



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
**MfeI (82)**  
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTGCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

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**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

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**AgeI (552)** **BspHI (560)** **XmaI (584)** **MseI (593)**  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCTACCTGAGATCACCGGTATCATGACCATGTTTAAAATGTCACCCGGCCCTGGCCAG  
1 M T M F E N V T R A L A R

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**XhoI (611)** **Eco47III (653)**  
601 ACAGCTAAACCCCTCGAGGGACCTGACACCACTTGACAGCCTCATCGACTTCAAGCGCTTCCATCCCTTCTGCCTGGTGTGAGGAAGAGGAAGAGCAGC  
13 Q L N P R G D L T P L D S L I D F K R F H P F C L V L R K R K S T  
701 CTCTTCTGGGGGCGCGTACGTCGACCCGACTACACGCTGTGGATGTGCTTGAGCCCGCAGCTCACCTCAGACCCAACAGACACTGGGAATTTTG  
47 L F W G A R Y V R T D Y T L L D V L E P G S S P S D P T D T G N F  
801 GCTTTAAGAATATGCTGGACCCGAGTGGAGGAGATGTGGATGTACCAAAGACGGTGAAGGTGAAGGGAACGGCAGGGCTCTCGAGAACAGCACTCT  
80 G F K N M L D T R V E G D V D V P K T V K V K G T A G L S Q N S T L

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**DraIII (911)** **BstXI (926)**  
901 GGAGTCCAGACACTCAGTGTGGCTCCCAAGGCCCTGGAGACCGTGCAGGAGAGGAAGCTGGCAGCAGACCACCCATTCTGAAGGAGATGCAAGATCAA  
113 E V Q T L S V A P K A L E T V Q E R K L A A D H P F L K E M Q D Q

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**NgoMIV (1063)**  
1001 GGGGAGAACCTGTATGTGGTGTGGAGTGGTGGAGACGGTGCAGGAGGTCACTGGAGCGAGCCGCAAGGCAGAGGCTGCTTCTCCCTCCCTTCT  
147 G E N L Y V V M E V V E T V Q E V T L E R A G K A E A C F S L P F

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**BamHI (1120)** **PvuII (1186)**  
1101 TCGCCCCATTGGGGCTACAGGGATCCATAAATCACAAGGAGGCTGTAACCATCCCCAAGGGCTGCGTCTGGCCTTTCGAGTGAGACAGCTGATGGTCAA  
180 F A P L G L Q G S I N H K E A V T I P K G C V L A F R V R Q L M V K  
1201 AGGCAAAGATGAGTGGGATATCCACATATCTGCAATGATAACATGCAAACCTTCCCTCCTGGAGAAAAGTCAAGGAGAGGAGAAGGTATCCTTATCCAG  
213 G K D E W D I P H I C N D N M Q T F P P G E K S G E E K V I L I Q

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**XmnI (1345)**  
1301 GCATCTGATGTTGGGACGTACACGAAGGCTCAGGACACTAAAAGAAGAAGTTCAGAGAGAGACCCAACAAGTGGAGAAGCTGAGCCGAGTAGGGCAAA  
247 A S D V G D V H E G F R T L K E E V Q R E T Q Q V E K L S R V G Q

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**XbaI (1479)**  
1401 GCTCCCTGCTCAGCTCCCTCAGCAAACCTCTAGGGAAGAAAAAGGAGCTACAAGACCTTGAGCTCGCACTTGAAGGGCTCTAGACAAGGGACATGAAGT  
280 S S L L S S L S K L L G K K K E L Q D L E L A L E G A L D K G H E V  
1501 GACCCTGGAGGCACTCCCAAAAGATGCTCTGCTATCAAAGGAGGCCGTGGGCGCCATCCTCTATTTGTTGGAGCCCTAACAGAGCTAAGTGAAGCCCAA  
313 T L E A L P K D V L L S K E A V G A I L Y F V G A L T E L S E A Q

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**NcoI (1619)**  
1601 CAGAAGCTGCTGGTGAATCCATGGAGAAAAAGATCCTACCCGTGCAGCTAAAGCTGGTGGAGAGCACGATGGAACAGAATCTCTGCTGGATAAAGAGG  
347 Q K L L V K S M E K K I L P V Q L K L V E S T M E Q N F L L D K E  
1701 GTGTTTTCCCTGCAACCTGAGCTGCTCTCCCTTGGGACGAGGAGCTGACCCCTCACGAGGCTCTAGTCGGGCTGAGTGGCCTGGAAGTGCAGAG  
380 G V F P L Q P E L L S S L G D E E L T L T E A L V G L S G L E V Q R

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**SmaI (1820)**  
1801 ATCGGGCCCCAATATATGTTGGACCCAGACACCCCTCCCTCGCTCTGTGCTCTTTATGCAGGCTCTCTCTCCCTCAGCAGCTTACCAAGGCCCTCTAA  
413 S G P Q Y M W D P D T L P R L C A L Y A G L S L L Q Q L T K A S •

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**MseI (1929)** **NheI (1923)**  
1901 TTTGCCTTTTACGTCTGCTTCATGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTT

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**HpaI (2061)** **MfeI (2072)**  
2001 TATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAACAAGTTAACAAACAACATTGCATTCATTTTATGTTTCAGGTT

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**EcoRI (2157)**  
2101 CAGGGGAGGTGTGGGAGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACTTTAACCTCCAAATCA  
2201 AGCCTTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATG

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**SspI (2396)**  
2301 GAGTTTAAAGATATAGTGTATTTCCCAAGTTTGAAGTACTGCTCTTCATTTCTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAATA

SwaI (2410)  
 2401 TTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGT  
 2501 AGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGGATGAGTTCC  
 2601 TCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGA  
 129 E I T T K V L K G 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  
 BstXI (2700)  
 2701 CCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCCGTTGCTCACAGCAGACCCAATGGC  
 96 V R I S R D V E 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  
 2801 AATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCCGACATGG  
 63 I A E A C V T V R G I Y A E I H V A S I I E G T K T R I A A G V H  
 BbsI (2981)  
 XmnI (2977)  
 2901 TGCTTGTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCGACTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCC  
 29 H K N D E Y L M T I K E T A V E V L E L D Q Q S I N F T K M  
 AseI (3043)  
 3001 TATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAC  
 SpeI (3198)  
 3101 GAGCTCTGCTTATATAGACCTCCACCCTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTAC  
 3201 TAGTCAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGACTGCCAAAACCGC  
 SnaBI (3326)  
 3301 ATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTAC  
 NdeI (3431)  
 3401 CGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCGAGTTTACCGTAAATACTCCACCCATTGACGTCAATG  
 3501 GAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAAGT  
 PacI (3617)  
 PstI (3610)  
 SdaI (3609)  
 BspLU11I (3627)  
 3601 TATGTAACGCTGCAGGTTAATAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGGTGGCGTTTTTCCATAGGCT  
 3701 CCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCC  
 3801 CTCGTGCGCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGTTTTCTCATAGCTCAGCTGTAGGT  
 ApaLI (3941)  
 3901 ATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGACGAAACCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGA  
 4001 GTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTTCTTGAAG  
 4101 TGGTGGCCTAACTACGGTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCG  
 4201 GCAAACAACACCAGCTGGTAGCGGTGTTTTTTTTGTTGCAAGCAGCAGATTACCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTCTAC  
 EagI (4377)  
 PacI (4357) SwaI (4366) NotI (4376)  
 4301 GGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCCAATAAAATATCTTTAT  
 4401 TTTCATTACATCTGTGTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAAACAAAACGAAAACAAAACAACTAGCAAAATAGGCTGT  
 4501 CCCAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA