



**EcoRI (23)**  
**NotI (2)** **XbaI (19)** **SdaI (38)**  
1 GCGGCCGCGTCGACGATATCTAGAATTCGGATCCTGCAGGGCCCACTGAGCCACAGCCTAAGGCAGTGGACAGTCCACTTTGAGGCTCTCACCATCTA  
101 GGAGACATCTCAGCATGAACATAGCCACATCTGTCTATTAGAAAACATGTTTTATTAAGAGGAAAAATCTAGGCTAGAAGTCTTTATGCTCTTTTTCT  
201 CTTTATGTTCAAATTCATATACTTTTAGATCATTCTTAAGAAGAATCTATCCCCTAAGTAAATGTTACTACTGACTGGATAGTGTGGTGTCTCACT  
301 CCCAACCCCTGTGTGGTACAGTGCCTCTCCAGCCCTGGCCCTCTCTGATTCTGAGAGCTTTGGGTGCTCCTCATTAGGAGGAAGAGAGGAA  
401 GGGTGTTTTTAATATTCTCACCATTACCCATCCACCTCTTAGACACTGGGAAGAATCAGTTGCCACTCTTGGATTTGATCCTCGAATTAATGACCTCT  
501 ATTTCTGTCCCTGTCCATTTCAACAATGTGACAGGCCTAAGAGGTGCCTTCTCCATGTGATTTTTGAGGAGAAGTTCTCAAGATAAGTTTTCTCACAC  
601 CTCTTTGAATTACCTCCACCTGTGTCCCATCACCATTACCAGCAGCATTGGACCCTTTTTCTGTTAGTCAGATGCTTCCACCTCTGAGGGTGTATA  
701 CTGTATGCTCTCTACACAGGAATATGACAGGAAATAGAAAAGGAAATCGCATTACTATTAGAGAGAAGAAGACCTTTATGTGAATGAATGAGAGTC  
801 TAAAATCTAAGAGAGCCATATAAAAATTATTACCAGTCTAAAACACAAAAGTTACACTAACAGTAACTAGAATAATAAAAACATGCATCACAGTTGC  
901 TGGTAAAGCTAAATCAGATATTTTTTCTTAGAAAAGCATTCCATGTGTGTTGAGTGTGACAGGAGTGCCTTCAGTCAATATGCTGCCTGTAATTT  
**PvuII (1090)**  
1001 TTGTTCCCTGGCAGAATGATTGTCTTTCTCCCTTTAAATCTTAAATGCAAACTAAAGGCAGCTCTGGGCCCTCCCAAAGTCAGCTGCCTGCAA  
1101 CCAGCCCCACGAAGACAGAGGCTGAGCTCCCTGGTCAAATAGGGGGCTAGGGAGCTTAACCTCGCTCGATAAAGCTGTGTCCCAAGTGTCTGCTC  
1201 CTGTTCCAGGGCACCAGCCTGGAGGGTGGTGGCTCACTGGTGGCTGATGCTTACCTTGTGCCCTCACACCAGTGGTCACTGGAACCTTGAACACT  
1301 TGGCTGTCGCCGGATCTGCAGATGCAAGAACTCTGGAAGTCAAATACTGCCAATTCTCCAGGGCAGATACCTGTGAACATCCAAAACCATGCCAC  
**NdeI (1427)**  
1401 AGAACCTGCCTGGGGTCTACAACACATATGGACTGTGAGCACCAAGTCCAGCCCTGAATCTGTGACCACCTGtCTAGTGCCTGGAGAGCATGGGGAGA  
1501 CCCGGGACCTGCTGGGTTTCTGTGCACAAAGGAAAATAATCCCCTGGTGTGACAGACCAAGGACAGAACACAGCAGAGGTGAGCACTGGGAAGAC  
1601 AGGTTGCTCCCAGGGATGGGGTCCATCCACCTTGCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAAGGAAAAAAGAGGAGGACAAAAGAGGC  
**ScaI (1773) AvrII (1782)**  
1701 AGAAATGAGAGGGGAGGGACAGAGGACCTGAATAAAGACCACCCATGACCCAGTGTGCTGAGAAGTACTCTGCCCTAGGAAGAGACTCAGGG  
1801 CAGAGGGAGGAAGGACAGCAGACAGCAGTACAGCAGCCTTGACAAAACGTTCTGGAACCTCAAGCTTTCTCCACAGAGGAGGACAGAGCAGACAG  
**NcoI (1906)**  
1901 AGAGACCATGGAATCAAGGTGCTGTTGCCCTCATCTGTATTGCTGTGTGCTGAGGCAAAACCCTGAAATCAATGAAGACCTCAATATAGCTGCTGTG  
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 (2021)**  
2001 GCCTCAACTTTGCCACCACAGATCTTGAGACTGACCTGTTCAACCACTGGGAGACCATGAATGTGATTAGCACTGACACAGAGCAGGTGAACACAGATG  
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  
2101 CTGACAGGGCAAGCTGCCTGGCAAAAACTCCCCAGATGTCTGAGGGAGCTGGAGGCCAATGCCAGAAGGGCTGGTGCACAAGAGGCTGCCTCAT  
65> 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 A G C T R G C L I  
2201 TTGCTCTCCACATTAAGTGCACCCCTAAGATGAAGAAATTTATCCCTGGCAGGTGCCACACTTATGAAGGTGAAAAGGAGTCTGCTCAGGGAGGGATT  
98> 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  
2301 GGAGAGGCAATTGTTGATATCCAGAGATTCTGGCTTCAAGGATAAGGAGCCACTGGACAGTTTATTGCTCAAGTGGACCTCTGTGCTGATTGCACCA  
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  
2401 CTGGCTGTCTGAAGGGCTTGCATGTCAGTGTCTGACCTCTGAAGAAGTGGCTTCCCAAGAGGTGTACCCTTTTCCAGCAAGATTCAGGGTAG  
165> 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 T F A S K I Q G R  
**NheI (2540)**  
2501 GGTGGACAAAATCAAGGGTCTGGCTGGGACAGATGATAGCTAGCTGGCAGACATGATAAGATACATTGATGAGTTTGGACAAAACCACACTAGAATGC  
198> V D K I K G L A G D R •  
2601 AGTGAAAAAATGCTTTATTGTGAAATTTGTGATGCTATTGCTTTATTGTAACCATTATAAGCTGCAATAAACAAGTTAACACAACAATTGCATTCA  
2701 TTTTATGTTTCAGTTTCAGGGGAGGTGTGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAATGTGGTATGGAATTAATTCTAAAATACAGCATAGCA  
**SgrAI (3447)**  
2801 AAACCTTAACTCCAATCAAGCTCTACTTGAATCCTTTCTGAGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTG  
2901 CAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTCCCAAGTTTGAAGTACTCTTCAATTTTATGTTTTAAATGCACTGACCTCCCAC  
3001 ATTCCTTTTTAGTAAAATATTAGAAAATATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTC  
3101 ATAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAGGAACCTTAAATAGAAAATTGGACAGCAAGAAAGCGAGCTTACTAGCTTATCCTCAGTCTCTG  
125< • D Q  
3201 CTCTCTGCCACAAAGTGACCGAGTGTCCGGCCGGTGTCCGAGGGGCAACTCCCGCCCCACGGCTGCTGCCGATCTGGTATGCGCCGGCCGGAG  
122< 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  
3301 GCGTCCCGAAGTTGCTGGACACGACCTCCGACACTCGCGTACAGCTCGTCCAGGCCGCGCACCCACACCCAGGCCAGGGTGTTCGCGCACCACT  
88< 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 L T N D P V V Q  
**SgrAI (3447)**  
3401 GGTCTGGACCGCTGATGAACAGGGTCACTGCTGCCGACACACCGCGAAGTCTCTCCAGAACTCCCGGAGAACCCGAGCCGGTCTGTTCCA  
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  
3501 GAACCTGACCGCTCCGCGCAGCTCGCGCGGTGAGCACCAGGACCGCACTGGTCAACTTGGCCATGATGGCTCTCTGTGAGGAGGAAAGAGAGA  
22< F E V A G A V D R A T L V P V A S T L K A M

3601 AGGTTAGTACAATTGCTATAGTGAGTTGTATTATACTATGCAGATATACTATGCCAATGATTAATTGTCAAACTAGGGCTGCAGGTTAATTAAGAACATG  
3701 TGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGAC  
3801 GCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCCTGCCGCT  
3901 TACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAG  
4001 CTGGGCTGTGTGCACGAACCCCGTTAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCAC  
4101 TGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAAC  
4201 AGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGGTTTT  
4301 TTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCAC  
4401 GTAAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCA