



**PvuI (7)**  
**SgfI (6)**  
1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA  
101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGTCTGTACTGGCTCCGCCTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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**HindIII (245)**  
**Psp1406I (203)** **PvuII (239)** **Bsu36I (291)**  
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCGCCCTACCTGAGGCC  
301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCTGACCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

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**AgeI (552)** **NcoI (568)**  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCTACCTGAGATCACCGGTAGGAGGGCCACCATGGCTGGTGATCTTTCAGCAGGTTTCTTC  
1▶ M A G D L S A G F F

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**ScaI (638)**  
601 ATGGAGAACTTAATACATACCGTCAGAAGCAGGGAGTAGTACTTAAATATCAAGAACTGCCTAATTCAGGACCTCCACATGATAGGAGGTTTACATTTCC  
11▶ M E E L N T Y R Q K Q G V V L K Y Q E L P N S G P P H D R R F T F

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**BstAPI (756)**  
701 AAGTTATAATAGATGGAAGAGAATTTCCAGAAGGTGAAGGTAGATCAAAGAAGGAAGCAAAAATGCCGACGCAAAATAGCTGTTGAGATACTTAATAA  
44▶ Q V I I D G R E F P E G E G R S K K E A K N A A A K L A V E I L N K

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**NcoI (859)** **StuI (875)**  
801 GGAAAAGAAGGCAGTTAGTCCTTTATTATTGACAACAACGAATTTCTCAGAAGGATTATCCATGGGAATTACATAGGCCCTTATCAATAGAATTGCCAG  
77▶ E K K A V S P L L L T T T N S S E G L S M G N Y I G L I N R I A Q  
901 AAGAAAAGACTAACTGTAATATTGAACAGTGTGCATCGGGGTGCATGGGCCAGAAGGATTTTCATTATAAATGCAAAATGGACAGAAAAGATATAGTA  
111▶ K K R L T V N Y E Q C A S G V H G P E G F H Y K C K M G Q K E Y S  
1001 TTGGTACAGTTCTACTAAACAGGAAGCAAAACAATTTGGCCGCTAAACTGCATATCTCAGATATTATCAGAAGAACTCAGTAAATCTGACTACCT  
144▶ I G T G S T K Q E A K Q L A A K L A Y L Q I L S E E T S V K S D Y L  
1101 GTCCTCTGGTTCTTTTGTACTACTGTGAGTCCCAAAGCAACTCTTGTAGTACCAGCACACTCGCTTCTGAATCATCATCTGAAGGTGACTTCTCAGCA  
177▶ S S G S F A T T C E S Q S N S L V T S T L A S E S S S E G D F S A

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**PmeI (1231)** **BglII (1290)**  
1201 GATACATCAGAGATAAATTCTAACAGTGACAGTTTAAACAGTCTTCTGTTGCTTATGAATGGTCTCAGAAATAATCAAAGGAAGGCAAAAAGATCTTTGG  
211▶ D T S E I N S N S D S L N S S S L L M N G L R N N Q R K A K R S L

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**Bst1107I (1337)**  
1301 CACCCAGATTTGACCTTCTGACATGAAAGAAACAAAGTATACTGTGGACAAGAGGTTTGGCATGGATTTTAAAGAAATAGAATTAATTGGCTCAGGTGG  
244▶ A P R F D L P D M K E T K Y T V D K R F G M D F K E I E L I G S G G

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**MscI (1403)**  
1401 ATTTGGCCAAAGTTTTCAAAGCAAAACACAGAATTGACGAAAGACTTACGTTATTAACAGTGTAAATATAAATACGAGAAGCGGAGCGTGAAGTAAAA  
277▶ F G Q V F K A K H R I D G K T Y V I K R V K Y N N E K A E R E V K

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**SspI (1524)**  
1501 GCATTGGCAAAACTTGATCATGTAATATTGTTCACTACAATGGCTGTTGGGATGGATTTGATTATGATCCTGAGACCAGTGAATCTCTTGGAGCA  
311▶ A L A K L D H V N I V H Y N G C W D G F D Y D P E T S D D S L E S  
1601 GTGATTATGATCCTGAGAACAGCAAAAATAGTTCAAGGTCAAAGACTAAGGAATCTGTGATAAAGGGACCTTGAACAATGGATTGAAAAAGAAGAGG  
344▶ S D Y D P E N S K N S S R S K T K E F C D K G T L E Q W I E K R R G

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**BglII (1790)**  
1701 CGAGAACTAGACAAAGTTTTGGCTTTGGAACCTTTGAACAAATAACAAAAGGGTGGATTATACATTCAAAAAATTAATTCATAGAGATCTTAAG  
377▶ E K L D K V L A L E L F E Q I T K G V D Y I H S K K L I H R D L K  
1801 CCAAGTAAATATCTTAGTAGATACAAAACAAGTAAAGATTGGAGACTTTGGACTTTGAACTCTGAAAAATGATGAAAAGCAACAAGGAGTAAGG  
411▶ P S N I F L V D T K Q V K I G D F F G L V T S L K N D G K R T R S K  
1901 GAACCTTTCGATACATGAGCCCAGAACAGATTTCTCGCAAGACTATGGAAAGGAAGTGGACCTCTACGCTTTGGGCTAATCTTGTGAACCTTCTCA  
444▶ G T L R Y M S P E Q I S S Q D Y G K E V D L Y A L G L I L A E L L H  
2001 TGTATGTGACACTGCTTTTGAACATCAAAGTTTTTACAGACCTACGGGATGGCATCATCTCAGATATATTTGATAAAAAAGAAAAACTCTTCTACAG  
477▶ V C D T A F E T S K F F T D L R D G I I S D I F D K K E K T L L Q

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**Bsu36I (2118)** **BspLU11I (2199)**  
2101 AAATTACTCTCAAAGAAACCTGAGGATCGACCTAACACATCTGAAATACTAAGACCTTGACTGTGTGGAAGAAAAGCCAGAGAAAAATGAACGACACA  
511▶ K L L S K K P E D R P N T S E I L R T L T V W K K S P E K N E R H

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**MscI (2257)** **NheI (2251)**  
2201 CATGTTAGAGCCCTTCTGAAAAAGTATCCTGCTTCTGATATGCAGTTTTCCGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCA  
544▶ T C •

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**HpaI (2389)**  
2301 CAACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAACACAA  
2401 CAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGGTATGGAATTCAAAATACA

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2501 GCATAGCAAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTA

**SapI (2667)**

2601 GCTGTTTGAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCAAGGTTTGAAGTACTCTTCATTTCTTTATGTTTTAAATGCACTGA

SspI (2724)      SwaI (2738)

2701 CCTCCACATTCCCTTTTATGATAAATTCAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAA

2801 GGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTT

141 ← • N  
SacI (2999)

2901 CCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTATCTCAATGAGCACAAAGCAGTCAGAGCATAGTCAGAGATG  
139 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 C D P A Y D S I

**BstXI (3028)**

3001 AGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCT  
105 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 A V I T D F D K Q

StuI (3163)

3101 GCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGT  
72 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 V A S I I E G T

3201 CTTGGTCTGATGGCCGCCGACATGGTGTGTTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAG  
39 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 V L E L D Q Q S

**BbsI (3309)**

3301 ATGTTGAAGGCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGT  
5 I N F T K M ←

SacI (3428)

3401 CTCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTAC

**SpeI (3526)**

3501 GACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCC

**SnaBI (3654)**

3601 ACGCCATTGATGTAAGTCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTCCCAAGTAGGAAAGTCCCATAAGGTCATGTAC

**NdeI (3759)**

3701 TGGCATAATGCCAGGCGGGCCATTTACCGTCAATGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGTACTGCAAGTGGGAGTTTACC

3801 GTAAATACTCCACCATTGACGTCAATGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATATTGACGTCAATGGGCGGGGTCGTTGGGCGG

PacI (3945)

**PstI (3938)**  
**SdaI (3937)**      BspLU11I (3955)

3901 TCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGACAGGTTAATAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGG

4001 CCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAG

4101 ATACCAGGCGTTTCCCCGGAAGTCCCTCGTGCCTCTCTGTTCCGACCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTG

**ApaLI (4269)**

4201 GCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTGAGCCGACCGCT

4301 GCGCCTTATCCGTAACATATCGTCTTGTAGTCCAACCCGTAAGACACGACTTATCGCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTA

4401 TGTAGGCGGTGTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTC

4501 GGAAAAAGAGTTGGTAGCTCTTGATCCGCAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGGTGAAGCAGCAGATTACGCGCAGAAAAAAGGAT

PacI (4685)    SwaI (4694)

4601 CTCAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAA

**EagI (4705)**  
**NotI (4704)**

4701 ATCAGCGCGCGCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTAATCGTAACTAACATACGCTCTCCATCAAAACAAACGA

4801 AACAAACAAACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA