



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA MfeI (82)  
101 GAGAAGTGGCGCGGGTAAACTGGAAAGTGATGCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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**HindIII (245)**  
**Psp1406I (203)** 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACAGCGCCGCCGCCCTACCTGAGGCC **Bsu36I (291)**  
301 GCCATCCACGCGGTTGAGTCGCGTTTCTGCCGCTCCCGCCTGTGGTGCTCCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGTCTTTGTTTCGTTT

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**AgeI (552)** **BspLU11I (560)** **SacII (588)**  
501 TCTGTTTGTCCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCAACATGTGCGTGGGGGCTCGGCGGTGGCCGCGGCCGTG **1 M C V G A R R L G R G P C**  
**AgeI (680)**  
601 TGGGCTCTGCTCCTCTGGGCTGGGGCTGAGCACCGTGCAGGGGCTCCACTGTGTCGGGGACACCTACCCAGCAACGACCGGTGCTGCCACGAGTGC **13 A A L L L L G L G L S T V T G L H C V G D T Y P S N D R C C H E C**

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**BsrBI (732)** **DraIII (744)** **Tth111I (781)**  
701 AGGCCAGGCAACGGGATGGTGAAGCCGCTGCAGCCGCTCCAGAACACGGTGTGCCGTCGCGGGCCGGGCTTCTACAACGACGTGGTCAGCTCCAAGC **47 R P G N G M V S R C S R S Q N T V C R P C G P G F Y N D V V S S K**

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**BstAPI (803)** **DraIII (813)** **BsrBI (841)** **PvuII (850)** **Tth111I (871)**  
801 CGTGCAAGCCCTGCACGTGGTGAACCTCAGAAGTGGGAGTGAAGCGGAAGCAGCTGTGCACGGCCACACAGGACACAGTCTGCCGCTGCCGGGCGGGCAC **80 P C K P C T W C N L R S G S E R K Q L C T A T Q D T V C R C R A G T**

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**StuI (977)**  
901 CCAGCCCCTGGACAGCTACAAGCCTGGAGTTGACTGTGCCCCCTGCCCTCCAGGGCACTTCTCCCAGGCGACAACAGGCTGCAAGCCTGGACCAAC **113 Q P L D S Y K P G V D C A P C P P G H F S P G D N Q A C K P W T N**

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**BstAPI (1017)** **NgoMIV (1029)** **SmaI (1067)**  
1001 TGCACCTTGGCTGGGAAGCACACCTGCAGCCGCGCCAGCAATAGCTCGGACGCAATCTGTGAGGACAGGGACCCCGAGCCACGCAGCCCGAGGAAACCC **147 C T L A G K H T L Q P A S N S S D A I C E D R D P P A T Q P Q E T**

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**Bsp120I (1101)** **SmaI (1161)** **XmaI (1189)**  
1101 AGGGCCCCCGGCCAGGCCATCACTGTCCAGCCCACTGAAGCCTGGCCAGAACCTCACAGGACCTCCACCCGGCCCGTGGAGGTCCCGGGGGCCG **180 Q G P P A R P I T V Q P T E A W P R T S Q G P S T R P V E V P G G R**

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**Bsp120I (1245)** **BstXI (1256)** **BspEI (1280)**  
1201 TGGGTTGCCGCATCCTGGCCTGGGCTGGTGTGGGCTGCTGGCCCTGCTGGCCCTGTACCTGCTCCGGAGGACAGAGGCTG **213 A V A A I L G L G L V L G L L G P L A I L L A L Y L L R R D Q R L**

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**BspEI (1337)** **BglIII (1388)**  
1301 CCCCCGATGCCACAAGCCCCCTGGGGAGGAGTTCGGACCCCATCCAAGAGGAGCAGGCCGACGCCACTCCACCCTGGCCAAGATCTGACGCT **247 P P D A H K P P G G G S F R T P I Q E E Q A D A H S T L A K I •**  
1401 AGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTG

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**HpaI (1535)** **MfeI (1546)**  
1501 CTTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAAACAACAATTGCATTTTATGTTTCAGGTTCAAGGGGAGGTGTGGAGGTTTTTTA

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**EcoRI (1631)**  
1601 AAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTAACTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAG  
1701 GGATGAATAAGGCATAGGCATCAGGGCTGTTGCCAATGTGCATTAGCTGTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGATTTTCCC

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**SapI (1813)** **SspI (1870)** **SwaI (1884)**  
1801 AAGTTTGAAGTACTCTTCATTCTTTATGTTTTAAATGCACTGACCTCCCACATCCCTTTTATGTAATAATTCAGAAATAATTTAAATACATCATT  
1901 GCAATGAAATAAATGTTTTTATTAGCAGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAAGGAACC  
2001 TTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGTTGCC  
**141 • N R T Y K L P I L E E I T T K V L K G**

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**SacI (2145)** **BstXI (2174)**  
2101 ATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCCCTGATGGATCTGTCCACCTCA **121 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 R D V E**  
2201 TCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGCTGCTCAGCAGACCCCAATGGCAATGGCTTACAGCACAGACGTGACCC **87 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 C V T V R**

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**StuI (2309)**  
2301 TGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCACTTGGTCTGATGGCCGCCGACATGGTCTTGTGCTCCTCATAGAGCATGGT **54 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 Y L M T**

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**BbsI (2455)** **XmnI (2451)**  
2401 GATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTCTTGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCC **21 I K E T A V E V L E L D Q Q S I N F T K M**

2501 <sup>AseI (2517)</sup> GATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCCTAAACGAGCTCTGCTTATATAGACCTCCCAC <sup>SacI (2574)</sup>

2601 CGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCATTGACGT <sup>SpeI (2672)</sup>

2701 CAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAA

<sup>SnaBI (2800)</sup>  
2801 TACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTA

<sup>NdeI (2905)</sup>  
2901 CTTGGCATATGATACACTTGATGTACTGCCAAGTGGGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGG

<sup>PacI (3091)</sup>  
3001 GAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATTAAG <sup>SdaI (3083)</sup>

<sup>BspLU11I (3101)</sup>  
3101 AACATGTGAGCAAAAGGCCAGCAAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAA

3201 ATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCT

3301 GCCGTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCG

<sup>ApaLI (3415)</sup>  
3401 TCCAAGCTGGGCTGTGTGCACGAACCCCCGTTAGCCCGACCCTGCGCCTTATCCGGTAACACTATCGTCTTGTAGTCCAACCCGTAAGACACGACTTAT

3501 CGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAG

3601 AAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGT

3701 GGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTCTACGGGCTGACGCTCAGTGGAAACGAAA

<sup>PacI (3831) SwaI (3840) EagI (3851) NotI (3850)</sup>  
3801 ACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTT

3901 TTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAA

4001 CATTTCTCTATCGAA