



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

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

**Psp1406I (203)** **HindIII (245)** **Bsu36I (291)**  
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACGCGCCCGCCCTACCTGAGGCC

301 GCCATCCACGCGGTTGAGTCGCGTTTCTGCCGCCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTAAAGCTCAGGTGCAGACC

**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGTCTTTGTTTCGTTT

**NcoI (560)**  
**BstEII (555)**  
**AgeI (552)**  
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCGCTACCTGAGATCACCGGTACCATTGGGGCGCGCGGACGCCATCCTGGATGCGCTGGA  
1 M G R A R D A I L D A L E

**XcmI (698)**  
**NcoI (698)**  
**SacII (679)**  
601 GAACCTGACCGCCGAGGAGCTCAAGAAGTTCAAGCTGAAGCTGCTGTCGGTGCCGCTGCGCGAGGGCTACGGGCGCATCCCGGGGGCGCGCTGCTGTCC  
13 N L T A E E L K K F K L K L L S V P L R E G Y G R I P R G A L L S

**SdaI (792)**  
701 ATGGACGCTTGGACCTCACCGACAAGCTGGTCAGCTTCTACCTGGAGACCTACGGCGCCGAGCTCACCGCTAACGTGCTGCGCGACATGGGCGCTGCAGG  
47 M D A L D L T D K L V S F Y L E T Y G A E L T A N V L R D M G L Q

**BstXI (831)** **BamHI (857)** **StuI (891)**  
801 AGATGGCCGGGACGCTGCAGGCGCCACGACCGAGGGCTTGGAGCCGCGCCAGCTGGGATCCAGGCCCTCCTCAGTCGGCAGCCAAGCCAGGCTGCAG  
80 E M A G Q L Q A A T H Q G S G A A P A G I Q A P P Q S A A K P G L H

**NruI (929)** **Psp1406I (943)**  
901 CTTTATAGACCAGCACCGGGCTGCGCTTATCGCGAGGGTCACAAACGTTGAGTGGCTGCTGGATGCTGTGTACGGGAAGTCTGACGGATGAGCAGTAC  
113 F I D Q H R A A L I A R V T N V E W L L D A L Y G K V L T D E Q Y

**SapI (1044)** **XmnI (1041)** **XcmI (1060)**  
1001 CAGGCAGTGCGGGCGAGCCACCAACCAAGCATGCGGAAAGCTCTTTCAGTTTACACACCGCCTGGAAGTGGACCTGCAAGGACTTGTCTCTCCAGG  
147 Q A V R A E P T N P S K M R K L F S F T P A W N W T C K D L L L Q

**Bsu36I (1101)** **BsrBI (1138)** **MscI (1182)**  
**NheI (1176)**  
1101 CCCTAAGGGAGTCCAGTCTACCTGGTGGAGGACCTGGAGCGGAGCTGAGGCTCCTCCAGCAACACTCCGGTCCGCTAGCTGGCCAGACATGATAAGA  
180 A L R E S Q S Y L V E D L E R S •

1201 TACATTGATGAGTTGGACAACCACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAA

**HpaI (1314)** **MfeI (1325)**  
1301 GCTGCAATAAACAAGTTAAACAACAATAATGCATTTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAA

**EcoRI (1410)**  
1401 ATGTGGTATGGAATCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCAT

**SapI (1592)**  
1501 CAGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTCTTTTCATGGAGTTAAGATATAGTGATTTTCCCAAGGTTTGAAGTACTGCTCTTCA

**SspI (1649)** **SwaI (1663)**  
1601 TTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTATGATAAATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTT

1701 TATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTGTAGTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCA

1801 AGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGGGGGATGAGTTCCCTCAATGGTGGTTTTGACCAGCTTGCATTCATCTCAATGAGCACAAA  
1-1-1 • N R T Y K L P I L E E I T T K V L K G N M E I L V F

**BstXI (1953)**  
1901 GCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACA  
114 C D P A Y D S I L E R C M G C P S V V R I S R D V E D S Y P H R V

**StuI (2088)**  
2001 GCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGT  
80 A V I T D F D K Q G N S V A S G I A I A E A C V T V R G I Y A E I H

2101 GGACAGCAGAGATGATCTCCCGAGTCTGGTCTGATGGCCGCCCCGACATGGTCTTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTC  
47 V A S I I E G T K T R I A A G V H H K N D E Y L M T I K E T A V E

**BbsI (2234)**  
**XmnI (2230)** **AseI (2296)**  
2201 CACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCCTATAGTGGTTCGATTTATACTATGCGGATATACTATGCGGATGATTA  
14 V L E L D Q Q S I N F T K M

2301 ATTGTCAAACAGCGTGGATGGCTCTCCAGCTTACTGACGGTCACTAAACAGACTGCTTATATAGACCTCCACCGTACACGCCCTACCGCCATT

**SpeI (2451)**  
2401 TCGTCAATGGGGCGGAGTTGTTACGACATTTGGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGGAA

2501 ATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGT **SnaBI (2579)**

2601 AGGAAAGTCCATAAAGTCAATGTACTGGGCATAATGCCAGGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGA **NdeI (2684)**

2701 TGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACG

2801 TCAATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAGGCCAG **SdaI (2862) PacI (2870) BspLU11I (2880)**

2901 CAAAAGGCCAGGAACCGTAAAAAGGCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGT

3001 GCGGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGTCCCTCGTGCGCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTC

3101 CGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCAC **ApaLI (3194)**

3201 GAACCCCGTTCAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTG

3301 GTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTG

3401 CGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCCAGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAG

3501 CAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGG

3601 **EagI (3630)**  
**PacI (3610) SmaI (3619) NotI (3629)**  
TCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGAATAAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACA

3701 TACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA