



**PvuI (7)**  
**SgfI (6)** **MfeI (82)**  
1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTGTGCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

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**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCTGACCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

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**AgeI (552) NcoI (560)**  
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCTACCTGAGATCACCGGTACCATTGATTATCAAGTGTCAAGTCCAATCTATGACATCAA  
1 M D Y Q V S S P I Y D I N  
**BsrBI (664)**  
601 TTATTATACATCGAGCCCTGCCAAAAATCAATGTGAAGCAATCGCAGCCCGCCTCCTGCCTCCGCTCTACTCACTGGTGTTCATCTTTGGTTTTGTG  
13 Y Y T S E P C Q K I N V K Q I A A R L L P P L Y S L V F I F G F V

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**SapI (744)**
**MscI (776)**  
701 GGCAACATGCTGGTCATCCTCATCTGATAAACTGCAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCC  
47 G N M L V I L I L I N C K R L K S M T D I Y L L N L A I S D L F F

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**XcmI (837)**  
801 TTCTTACTGTCCCTTCTGGGCTCACTATGCTGCCGCCAGTGGGACTTTGAAATACAATGTGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTT  
80 L L T V P F W A H Y A A A Q W D F G N T M C Q L L T G L Y F I G F F

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**Acc65I (938)**  
901 CTCTGGAATCTTCTTCATCATCCTCCTGACAATCGATAGGTACTTGGCTGTGCTCCATGCTGTGTTTGCCTTAAAAGCCAGGACGGTCACCTTTGGGGTG  
113 S G I F F I I L L T I D R Y L A V V H A V F A L K A R T V T F G V

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**BglII (1063)**
**PstI (1092)**  
1001 GTGACAAGTGTGATCACTTGGGTGGTGGCTGTGTTTGCCTCTCCAGGAATCATCTTACCAGATCTCAAAAAGAAGGTCTTCATTACACCTGCAGCT  
147 V T S V I T W V V A V F A S L P G I I F T R S Q K E G L H Y T C S

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**BsaBI (1152)**  
1101 CTCATTTTCCATACAGTCAGTATCAATTCTGGAAGAATTTCCAGACATTAAGATAGTCATCTTGGGCTGGTCTGCGCTGCTTGTGATGGTCATCTG  
180 S H F P Y S Q Y Q F W K N F Q T L K I V I L G L V L P L L V M V I C

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**BspHI (1280)**  
1201 CTACTCGGAATCCTAAAACTCTGCTTCCGGTGTGAAATGAGAAGAAGAGGCACAGGGCTGTGAGGCTTATCTTACCATCATGATTGTTTATTTTCTC  
213 Y S G I L K T L L R C R N E K K R H R A V R L I F T I M I V Y F L

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**EcoRI (1345)**  
**XcmI (1341)**  
1301 TTCTGGGCTCCCTACAACATTGCCTTCTCCTGAACACCTTCCAGGAATTCCTTGGCCTGAATAATTGCAGTAGCTCTAACAGTTGGACCAAGCTATGC  
247 F W A P Y N I V L L L N T F Q E F F G L N N C S S S N R L D Q A M  
1401 AGGTGACAGAGACTCTTGGGATGACGCACTGCTGCATCAACCCATCATCTATGCCTTGTGCGGGAGAAGTTCAGAACTACCTCTTAGTCTTCTTCCA  
280 Q V T E T L G M T H C C I N P I I Y A F V G E K F R N Y L L V F F Q  
1501 AAAGCACATTGCCAAACGCTTCTGCAAATGCTGTTCTATTTTCCAGCAAGAGGCTCCCGAGCGAGCAAGCTCAGTTTACACCCGATCCACTGGGGAGCAG  
313 K H I A K R F C K C C S I F Q Q E A P E R A S S V Y T R S T G E Q

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**MscI (1664)**  
1601 GAAATATCTGTGGGCTTGTGACACGGACTCAAGTGGGCTGGTACCAGTCAGAGTTGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGAA  
347 E I S V G L •

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**HpaI (1796)**  
1701 CAAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAACAAGTTA

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**MfeI (1807)**
**EcoRI (1892)**  
1801 ACAACAACAATTGCATTCATTTTATGTTTCAGGTTCCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATCTA  
1901 AAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATG

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**SapI (2074)**  
2001 TGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGAGTAAAGATAGTGTATTTTCCCAAGGTTTGAAGTCTTCTTATGTTTAAAT

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**SspI (2131)**
**SwaI (2145)**  
2101 GCACTGACCTCCACATTCCCTTTTGTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGA

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**EcoO109I (2206)**  
2201 TGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGAACAAGGAACCTTAAATAGAAATTTGGACAGCAAGAAAGCGAGCTTCTAGC

2301 TTTAGTTCCTGGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGTTGCCATTTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTC  
141 ◀ • 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 C D P A Y D  
SacI (2406) BstXI (2435)

2401 AGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAG  
108 ◀ 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 A V I T D F  
StuI (2570)

2501 TCCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTACAGCACAGCAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCT  
74 ◀ 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 V A S I I E  
2601 CCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGTGTTGTCCCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTG  
41 ◀ 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 V L E L D Q  
AseI (2778)

2701 CTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGG  
8 ◀ Q S I N F T K M ◀  
SacI (2835)

2801 ATGGCGTCTCCAGCTTATCTGACGGTCTACTAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAG

2901 TTGTTACGACATTTTGGAAAGTCCCCTGTTGATTTACTAGTCAAAAACAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAAC  
SpeI (2933)

3001 GCTATCCACGCCATTGATGTACTGCCAAAACGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAGGT  
SnaBI (3061)

3101 CATGTAAGTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTAAGTGGGCA  
NdeI (3166)

3201 GTTACCCTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGT

3301 TGGGCGTCCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGT  
PacI (3352) PstI (3345) SdaI (3344) BspLU11I (3362)

3401 AAAAAAGCCGCTTGTGGCGTTTTTTCATAGGCTCCGCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCAAACCCGACAGGAC  
3501 TATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGGCTCTCTGTCCGACCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGG

3601 AAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCAGCCC  
ApaLI (3676)

3701 GACCGTGGCGCTTATCCGTAAGTATCGTCTTGTGTTGACCAACCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAG  
3801 CGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGT  
3901 TACCTTCGAAAAAGAGTTGGTAGCTCTTGTATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGGCAGAAAA  
PacI (4092)

4001 AAAGGATCTCAAGAAGATCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAA

EagI (4112)  
SwaI (4101) NotI (4111)

4101 CATTTAAATCAGCGGCCCAATAAAATATCTTTATTTTTCATTACATCTGTGTGGTTTTTTGTGTAATCGTAACATAACATACGCTCTCCATCAAAC  
4201 AAAACGAAAACAAAACAACTAGCAAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA