



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTGTGCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

**HindIII (245)**  
**Psp1406I (203)** 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCCGCCGCTACCTGAGGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

501 TCTGTTTGTCCGGCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTTCATGACAGTGAAGACCTGTCATGGCCAGCCATGGTCAA

601 GTACTTGTGCTGTCGATATTGGGGCTTGCCTTCTGAGTGAGGCGGAGCTCGAAAATCCCAAAGTAGGACATACTTTTTCCAAAAGCCTGAGAGT

13▶ Y L L L S I L G L A F L S E A A A R K I P K V G H T F F Q K P E S

701 TGCCCGCTGTGCCAGGAGTAGTATGAAGCTTGACATTGGCATCATCAATGAAAACAGCGCTTCCATGTACGTAACATCGAGAGCCGCTCCACCT

47▶ C P P V P G G S M K L D I G I I N E N Q R V S M S R N I E S R S T

**Acc65I (836)**  
801 CCCCTGGAATTACACTGTCACCTGGGACCCCAACCGGTACCCCTCGGAAGTTGTACAGGCCAGTGTAGGAACTTGGGCTGCATCAATGCTCAAGGAAA

80▶ S P W N Y T V T W D P N R Y P S E V V Q A Q C R N L G C I N A Q G K

901 GGAAGACATCTCCATGAATCCGTTCCCATCCAGCAAGAGACCTGGTCGTCGGAGGAAGCACCAAGGCTGCTCTGTTTCTTCCAGTTGGAGAAGGTG

113▶ E D I S M N S V P I Q Q E T L V V R R K H Q G C S V S F Q L E K V

**DraIII (1039)** **PvuII (1070)**  
1001 CTGGTGACTGTTGGTGCACCTGCGTCAACCCTGTCATCCACCATGTGACGTAAGAGGTGCATATCCACTCAGCTGAAGAAGCTGTAGAAATGCCACTCC

147▶ L V T V G C T C V T P V I H H V Q •

**MscI (1116)**  
**NheI (1110)**  
1101 TTACCCAGTGTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGACAAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAAT

1201 TGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACAATTGCATTCATTTTATGTTTCAGGTTACAGGGGAGGTGT

**HpaI (1248)** **MfeI (1259)**

1301 GGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACCTTTAACCTCAAATCAAGCCTCTACTTGA

1401 ATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATAT

**SapI (1526)** **SspI (1583)** **SwaI (1597)**  
1501 AGTGTATTTTCCAAGTTTGAAGTCTCTTCAATTTCTTTATGTTTTAAATGCACTGACCTCCCACATTCCTTTTTAGTAAAATATTCAGAAAATAATT

1601 TAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTATAATATCCCCAGTTTAGTAGTTGGACTTAGG

1701 GAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTT

141▶ N R T Y K L P I L E E I T T K

1801 TGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGA

125▶ V L K G N M E I L V F C D P A Y D S I L E R C M G C P S V V R I S

1901 TCTGTCCACCTCATCAGAGTAGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCA

92▶ R D V E D S Y P H R V A V I T D F D K Q G N S V A S G I A I A E A

**StuI (2022)**  
2001 CAGACAGTGACCCTGCCAATGTAGGCCATGTGGACAGCAGAGATGATCTCCCGTCTTGGTCTGATGGCCGCCCGACATGGTGTGTTGTCTCT

58▶ C V T V R G I Y A E I H V A S I I E G T K T R I A A G V H H K N D E

**XmnI (2164)**  
2101 CATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTCATGGTGGCCCTCTATAGTGAGTCGT

25▶ Y L M T I K E T A V E V L E L D Q Q S I N F T K M

**AseI (2230)** **SacI (2287)**  
2201 ATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCATAACGAGCTCTGCTTAT

2301 ATAGACCTCCCACGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAACAAA

2401 CTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAA

**SnaBI (2513)**

2501 TAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTC

**NdeI (2618)**

2601 AATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATT

**PstI (2797)**  
**SdaI (2796)**

2701 GCGTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTG

**PacI (2804)** **BspLU11I (2814)**

2801 CAGGTTAATTAGAACATGTGAGCAAAAGGCCAGAAAAGGCCAGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTTCATAGGCTCGCCCCCTGAC



2901 GAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCCTCTC

3001 CTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCCTTTCCTTCGGAAGCGTGGCGCTTTCATAGCTCACGCTGTAGGTATCTCAGTTCGGT

**ApaLI (3128)**

3101 GTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTA

3201 AGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACT

3301 ACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCAC

3401 CGCTGGTAGCGGTGGTTTTTTTGTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCT

**EagI (3564)**

**PacI (3544)** **Swal (3553)** **NotI (3563)**

3501 CAGTGAACGAAAACCTACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCT

3601 GTGTGTTGGTTTTTTTGTGTAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAAACTAGCAAATAGGCTGTCCCGAGTGCAAGT

3701 GCAGGTGCCAGAACATTTCTCTATCGAA