



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA **MfeI (82)**

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

**HindIII (245)**  
**Psp1406I (203)** 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCGCCCTACCTGAGGCC **PvuII (239)** **Bsu36I (291)**

301 GCCATCCACGCGGTTGAGTCGCGTTTCTGCCGCTCCCGCCTGTGGTGCTCCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCGGCTCTCCACGCTTGGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

**NcoI (560)**  
**BstEII (555)**  
**AgeI (552)** 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTACCATTGGCTTCATCCTCCTCCGTCCAGCCTCCTCACTCC **BsaBI (666)** **XcmI (687)**

601 GTCCAAGAAGCCTCGAGACAAGATAGCTGACTGGTTCAGGCGAGGCTCTGTTGAAGAAGCCCAAGAAGATGCCGATCTCCAGGAAAGCCACCTCTATGAT **BsaBI (666)** **XcmI (687)**  
13▶ S K K P R D K I A D W F R Q A L L K K P K K M P I S Q E S H L Y D  
701 GGTTACAGACAGCCACACAGGATGGTCTCTACCCTCGAGCTCAGCTCACCCCGAGTACAGTTCACCCGAGAGCGGTAGCTCACCTCGAGCTGCA  
47▶ G S Q T A T Q D G L S P S S C S S P P S H S S P E S R S S P S S C

801 GTTCAGGAATGTCACCTACCTCGCCACCAACACACGTGGACAGCAGCAGCAGCAGTGGCCGCTGGAGCAAAGACTACGATGTCTGCTGTGCCACAG **BbrPI (832)**  
80▶ S S G M S P T S P P T H V D S S S S S S G R W S K D Y D V C V C H S

901 TGAGGAGGACTTGGAGGGGCCAGGAGCTGGTCTCCTACTTGGAGGGTAGCCAGGCCAGTCTACGCTGCTTCTGCAGTTCGGGATGCAGCCCGGT **XmaI (993)**  
113▶ E E D L E A A Q E L V S Y L E G S Q A S L R C F L Q L R D A A P G

1001 GCGCCATTGTTTCGGAGCTATGCCAGGCACTGAGTCGTAGTCACTGCCGTGTGCTGCTCATCACTCCAGGCTTCCTTCGGGACCCTGGTGCAAGTACC **SmaI (1079)**  
147▶ G A I V S E L C Q A L S R S H C R V L L I T P G F L R D P W C K Y  
1101 AGATGCTGCAGGCCCTGACGGAGCCCGCGTCCGAGGGTTGACCATACCCCTGCTGTCGGCCTGTCCAGAGCCGCTATCCGCCGAACCTCCGATT  
180▶ Q M L Q A L T E A P A S E G C T I P L L S G L S R A A Y P P E L R F  
1201 CATGACTATGTGGATGGCAGAGGCAAGGACGGAGGCTTTTACCAAGTCAAGGAGGCTTTATACACTATCTGGAGACTAAGCTGACACTTGGGCTTT  
213▶ M Y Y V D G R G K D G G F Y Q V K E A V I H Y L E T L S •

**MseI (1336)**  
**NheI (1330)** 1301 CATAAGAAAAGCTGGGAATAGCTCACAGCAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGA AAA

1401 AATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAACAAGTTAAACAACAACCTGATTATTTATGTT

**EcoRI (1564)** 1501 TCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAATAACAGCATAGCAAACTTTAACCTC  
1601 CAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTC

1701 TTTTCATGGAGTTAAGATATAGTGTATTTTCCAAGGTTTGAAGTCTCTTCACTTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTATG

**SspI (1803)** **SwaI (1817)** 1801 TAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCA  
1901 GTTTAGTAGTTGGACTTAGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGAT  
141▶ • N R T Y K L P I

2001 GAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAGCAGTCAAGGAGCATAGTCAAGATGAGCTCTGTCATGCCACAG **SacI (2078)**  
132▶ L E E I T T K 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

2101 GGGCTGACCACTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACC **BstXI (2107)**  
98▶ P S V V R I S 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

2201 CAATGGCAATGGCTTCAGCACAGACAGTACCCTGCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAAGTCTTGGTCTGATGGCCGCCCC **StuI (2242)**  
65▶ I A I A E A 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

2301 GACATGGTGTGTTGTCCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTG **BbsI (2388)** **XmnI (2384)**  
32▶ V H H K N D E 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

2401 GCCCTCTATAGTGAAGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTC **AseI (2450)**

2501 <sup>SacI (2507)</sup> ACTAAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCCTT

2601 <sup>SpeI (2605)</sup> GATTTACTAGTCAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCA

2701 <sup>SnaBI (2733)</sup> AAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGC

2801 <sup>NdeI (2838)</sup> CATTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCGAGTTTACCGTAAATACTCCACCCATTGAC

2901 GTC AATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGGGGGGTCTGGGCGGTTCAGCCAGGCGGGCCATTTAC

3001 <sup>PacI (3024)</sup> <sup>SdaI (3016)</sup> <sup>BspLU111 (3034)</sup> CGTAAGTTATGTAACGCTGCAGGTTAATTAAAGAACATGTGAGCAAAGGCCAGGAAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTTCC

3101 ATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGG

3201 AAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGC

3301 <sup>ApaLI (3348)</sup> TG TAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTT CAGCCGACCGCTGCGCCTTATCCGGTAACTATC

3401 GTCTTGAGTCAAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTT

3501 CTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGAACGATTTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCT

3601 TGATCCGGCAAACAACCCGCTGGTAGCGGTGGTTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCT

3701 <sup>EagI (3784)</sup> <sup>PacI (3764)</sup> <sup>SwaI (3773)</sup> <sup>NotI (3783)</sup> TTTCTACGGGGTCTGACGCTCAGTGAACGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATA

3801 TCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTTGTAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAAT

3901 AAGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA