



Bsp120I (6)
PstI (6)
SdaI (6) SpeI (13)
1 CCTGCAGGGCCaCTAGtGTTTCATCGGAGCCAGGTTTACTCCCTTAAGTGAAATTTCTTCCCCACTCCCTCCTTGGCTTTCTCCAAGGAGGAAACC

101 AGGCTACTGAAAGTCCGGCTGGGCGGGGACTGTGGTTCAGGGTAGAACTGCGTGTGGAACGGGACAGGAGCGTTAGAAGGTGGGCTATTCCG

201 GGAAGTGGTGGGGGAGGAGCCAAAAGTAGCACCTAGTCCACTCATTATCCAGCCCTTATTCTCGGCCCCGCTCTGCTTCACTGACCCGGGAG

301 GCGCGGGAAGTGGAGTGGGAGACCTAGGGTGGGCTTCCGACCTTGTGTACAGGACCTGCACCTAGCTGGCTTTGTTCCCATCCCCACGTTAGTTGT

401 TGCCCTGAGGCTAAACTAGAGCCAGGGGCCCAAGTTCAGACTGCCCTCCCCCTCCCCGGAGCCAGGGAGTGGTGGTAAAGGGGGAGGCCAG

501 CTGGAGAACAACGGGTAGTCAGGGGTTGAGCGATTAGAGCCCTGTACCTACCCAGGAATGTTGGGGAGGAGGAGGAAGAGGTAGGAGGTAGGGGA

601 GGGGGCGGGTTTTGTCACTGTCACTGCTCCGGTGTGCTAGGGCGGGCGGGGAGTGGGGGACCGGTATAAAGCGGTAGGCCCTGTGCCG

701 CTCACCTCTCAAGCAGCCAGCGCTGCCTGAATCTGTTTCCGCCCTCCCCACCCATTTACCACCACCATGGGGGTTCTCATCATCATCATCAT

801 GGTATGGCTAGCATGACTGGTGGACAGCAATGGGTCGGGATCTGTACGACGATGACGATAAGGTACCTAAGGATCAGCTTGGAGTTGATCCCGTCGTT

901 TACAACGTCGTGACTGGGAAAACCTGGCGTTACCCAACTAATCGCTTGCAGCACATCCCCCTTCCGACGCTGGCGTAATAGCGAAGGCCCCGCAC

1001 CGATCGCCCTCCCAACAGTTGCGCAGCCTGAATGGCAATGGCGTTCGCTGGTTCCGGCACCAGAAGCGGTGCCGAAAGCTGGCTGGAGTGGCAT

1101 CTTCTGAGGCGGATGCTGCTGCTCCCTCAAAGTGGCAGATGCACGGTACGATGCGCCATCTACACCAACGTAACCTATCCATTACGGTCAATC

1201 CGCGCTTTGTTCCACGAGAAATCCGACGGGTTGTTACTCGCTCACATTTAATGTTGATGAAAGCTGGCTACAGGAAGCCAGACGCAATATTTTTGA

1301 TGGCTTAACTCGCGCTTTCATCTGTGGTGCACGCGCTGGTTCGGTACGGCCAGGACAGTCGTTTGGCGTCTGAATTTGACCTGAGCGCATTTTTA

1401 CGCGCCGAGAAAACCGCTCGCGGTGATGGTGTGCTGGTGGAGTGACGGCAGTTATCTGGAAGATCAGGATATGTGGCGGATGAGCGGCATTTTCCGTG

1501 ACGTCTCGTTGCTCATAAACCGACTACACAAATCAGCGATTTCCATGTTGCCACTCGCTTAAATGATGATTTACGCGCGCTGTACTGGAGGCTGAAGT

1601 TCAGATGTGCGCGAGTTCGCTGACTACCTACGGGTAACAGTTTCTTATGGCAGGGTAAACGCAAGTCCGACGCGCCAGCGCCTTTCCGGCGGTGAA

1701 ATTATCGATGAGCGTGGTGGTATGCCGATCGCGTCACTACGCTGACAGCTCGAAAACCGAAACTGTGGAGCGCCGAAATCCCGAATCTCTATCGT

1801 CGGTGTTGAACTGCACCCCGACGCGCTGATTGAAGCAGAAGCCTGCGATGTCGTTTCCGCGAGGTCGGATGAAATGGTCTGCTGCTGCT

1901 GAACGGCAAGCCGTTGCTGATTCGAGGCGTTAACCGTACGAGCATCATCTCTGATGGTCAAGTCATGGATGAGCAGACGATGGTGCAGGATATCCTG

2001 CTGATGAAGCAGAACAACCTTAAACCGCGTGCCTGTTCCGATTATCCGAACCATCCGCTGTGGTACACGCTGTGCGACCGCTACGGCCTGTATGTGGTG

2101 ATGAAGCCAATATTGAAACCCACGGCATGGTGCATGAATCGTCTGACCGATGATCCGCGCTGGCTACCGCGATGAGCGAACCGCTAACGCAATGGT

2201 GCAGCGCGATCGTAATCACCCGAGTGTGATCATCTGCTGCTGGGAATGAATCAGGCCACGGCGCTAATCACGACGCGCTGATCGCTGGATCAATCT

2301 GTCGATCCTTCCCGCCGGTGCAGTATGAAGCGGGCGGAGCCGACACCACCGCATATTATTTCCCGATGATCGCGCGGTGGATGAAGACCGAGC

2401 CCTTCCCGGCTGTGCCGAAATGGTCCATCAAAAATGGCTTTCGCTACTGGAGAGACGCGCCGCTGATCCTTTGCAATACGCCACCGGATGGGTAA

2501 CAGTCTTGGCGTTTCGTAATAACTGGCAGCGTTCGTCAGTATCCCGTTTACAGGGCGGCTTTCGCTGGGACTGGTGGATCAGTCTGCTGATTA

2601 TATGATGAAAACGGCAACCCGTTGCTGCGCTTACGGCGGTGATTTGGCGATACGCCAAGCATGCCAGTTCTGTATGAAGGCTGGTCTTTGCCGACC

2701 GCACCGCGATCCAGCGTACGGAAGCAAAACACCAGCAGGTTTTTCCAGTTCGGTTTATCCGGGCAACCATCGAAGTGACCAGCGAATACCTGTT

2801 CCGTCATAGCGATAACGAGCTCCTGCACTGGATGGTGGCTGGATGTAAGCCGCTGGCAAGCGGTGAAGTGCCTCTGGATGCTCCACAAGGTAA

2901 CAGTTGATTGAACCTGCCTGAACCTACCGCAGCCGAGAGCCGCGGCAACTGCTGCTACAGTACGCTAGTGAACCGAAGCGGACCGCATCGAGA

3001 CCGGACACATCAGCGCTGCGCAGCAGTGGCGTCTGGCGGAAACCTCAGTGTGACGCTCCCGCGCGTCCACGCCATCCCGCATCTGACCCAGGCA

3101 AATGATTTTTGCATCGAGTGGGTAATAAGCGTTGGCAATTTAACGCCAGTCAGGCTTTCTTTCACAGATGTGGATTGGCGATAAAAAACAATGCTG

3201 ACGCCGCTGCGGATCAGTTCACCCGTCACCCGCTGGATAACGACATTTGGCGTAAGTGAAGCGACCCGATTGACCCTAACGCTGGTGGTGAAGCGTGG

3301 AGGCGCGGGCCATTACAGCGGAAGCAGCGTGTGGTGCAGTGCACGGCAGATACACTTGTGATGCGGTGCTGATTACGACCGCTCAGCGTGGCAGCA

3401 TCAGGGGAAAACCTTATTATCAGCCGAAAACCTACCGGATTGATGGTCAAAATGGCGATTACCGTTGATGTTGAAGTGGCGAGCGGATACACCG

3501 CATCCGGCGCGGATTGGCCTGAACCTGCCAGCTGGCGCAGTACGAGAGCGGGTAAACTGGCTCGGATAGGGCGCAAGAAAACCTACCCGACCGCCTTA

