTCCCTTCTTTCCACAC
201 GCACAACCACCCACCCCTGTGGCCTGAGCTGTCTGCCTGCCACAATGGCACCTGCCCTAAAATAGCTTCCCATGTGAGGGCTAGAGAAAAGGAAAAAG
301 ATTAGACCTCCTGGATGAGAGAGAGAAAAGTGAAGGAGGGCAGGGGAGGGGACAGCGAGCCATTGAGCGATCTTTGTCAAGCATCCCAGAAGGTATAA

NotI (2)

401 AAACGCCCTTGGGACCAGGCAGCCCTCAAACCCAGCTGTTGGGGCCAGGACACCCAGTGAGCCATACTTGTCTTTTTGTCTTCTTCAGACTGGCCAT
501 GGTTCGGGGCCCTGCATGCTGCTGCTGCTGCTGCTGCTGGGCTGAGGCTACAGCTCTCCCTGGGCATCATCCCAGTTGAGGAGGAGAACCAGGACTTC
1 V L G P C M L L L L L L L L G L R L Q L S L G I I P V E E E N P D F
601 TGGAACCGCGAGGACGCGAGGCCCTGGGTGCCGCAAGAAGCTGCAGCCTGCACAGACAGCCGCAAGAACCTCATCATCTTCTGGGCGATGGGATGG
35 W N R E A A E A L G A A K K L Q P A Q T A A K N L I I F L G D G M

NdeI (792)

701 GGTGTCTACGGTACAGCTGCCAGGATCCTAAAAGGGCAGAAGAAGGACAAACTGGGCGCTGAGATACCCCTGGCTATGGACCGCTTCCCATATGTGGC
68 G V S T V T A A R I L K G Q K K D K L G P E I P L A M D R F P Y V A
801 TCTGTCCAAGACATACAATGTAGACAAACATGTGCCAGACAGTGGAGCCACAGCCACGGCTACCTGTGCGGGTCAAGGGCAACTTCCAGACCATTGGC
101 L S K T Y N V D K H V P D S G A T A T A Y L C G V K G N F Q T I G
901 TTGAGTGCAGCCGCGCTTAACCAAGTGAACACAGCAGCGGGCAACGAGGTCTCCGTGATGAATCGGGCAAGAAAGCAGGAAGTCAAGTGGGAG
135 L S A A A R F N Q C N T T R G N E V I S V M N R A K K A G K S V G
1001 TGGTAACCACACACGAGTGCAGCAGCCTCGCCAGCGGCACCTACGCCACACGGTGAACCGCAACTGGTACTCGGACGCGGACGTGCCTGCCTCGGC
168 V V T T T R V Q H A S P A G T Y A H T V N R N W Y S D A D V P A S A
1101 CCGCCAGGAGGGGTGCCAGGACATCGTACGCAGCTCATCTCAAATGGACATTGATGTGATCCTGGGTGGAGGCGAAAGTACATGTTTCGCATGGGA
201 R Q E G C Q D I A T Q L I S N M D I D V I L G G G R K Y M F R M G
1201 ACCCCAGACCTGAGTACCCAGATGACTACAGCAAGGTGGGACCAGGCTGGACGGGAAGAATCTGGTGCAGGAATGGCTGGYAGCGCCAGGTTGCC
235 T P D P E Y P D D Y S Q G G T R L D G K N L V Q E W L A K R Q G A
1301 GGTATGTGTGAACCGCACTGAGCTCATGCAGGCTCCCTGGACCGTGTGTACCATTCTCATGGTCTCTTTGAGCCTGGAGACATGAAATACGAGAT
268 R Y V W N R T E L M Q A S L D P S V T H L M G L F E P G D M K Y E I

SacII (1479)

1401 CCACCGAGACTCCACACTGGACCCCTCCTGATGGAGATGACAGAGGCTGCCCTGCGCTGCTGAGCAGGAACCCCGCGGCTTCTCTCTTCGTGGAG
301 H R D S T L D P S L M E M T E A A L R L L S R N P R G F F L F V E
1501 GGTGGTCGCATCGACACCGTTCATCACGAAAGCAGGGCTTACCGGCACTGACTGAGACGATCATGTTCCAGCAGCCATTGAGAGGGCGGGCCAGCTCA
335 G G R I D H G H H E S R A Y R A L T E T I M F D D A I E R A G Q L
1601 CCAGCGAGGAGGACAGCTGAGCCTGCTACTGCCAGCCTCCACGTCTTCTCTCGGAGGCTACCCCTGCGAGGCTCCATCTTCGGGCTGGC
368 T S E E D T L S L V T A D H S H V F S F G G Y P L R G S S I F G L A
1701 CCCTGGCAAGGCCGGGACAGGAAGCCTACACGGTCTCCTATACGAAACGGTCCAGGCTATGTGCTCAAGGACGGCGCCGGCCGGATGTTACCGAG
401 P G K A R D R K A Y T V L L Y G N G P G Y V L K D G A R P D V T E
1801 AGCGAGAGCGGGAGCCCGAGTATCGGCAGCAGTCAAGTGGCCCTGGACGAAGACCCACGCAGGCGAGGAGCTGGCGGTGTTTCGCGCGCGCCCGC
435 S E S G S P E Y R Q Q S A V P L D E E T H A G E D V A V F A R G P
1901 AGGCGCACCTGGTTCACGGCGTGCAGGAGCAGACCTTCATAGCGACGTGATGGCCTTCGCGCCTGCTGGAGCCCTACACCGCTGCGACCTGGCGCC
468 Q A H L V H G V Q E Q T F I A H V M A F A A C L E P Y T A C D L A P

NheI (2063)

2001 CCCC CGCGCACCACCGACCGCGCACCCGGGGCGGTCCCGGTCCAAGCGTCTGGATTGAAGCTAGCTGGCCAGACATGATAAGATAACATTGATGAGTT
501 P A G T T D A A H P G R S R S K R L D
2101 TGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAA

MfeI (2212)

2201 GTTAACAACAACAATTGCATTATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAAACTCTACAAATGTGGTATGGAAT
2301 TAATTCTAAAATACAGCATAGCAAAACTTTAACTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGT
2401 TGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAAGATATAGTGTATTTTCCCAAGGTTTGAACAGCTCTTCATTCTTTATG
2501 TTTTAAATGCACTGACCTCCACATTTCCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAG
2601 AATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTAGTAGTTGACTTAGGGAACAAAGGAACCTTAAATAGAAATTGGACAGCAAGAAAGCGAG
2701 CTTCTAGCTTATCCTCAGTCTCCTCTGCCCACAAGTGCAGCAGTTGCGCGGGTGCAGGCGGCTCAGGCGGCACTCCCGCCACAGGCTCTCGCCGA
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 G I
2801 TCTCGGTCATGGCCGGCCGGAGGCGTCCCGGAAGTTCGTTGGACACGACCTCCGACCACTCGGCGTACAGCTCGTCCAGGCGCGCACCCACACCCAGGC
96 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 W V W A

SgrAI (2970)

2901 CAGGGTGTGTTCGGCACCACTGGTCTGGACCGCGCTGATGAACAGGGTCACTGCTGCCGACCAACCGGCAAGTCTCTCCACGAAGTCCCGG
63 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 D R
3001 GAGAACCCGAGCCGTCGGTCCAGAACTGACCGCTCCGGCGACGTGCGCGCGGTGAGCACCAGGAACTGGTCAACTGGCCATGATGGCTCCTC
29 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

MfeI (3133)

3101 CTGTGAGGAGGAAAGAGAAGAAGGTTAGTACAATTGCTATAGTGAGTTGATTATACTATGCAGATATACTATGCCAATGATTAATTGTCAAAGTAGG
3201 GCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCTTTTTCCATAGGCTCCGCCCC
3301 TGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCTTTCCCTGGAAGCTCCCTCGTGGC
3401 TCTCTGTTCCGACCCTGCCGTTACCGGATACTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTT
3501 CGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCAGCCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGTAGTCCAACCC
3601 GGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGTTAACAGGATTAGCAGGAGGATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCT

3701 AACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAA
3801 CCACCGCTGGTAGCGGTGGTTTTTTTGGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGA
3901 CGCTCAGTGGAACGAAAACACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCA