



**EcoRI (23)**  
1 **NotI (2)** **XbaI (19)** **SdaI (38)** **SpeI (45)**  
1 **GCGGCCGCGTCGACGATATCTAGAATTCGGATCCTGCAGGCCCACTAGTATAGGGCTGTCTGGGAGCCACTCCAGGGCCACAGAAATCTTGTCTCTGAC**  
101 **TCAGGGTATTTTGTCTTCTGTTTGTGTAATGCTCTTCTGACTAATGCAAACCATGTGTCCATAGAACCAGAAGATTTTCCAGGGGAAAAGGTAAGGA**  
**SfiI (295)**  
201 **GGTGGTGAGAGTGTCTGGTCTGCCCTTCCAGGGCTTCCCTGGGTTAAGAGCCAGGCAGGAAGCTCTCAAGAGCATTGCTCAAGAGTAGAGGGGGCCT**  
301 **GGGAGGCCAGGGAGGGGATGGGAGGGGAACCCAGGCTGCCCCCAACCAGATGCCCTCCACCCTCTCAACCTCCCTCCACGGCCTGGAGAGGTGGG**  
401 **ACCAGGTATGGAGGCTTGAGAGCCCTGGTTGGAGGAAGCCACAAGTCCAGGAACATGGGAGTCTGGGCAGGGGGCAAAGGAGGCAGGAACAGGCCATCA**  
501 **GCCAGGACAGGTGTAAGGCAGGCAGGAGTGTTCCTGCTGGGAAAAGGTGGGATCAAGCACCTGGAGGGCTCTTCAGAGCAAAGACAAACACTGAGGTGC**  
**NcoI (682)**  
601 **CTGCCACTCTACAGAGCCCCACGCCCGCCAGCTATAAGGGCCATGCACCAAGCAGGGTACCCAGGCTGCAGAGGTGCCATGGTTCTGGGGCCCTG**  
701 **CATGCTGCTGCTGCTGCTGCTGGGCTGAGGCTACAGCTCTCCCTGGGCATCATCCCAGTTGAGGAGGAGAACCCGGACTTCTGGAACCCGCGAGGCA**  
801 **GCCGAGGCCCTGGTGGCCCAAGAAGCTGCAGCCTGCACAGACAGCCGCCAAGAACCCTCATCTTCTGGCGATGGGATGGGGTGTCTACGGTGA**  
901 **CAGCTGCCAGGATCCTAAAAGGGCAGAAGAAGGACAAACTGGGGCTGAGATACCCCTGGCTATGGACCGCTTCCCATATGTGGCTCTGTCCAAGACATA**  
1001 **CAATGTAGACAAACATGTGCCAGACAGTGGAGCCACAGCCACGGCTACCTGTGCGGGTCAAGGGCAACTTCCAGACCATTGGCTTGAGTGCAGCCGCC**  
1101 **CGCTTAAACAGTGCACACGACACGCGGCAACGAGGTCATCTCCGTGATGAATCGGGCCAAAGAAAGCAGGGAAGTCACTGGGAGTGGTAACCACCACAC**  
1201 **GAGTGACGACGCTCGCCAGCCGACCTACGCCACACGGTGAACCGCAACTGGTACTCGGACCGCAGCTGCCTGCCTCGGCCCGCAGGAGGGGTG**  
1301 **CCAGGACATCGTACGACGCTCATCTCAACATGGACATTGATGTGATCTGGGTGGAGGCCAAAGTACATGTTTCGCATGGGAACCCAGACCCTGAG**  
1401 **TACCCAGATGACTACAGCCAAGGTGGGACCAGGCTGGACGGGAAGAATCTGGTGCAGGAATGGCTGGCGAAGCCAGGGTGCCTGGTATGTGTGGAACC**  
1501 **GCACGTGAGCTCATGCAAGCTTCCCTGGACCCGCTGTGACCCATCTCATGGGCTCTTTGAGCCTGGAGACATGAAATACGAGATCCACAGACTCCAC**  
1601 **ACTGGACCCCTCCCTGATGGAGATGACAGAGGCTGCCCTGCGCTGCTGAGCAGGAACCCCGCGGCTTCTTCTCTCGTGGAGGGTGGTCGCATCGAC**  
1701 **CACGTGCATCACGAAAGCAGGGCTTACCGGCACTGACTAGACGATCATGTTTCGACGACGCCATTGAGAGGGCGGCCAGCTCACCAGCGAGGAGGACA**  
1801 **CGCTGAGCCTCGTCACTGCCGACCACTCCACGCTTCTCCTTCCGAGGCTACCCCTGCGAGGGAGCTCCATCTTCCGGGCTGGCCCTGGCAAGGCCCG**  
1901 **GGACAGGAAGGCTACACGGTCTCTATACGAAACGGTCCAGGCTATGTGCTCAAGGACGGCGCCCGCCGGATGTTACCAGAGCGAGAGCGGGAGC**  
2001 **CCCCAGTATCGGCAGCAGTCAAGTGCCTGGACGAAAGAGACCCAGCAGGCGAGGACGTGGCGGTGTTCCGCGCGGCCCGCAGGCGCACCTGGTTC**  
2101 **ACGGCGTGCAGGAGCAGACCTTCATAGCGACGTCATGGCCTTCCCGCCTGCTGGAGCCCTACACCGCTGCGACCTGGCGCCCCCGCGGCACCAC**  
2201 **CGACGCCGCGCACCCGGGGCGTCCCGTCAAGCGTCTGGATTGAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAAC**  
2301 **TAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAAT**  
2401 **TGCATTCAATTTATGTTTACAGTTACAGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTAATTCTAAAATACA**  
2501 **GCATAGCAAAACTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTA**  
2601 **GCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGGTTTGAACACTGCTTTCATTTCTTTATGTTTTAAATGCACTGA**  
2701 **CCTCCACATTCCTTTTGTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAA**  
2801 **GGCCCTTCAATAATCCCCAGTTTGTAGTTGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTATCCT**  
2901 **CAGTCTGCTCTCTGCCACAAAGTGCACGAGTTGCCGGCGGGTGCAGCAGGGGCAACTCCCGCCCCACGGCTGCTCGCGATCTCGGTATGGCCG**  
3001 **GCCGGAGGCGTCCCGAAGTTCTGTTGACACGACCTCCGACCACTGGCGTACAGCTCGTCCAGGCGCGCACCCACACCCAGGCGAGGGTGTGTCGG**  
3101 **CACCACCTGGTCTGGACCGCTGATGAACAGGGTACGCTGCTCCCGACACACCGCGCAAGTCTCCTCCACGAAGTCCCGGGAGAACCAGGCGCCG**  
3201 **TCGGTCCAGAACTCGACCTCCGCGACCTCGCGCGGTGAGCACCAGGAAAGGCAAGTGGTCAACTGGCTCCTCTCTGTCAGGAGAGGAA**  
324 **spThr TrpPheGl uValAl aGl yAl aVal AspArgAl aThr LeuVal P roValAl aSer Thr LeuLysAl aMet**

3301 AGAGAAGAAGGTTAGTACAATTGCTATAGTGAGTTGTATTATACTATGCAGATATACTATGCCAATGATTAATTGTCAAACTAGGGCTGCAGGTTAATTA  
3401 AGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGGCTGGCGTTTTTTCATAGGCTCCGCCCCCTGACGAGCATCACAA  
←  
3501 AAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACC  
3601 CTGCCGTTACCGGATACCTGTCCGCCTTCTCCCTTCGGGAAGCGTGGCGCTTTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTT  
3701 GCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGTAAGACACGACTT  
3801 ATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACT  
3901 AGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGTGGTAGCG  
4001 GTGGTTTTTTTGGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTCTACGGGGTCTGACGCTCAGTGAACGA  
4101 AAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCA