



**XbaI (15) SdaI (29)**

**NotI (2) NsiI (14) EcoRI (19) SpeI (36)**

1 GCGGCCGCTATGCATCTAGAATTCCTGCAGGGCCCACTAGTCTGTAAGCTGGAAGTCTGGCAGTGTGAGCTGG

75 CCAACCCCTCAGGACCTCCTCCTTGTCCTGACTGAATGACTCACCTTGGCATAGACATAATGGTCAGGGGCGG

149 GCACACAGCCTGATTCCCCTGCACTCCAGGCCCTTCAATGCTTTCCGAGAAGTCCATTGAGCTGGGAGCTT

**NcoI (270)**

223 GTACTGCACCAAGGGCTGACATCCTGGCAGCCAGGGATGAAAGCAGCCCATGGGGCTACCCTTGCCGTATGCCT

297 CACTGGCGGCAGAGAACAAGGCTCTATTCAGCAAATGCCCTGGAGTAGACACCAGAAGTCCAAGCATGGGCAGA

371 GGAAGGCAGGCGTTGGGGGCTGGAGGGGAGCAGAGCTGTCTGTTTTCCAGAAGCCCAAGGGTACAGATGGCGCC

**BglII (481)**

445 TGGGGGGAACTGAGTGGAGGGGATAGATGGGCCTGAGATCTCAAACATCAACAGCCTCCTCCCCACCAACGAT

519 GAAGGTGGAGGTTGTTTTCCAGACCTACATATCCCCAGAGACCTGGTGTATGAAAATTCAAAGGAGGTAAGT

593 CTCCTGAGAGAACGGGGGCTCACAAATGAAGCCAGCTGTCTTACCCTATCAGGACCTACGTGCATTCTTCTG

667 TCCTGCCCCCTAAACACACAGCCAGAGGCTCAAATTGATTCTGGAGTCACAAAGGGGCTTGAACCCAGCCC

741 CCCACTCCTGAACTCCAGGAATGAGAAGATAGTATTGGAGGGTTTCAGAGGAGAGGGCTCTGCACATCTGTTGA

815 GAATGGGGTCCCAGGAGAGTGAATTTAGGCTGATCCCGGAGGAAGGGAATAGGCTCTTCAAGATCCTAGCAT

889 CTCACAGGCCACAGAGAAGTTCAGAGTTGGGGCAGCCCTGGCTTACAGGCTCTAAGAAGTGGAGGCAGTTTAC

963 CCAACCCAGCTGTGTGCATGCTGTCCCTCTCTGTCTCTGTCTGTCTCTCTCTGTCTCTCTGTGTGT

**BsrGI (1088)**

1037 GTGTGTGTGTGCTCACACACGTGTGTGTTTATCACACAAATGTTTCATGTGTGTGTACATACATGTGTTGAGGCC

1111 AGAGGTCAACCTCAGACACTGTTGACTTGTTGTATGAGATAACATTTCCCCTGGGACCTGGGATTTGCCAAT

1185 TAGTGTGACCCAGGAAGCCTACTTATTTTTCATTCTCAGCACTGCAGTTACAAGTATGCACTGTCAAACCAGGC

1259 CTTTTTTTTTTTTTTTTTCCAAACCAGGCCTTTTGTATTGCTCTGTGGCTAGAACTTGGGTCTCCATGCTTGA

1333 CAGGCAAGCGATTTATGGACTAAGCTGTTTCTCGGCCCTCTCTTGACCCATTTACCAGAAATGGGGTTTCCTT

1407 GATCAATGGTTAAGCCAGGCTGGTGTTCAGGAAACCCTTGACTCTGGGTACAGTGACCTTGGTGGGGTGAGA

1481 AGAGTTCTCTCCATAGCTGGGCTGGGGCCAGCTCCACCCCTCAGGCTATTCAATGGGGTGCTGCCAGGAAGT

**BspHI (1627)**

1555 CAGGGGCAGATCCAGTCCAGCCCGTCCCTCAATAAAGGCCCTGACATCCAGGAGCCAGCAGAAGCAGGGCATC

1629 ATGATGGAAATCAAGGTGCTGTTTGCCTCATCTGTATTGCTGTTGCTGAGGCAAAACCCACTGAAATCAATGA

1▶ M M E I K V L F A L I C I A V A E A K P T E I N E

**BglII (1745)**

1703 AGACCTCAATATAGCTGCTGTGGCCTCCAACCTTCCACCACAGATCTTGAGACTGACCTGTTACCAACTGGG

25▶ D L N I A A V A S N F A T T D L E T D L F T N W

1777 AGACCATGAATGTGATTAGCACTGACACAGAGCAGGTGAACACAGATGCTGACAGGGGCAAGCTGCCTGGCAAA

50▶ E T M N V I S T D T E Q V N T D A D R G K L P G K

1851 AAACCCCCAGATGTCTGAGGGAGCTGGAGGCCAATGCCAGAAGGGCTGGTTGCACAAGAGGCTGCCTCAT

75▶ K I P P D V I R F I F A N A R R A G C T R G C I I

1925 TTGCCTCTCCACATTAAGTGCACCCCTAAGATGAAGAAATTTATCCTGGCAGGTGCCACACTTATGAAGGTG  
99▶ C L S H I K C T P K M K K F I P G R C H T Y E G  
1999 AAAAGGAGTCTGCTCAGGGAGGGATTGGAGAGGCAATTGTTGATATCCAGAGATTCTGGCTTCAAGGATAAG  
124▶ 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  
2073 GAGCCACTGGACCAGTTTATTGCTCAAGTGGACCTCTGTGCTGATTGCACCACTGGCTGTCTGAAGGGCCTTGC  
149▶ E P L D Q F I A Q V D L C A D C T T G C L K G L A  
2147 CAATGTCCAGTGTCTGACCTCCTGAAGAAGTGGCTTCCCCAGAGGTGTACCACTTTTGCAGCAAGATTCAGG  
173▶ N V Q C S D L L K K W L P Q R C T T F A S K I Q  
NheI (2264)  
2221 GTAGGGTGGACAAAATCAAGGGTCTGGCTGGGGACAGATGATAGCTAGCTGGCCAGACATGATAAGATACATTG  
198▶ G R V D K I K G L A G D R •  
2295 ATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCT  
2369 TTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCA  
2443 GGGGGAGGTGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTAATTCTAAAATACA  
2517 GCATAGCAAACTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCA  
2591 TCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAGATATAGTGTAT  
2665 TTTCCCAAGGTTTGAAGTACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGT  
SspI (2743)  
2739 AAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGC  
2813 TCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGA  
2887 CAGCAAGAAAGCGAGCTTCTAGCTTATCCTCAGTCTGCTCCTCTGCCACAAAGTGCACGCAGTTGCCGGCCGG  
125▶ • D Q E E A V F H V C N G A P  
2961 GTCGCGCAGGGCGAAGTCCCAGCCACGGCTGCTCGCCGATCTCGGTCATGGCCGGCCCGAGGCGTCCCAGG  
110▶ D R L A F E R G W P Q E G I E T M A P G S A D R F  
3035 AGTTCGTGGACACGACCTCCGACCACTCGGCGTACAGCTCGTCCAGGCCGCGCACCCACACCCAGGCCAGGGTG  
85▶ N T S V V E S W E A Y L E D L G R V W V W A L T  
SgrAI (3171)  
3109 TTGTCCGGCACCACCTGGTCTGGACCGCGCTGATGAACAGGGTACGTCGTCGCCGACCACACCCGGCGAAGTC  
60▶ 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  
3183 GTCCTCCACGAAGTCCCGGGAGAACCAGCCGGTCCGTCAGAACTCGACCGCTCCGGCGACGTCGCGCGCGG  
36▶ D E V F D R S F G L R D T W F E V A G A V D R A T  
3257 TGAGCACCGGAACGGCACTGGTCAACTTGGCCATGATGGCTCCTCCTGTGAGGAGAGGAAAGAGAAGAAGGTTA  
11▶ L V P V A S T L K A M  
3331 GTACAATTGCTATAGTGAGTTGTATTATACTATGCAGATATACTATGCCAATGATTAATTGTCAAAGTAGGGCT  
3405 GCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCG  
3479 TTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGAC  
3553 AGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGCTTA  
3627 CCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGT  
3701 TCGGTGTAGGTGCTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTTCAGCCGACCGCTGCGCCTTATC  
3775 CGGTAACATATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGA  
3849 TTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGA  
3923 ACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAA  
3997 ACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAG  
4071 AAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATG

4145 GCTAGTTAATTAACATTTAAATCA