



**EcoRI (23)** **SdaI (38)**  
**NotI (2)** **XbaI (19)** **BamHI (29)** **SpeI (45)**  
1 CGGGCCGCGTCGACGATATCTAGAATTCGGATCCTGCGAGGGCCACTAGTCAGGGCCCCAACCCCCAAGCCCCATTTACAACACGCTGGCGCTACA

**BspEI (152)**  
101 GGCGCGTGACTTCCCCTTGTCTTGGGGCGGGGGGTGAGACTCCTATGTGCTCCGATTGGTCAGGCACGGCCTTCGGCCCCGCTCCTGCCACCGCAGA

**SacII (298)**  
201 TTGGCCGCTAGCCCTCCCCGAGCGCCCTGCCTCCGAGGGCCGGCGCACCATAAAAGAAGCCGCTAGCCACGTCCCCTCGCAGTTCGGCGGTCCCCGCGG

**HindIII (310)** **EcoNI (356)**  
301 GTCTGTCTCAAGCTTCGAGGGGCTCGCATCTCTCTTACGCGCCCGCCCTACCTGAGGCCGCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCCTC

401 CCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGGCGCTCCCTTGAGGCTACCTAG

**NcoI (595)**  
501 ACTCAGCCGGCTCTCCACGCTTTCCTGACCCTGCTTGCTCAACTCTACGCTTTGTTTCGTTTTCTGTTCTGCGCCGTTACAGATCCAAGCCACCATGG

601 AAATCAAGGTGCTGTTTGCCTCATCTGTATTGCTGTTGCTGAGGCCAAAACCACTGAAATCAATGAAGACCTCAATATAGCTGCTGTGGCCTCCAATTT  
2▶ 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 A S N F

**BglII (710)**  
701 TGCCACCACAGATCTTGAGACTGACCTGTTACCAACTGGGAGACCATGAATGTGATTAGCACTGACACAGAGCAGGTGAACACAGATGCTGACAGGGGC  
35▶ 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 A D R G  
801 AAGTCCTGGCAAAAACTCCCCAGATGTCTGAGGGAGCTGGAGGCCAATGCCAGAAGGGCTGGTTGCACAAGAGGCTGCCTCATTTCCTCC  
69▶ 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 C L S  
901 ACATTAAGTGCACCCCTAAGATGAAGAAATTTATCCCTGGCAGGTGCCACACTTATGAAGGTGAAAAGGAGTCTGCTCAGGGAGGATTGGAGAGGCAAT  
102▶ 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 G E A I  
1001 TGTTGATATCCCAGAGATTCCTGGCTCAAGGATAAGGAGCCACTGGACCAGTTTATTGCTCAAGTGGACCTCTGTGCTGATTGCACCACTGGCTGTCTG  
135▶ 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 T G C L  
1101 AAGGGCCTTGCAATGTCCAGTGTCTGACCTCCTGAAGAAGTGGCTTCCCCAGAGGTGTACCACTTTTGCCAGCAAGATTCAAGGTTAGGGTGGACAAAA  
169▶ 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 V D K

**NheI (1229)**  
1201 TCAAGGTCTGGTGGGACAGATGATAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGACAAAACCACAAGTGAATGCAGTGAIAAAAA  
202▶ I K G L A G D R •

1301 TGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTC

1401 AGGTTCAAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTAATTCTAAAATACAGCATAGCAAACTTTAACC

1501 TCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCT  
1601 TCTTTCATGGAGTTAAGATATAGTGATTTTCCCAAGGTTTGAAGTACTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTT

**SspI (1708)**  
1701 AGTAAATATTAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTATTAGGCAGAAATCCAGATGCTCAAGGCCCTTCATAATATCCCC  
1801 CAGTTTAGTAGTTGACTTAGGGAACAAAGAACCTTAAATAGAAATTGGACAGCAAGAAAGCAGGCTCTAGCTTATCCTCAGTCTGCTCCTCTGCCA  
125▶ D Q E E A V

1901 CAAAGTGCACGCAGTTGCCGGCCGGTTCGCGCAGGGCGAACTCCCGCCCCACGGCTGCTCGCGATCTCGGTTCATGGCCGGCCGGAGGCGTCCCGGAA  
118▶ 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 A D R F  
2001 GTTCTGGACACGACCTCCGACCACTCGCGTACAGCTCGTCAGGCCGCGCACCCACACCCAGGCCAGGGTGTGTCGGCACCACTGGTCTGGACC  
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 N D P V V Q D Q V

**SgrAI (2136)**  
2101 CGCTGATGAACAGGGTACGCTGCTCCCGACCACCGGCGAAGTCTCCTCCACGAAGTCCCGGAGAACCCGAGCCGGTCCGAGTCCAGAACTCGACCG  
51▶ 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 F E V A  
2201 CTCCGGCAGCTCGCGCGGGTGAACCGGAAACGGCACTGGTCAACTTGGCCATGATGGCTCCTCCTGTCAGGAGAGGAAAGAGAAGGTTAGTACA  
18▶ G A V D R A T L V P V A S T L K A M

2301 ATTGCTATAGTGAATGATTATACTATGCAGATATACTATGCAATGATTAATTGTCAAAGTGGGCTGCAGGTTAATTAAGAACATGTGAGCAAAAGG

2401 CCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAG

2501 AGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGTCCCTCGTGGCTCTCCTGTTCCGACCCTGCCGTTACCGGATACC

2601 TGTCCGCTTTCTCCCTCGGGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGT

2701 GCACGAACCCCCGTTACGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGTAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCC

2801 ACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGAACAGTATTTGGTA

2901 TCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGTATCCGGCAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGCAA

3001 GCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATT

3101 TTGGTCATGGCTAGTTAATTAACATTTAAATCA