



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

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

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**NgoMIV (441)**  
401 GGGCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGCCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

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**AgeI (552)** **BspHI (560)**  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTATCATGATGGGCCTCCTTGGCCTCTGCTGTGCTCCTGGC  
1▶ M M G L S L A S A V L L A

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**BbrPI (632)**  
601 CTCCTCCTGAGTCTCCACCTTGAAGTCCACACAGTGGGAGTGACATATCCAAGACCTGCTGCTTCCAATACAGCCACAAGCCCTTCCCTGGACCTGG  
13▶ S L L S L H L G T A T R G S D I S K T C C F Q Y S H K P L P W T W

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**EcoRI (712)** **PvuII (726)** **XcmI (787)**  
701 GTGCGAAGCTATGAATTCACAGTAACAGCTGCTCCACGGGCTGTGATATCACTACCAAAAGAGGCAAGAAAGTCTGTACCCATCCAAGGAAAAAT  
47▶ V R S Y E F T S N S C S Q R A V I F T T K R G K K V C T H P R K K

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**MscI (857)** **NheI (851)**  
801 GGGTGCAAAAATACATTTCTTTACTGAAAACCTCCGAAACAATTGTGACTCAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCA  
80▶ W V Q K Y I S L L K T P K Q L •

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**HpaI (989)**  
901 CAACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACCAAGTTAACAAACA

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**EcoRI (1085)**  
1001 CAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCTAAAATACA  
1101 GCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTA

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**SapI (1267)**  
1201 GCTGTTTGCAGCCTCACCTTCTTTTCATGGAGTTAAGATATAGTGATTTTTCCAAGGTTTGAAGTCTCTTCAATTTCTTTATGTTTTAAATGCACTGA

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**SspI (1324)** **Swal (1338)** **EcoO109I**  
1301 CCTCCACATTCCTTTTTAGTAAAATATTCAGAAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAA  
1401 GGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTT  
141▶ • N

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**SacI (1599)**  
1501 CCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATG  
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

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**BstXI (1628)**  
1601 AGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCT  
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

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**StuI (1763)**  
1701 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  
1801 CTTGGTCTGATGGCCGCCCGACATGGTGCTTGTCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAG  
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

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**BbsI (1909)** **XmnI (1905)** **AseI (1971)**  
1901 ATGTTGAAGGCTTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGT  
5▶ I N F T K M

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**SacI (2028)**  
2001 CTCCAGCTTATCTGACGGTTCACATAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTAC

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**SpeI (2126)**  
2101 GACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCCATGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCC

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**SnaBI (2254)**  
2201 ACGCCATTGATGTAAGTCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTCCCAAGTAGGAAAGTCCCATAAAGTTCATGTAC

2301 TGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACC  
2401 GTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGG

PacI (2545)  
PstI (2538)  
SdaI (2537)      BspLU11I (2555)

2501 TCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATTAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGG  
2601 CCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAG  
2701 ATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCTGTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTG

ApaLI (2869)

2801 GCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTGAGCCGACCGCT  
2901 GCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTA  
3001 TGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTC  
3101 GGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGAT

PacI (3285)   SwaI (3294)

3201 CCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAA

EagI (3305)  
NotI (3304)

3301 ATCAGCGCGCGCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGA  
3401 AACAAAACAACTAGCAAAATAGGCTGTCCCAAGTCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA