



**EcoRI (23)**  
**NotI (2)** **XbaI (19)** **SdaI (38)** **SpeI (45)**  
1 CCGGCCCGCTGACGATATCTAGAAATTCGGATCCTGCAGGGCCACTAGTAACAGCTGCAAGTCGTGGATATTTTATGGGTTTTCTCCTCACAAAATA  
101 CACTCTATAAGCAGAGATCCCCCCCACCCCCAAGAGAGGTGACGCAATGTCTCAAACACTACCACCACCCCAATAAAAAAGAAAGGAAGGG  
201 GGAGCGTCTTGAACCCCTTCGCTTACACAAGTCAGCCACTCCCTTTCTCCAGCGCTTCCCATCCCTTCCCCATCCCTAAAAAGTTTGATGAC  
301 CGCAAAGGAAACCGAAAAAAGTTGTCTTGCCTGCTGGCGGGCCATCAGCATCTCTTTTGTCTGCTGCGAACCCACAGTCCCCCGTGACGTACCC  
401 GGAGCCCGGGCAATCGCGCGCGGTGCTGCGCGCGCGGGCGGGCGGGTGGGGTGGGGCGGGCGGGACAGCCCGGGGTCTCTCTCCCC  
501 CGCCCCGGGCTCCAGAGGGCGGGAGGGACCGTCCATATAAGCCCCGGTCCCGGCTCGACGCCCGCGCGGTGTGCTGCACAGGGGGAGGA  
601 GAGGGAACCCAGGCGGAGCGGGAAGAGGGGACCTGCAGCCACAACCTTCTGTGCTCTGCATCCCTTGTCTCCACCCGTCCTCTCCCCACCC  
**BstXI (716)**  
701 TCTGGCCCCACCTTCTTGAGGCGACAACCCCGGAGGCATTAGAAGGATTTTTCCGCAGGTTGCGAAGGGAAGCAAACCTTGGTGGCAACTTGCCT  
**Neol (833)**  
801 CCCGGTGGGGCGTCTCTCCCCACCGTCTCACCATGGAAATCAAGGTGCTGTTGCCCTCATCTGATTGCTGTGCTGAGGCAAACCCACTGAAATC  
1 M E I K V L F A L I C I A V A E A K P T E I  
**BglII (948)**  
901 AATGAAGACCTCAATATAGCTGTGTGCCCTCCAACCTTTGCCACCACAGATCTTGAGACTGACCTGTTACCAACTGGGAGACCATGAATGTGATTAGCA  
23 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 I S  
1001 CTGACACAGACAGGTGAACACAGATGCTGACAGGGGCAAGCTGCTGGCAAAAACTCCCCCAGATGTCTGAGGGAGCTGGAGGCAATGCCAGAAG  
56 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 A R R  
1101 GGCTGGTGCACAAGAGGCTGCCTCATTGCTCTCCACATTAAGTGCACCCCTAAGATGAAGAAATTTATCCCTGGCAGGTGCCACATTATGAAGGT  
89 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 E G  
1201 GAAAAGGAGTCTGCTCAGGAGGATTGGAGAGCAATTGTTGATATCCAGAGATTCCTGGCTTCAAGGATAAGGAGCCACTGGACCAGTTTATTGCTC  
123 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 I A  
1301 AAGTGGACCTGTGCTGATTGCACCACTGGCTGTGAAGGGCCTTGCATGTCCAGTGTCTGACCTCTGAAGAAGTGGCTTCCCCAGAGGTGTAC  
156 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 R C T  
**NheI (1467)**  
1401 CACTTTTCCAGCAAGATTGAGGTAGGGTGGACAAAATCAAGGGTCTGGCTGGGACAGATGATAGCTAGCTGGCCAGACATGATAAGATACATTGATG  
189 T F A S K I Q G R V D K I K G L A G D R •  
1501 AGTTTGGACAAACCAACTAGAAATGCAAGTGAAGAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGTGAATAA  
1601 ACAAGTTAAACAACAATTCATTATTTATGTTTTCAGGTTTCAGGGGAGGTGTGGGAGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATG  
1701 GAATTAATCTAAAATACAGCATAGCAAAACCTTAACCTCCAATCAAGCCTCTACTGAAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGG  
1801 CTGTTGCCAATGTGATTAGCTGTTTGCAGCCTCACCTTCTTTCATGAGTAAAGATATAGTATTTTCCCAAGGTTTGAAGTAGCTCTTCATTTCTT  
**SspI (1946)**  
1901 TATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAG  
2001 CGAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAGGAACTTTAATAGAAATTTGGACAGCAAGAAAG  
2101 CGAGCTTCTAGCTTACTCTCAGTCTGCTCTCTGCCACAAAGTGCACGAGTTCGCCGCGGGTCCGCGAGGCGAACTCCCGCCCCACGGCTGCTCG  
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  
2201 CCGATCTCGGTATGGCGGCGCGAGGCGTCCCGAAGTTCGTGGACACGACCTCCGACACTCGGCGTACAGTCTGTCAGGCGCGCACCCACACCC  
97 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 W V W  
**SgrAI (2374)**  
2301 AGGCCAGGGTGTGTCCGGCACCCCTGGTCTGGACCGCGTGTGAACAGGGTCCAGTCTGTCGCGGACACACCGGCAAGTCTGCTCCACGAAGTC  
64 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 F D  
2401 CCGGGAGAACCAGCGCGTCCGAGACTCGACCGCTCCGCGCAGCTCGCGCGGTGAGCACCAGGAAAGGCACTGGTCAACTGGCCATGATGGCT  
31 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  
2501 CCTCCTGTGAGGAGGAAAGAGAAGGTTAGTACAATGCTATAGTGTGATTGATTATACATATGAGATATACTATGCAATGATTAATTGTCAAAC  
2601 TAGGGCTCAGGTTAATTAAGAATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCC  
2701 CCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGACTATAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGT  
2801 GCGCTCTCTGTTCCGACCCTGCGCTTACCGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGTTTCTCATAGCTCAGCTGTAGGTATCTC  
2901 AGTTCGGTGTAGGTGTTGCTCCAAGTGGGTGTGTGACGAACCCCGTTCAGCCGACCGTGCCTTATCCGGTAACTATCGTCTTGAGTCCA  
3001 ACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGT  
3101 GCCTAACTACGGCTACACTAGAAGAAGTATTTGGTATCTGCGCTGCTGTAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAA  
3201 CAAACCACCGCTGTAGCGGTGTTTTTTTGTGCAAGCAGCAGATTACCGCAGAAAAAAGGATCTCAAGAAGATCCTTGATCTTTCTACGGGGT  
3301 CTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCA