



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
**MfeI (82)** **EcoNI (96)**  
101 GAGAAGTGGCGCGGGTAAACTGGAAAGTATGATGCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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**HindIII (245)** **Bsu36I (291)**  
**Psp1406I (203)** **PvuII (239)** **EcoNI (287)**  
201 GTGAACGTTCTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCCGCCCTACCTGAGGCC  
301 GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCGCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

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**AgeI (552)** **BspLU11I (560)** **XbaI (588)**  
501 TCTGTTTGTCCGCGCTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTCAACATGTCCACCTCTTCCCTGAAGTGGATCTAGAGAATTT  
1 M S T S F P E L D L E N F

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**StuI (620)**  
601 TGAGTATGACGATTCTGCTGAGGCTGTATTTGGGCGACATTGTGGCCTTTGGAACCATCTTCTGTCCGTCTTCTACGCCCTCGTCTTACGTTCCGGT  
13▶ E Y D D S A E A C Y L G D I V A F G T I F L S V F Y A L V F T F G  
701 CTGGTGGGAAATCTGTTGGTGGTCTCGCTCTACCAACAGCCGGAAGCCCAAGAGCATCACTGACATCTACCTCCTGAACCTGGCCTTGGAGCAGCTGC  
47▶ L V G N L L V V L A L T N S R K P K S I T D I Y L L N L A L S D L

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**MscI (806)**  
801 TCTTTGTGGCCACCTTGCCTTCTGGACTCACTACCTCATCAGCCATGAGGGCCTCCACAATGCCATGTGCAAGCTCACGACTGCCTTCTTCTATTGG  
80▶ L F V A T L P F W T H Y L I S H E G L H N A M C K L T T A F F F I G

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**Acc65I (944)** **AgeI (941)**  
901 CTTCTTTGGGGGCATATTCTTTCATCACCCTCATCAGCATCGACCGGTACCTTGCATCGTCTGGCCGCAACTCCATGAACAACCGGACAGTGCAGCAC  
113▶ F F G G I F F I T V I S I D R Y L A I V L A A N S M N N R T V Q H  
1001 GGCCTCACCATTAGTCTGGGCGTCTGGGCGGCGGCATCTTAGTGGCGTCACCCAGTTCATGTTCAAAAGAGAAAGGACAACGAGTGTCTGGGTGACT  
147▶ G V T I S L G V W A A A I L V A S P Q F M F T K R K D N E C L G D

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**PstI (1111)** **SdaI (1110)** **BspHI (1181)**  
1101 ACCCCGAGGTCCTCGAGGAAATGTGGCCGTGCTCCGCAACTCGGAAGTCAACATCCTGGGCTTCCGCCCTGCCCTTGCTTATCATGAGCTTTTGTACTT  
180▶ Y P E V L Q E M W P V L R N S E V N I L G F A L P L L I M S F C Y F  
1201 CCGCATCATCAGACGCTGTTTTCTGCAAGAATCGCAAGAAGCCAGAGCCGTGAGACTCATCTCCTGGTGGTCTTTGCCCTTCTTCTCTTCTGGACA  
213▶ R I I Q T L F S C K N R K K A R A V R L I L L V V F A F F L F W T

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**BspHI (1310)** **Bsu36I (1374)**  
1301 CCATAACAACATCATGATTTTCTGGAGACTCTCAAGTTCTACAACCTTCTCCCAAGTTGTGACATGAAGAGGGACCTGAGGTTGGCCCTCAGTGTGACGG  
247▶ P Y N I M I F L E T L K F Y N F F P S C D M K R D L R L A L S V T  
1401 AGACAGTGGCGTTGAGCCACTGTTGCCCTCAACCCCTTATCTAGCCTTTGCGGGGAAAAGTTCAGAAGATACTGGGACACCTGTATAGGAAGTGCCT  
280▶ E T V A F S H C C L N P F I Y A F A G E K F R R Y L G H L Y R K C L  
1501 GGGCGTCTGTGGGTGATCCTGTCCACACCGGCTTCTGCCAGAGTCCCAGAGGAGCAGGCAGGACAGCATTCTGAGCAGTTTCACTCACTACAAGC  
313▶ A V L C G H P V H T G F S P E S Q R S R Q D S I L S S F T H Y T S

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**MscI (1659)** **NheI (1653)**  
1601 GAGGGAGATGGGTCTCTCTGCTCTGAAGGGTCTCCCGACCCTAGCTCCACGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAC  
347▶ E G D G S L L L •

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**HpaI (1791)**  
1701 CACAAGTGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAAC

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**MfeI (1802)** **EcoRI (1887)**  
1801 AACAAATGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCATAAATA  
1901 CAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCAT

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**SapI (2069)**  
2001 TAGCTGTTTGAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGGTTTGAAGTACTGCTCTTCAATTTCTTTATGTTTAAATGCACT

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**SspI (2126)** **SwaI (2140)**  
2101 GACCTCCACATTCCTTTTATGTAATAATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTC  
2201 AAGGCCCTTATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTAAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAG  
141▶ •

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**SacI (2401)**  
2301 TTCCTGGTACTTGGGGGATGAGTTCTCAATGGTGGTTTTGACCAGCTTGCATTCACTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGA  
139▶ 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 S I  
2401 TGAGCTCTCTGCACATGCCACAGGGGTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCCTT  
106▶ 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

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**StuI (2565)**  
2501 CTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCCAGCAGACAGTACCCTGCAATGAGGCTCAATGTGGACAGCAGAGATGATCTCCCA  
73▶ 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 G  
2601 GTCTTGGTCTGATGGCCGCCCCGACATGGTGTCTGTTGCTCCTCATAGAGCATGGTGTCTTCTCAGTGGCGACTCCACCAGCTCCAGATCCTGCTGAG  
39▶ 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 Q S

**XmnI (2707)** **AseI (2773)**  
 2701 AGATGTTGAAGGTCCTCATGGTGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGC  
 6 I N F T K M

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**SacI (2830)**  
 2801 GTCCTCAGCTTATCTGACGGTTCACATAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCATTGCGTCAATGGGGCGGAGTTGTT

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**SpeI (2928)**  
 2901 ACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAAATCCCCGTGAGTCAAACCGCTAT

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**SnaBI (3056)**  
 3001 CCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTCCCAAGTAGGAAAGTCCCATAAGGTCATGT

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**NdeI (3161)**  
 3101 ACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTA  
 3201 CCGTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGGTCTGTTGGGC

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**PstI (3340)** **SdaI (3339)** **PacI (3347)** **BspLU11I (3357)**  
 3301 GGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATTAAGAACATGTGAGCAAAAAGGCCAGCAAAAAGGCCAGGAACCGTAAAAA  
 3401 GGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAA  
 3501 AGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCG

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**ApaLI (3671)**  
 3601 TGGCGTTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTGAGCCGACCG  
 3701 CTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGG  
 3801 TATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCT  
 3901 TCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGG

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**PacI (4087)** **SwaI (4096)**  
 4001 ATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTATGGCTAGTTAATTAACATT

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**EagI (4107)**  
**NotI (4106)**  
 4101 AAATCAGCGGCCGAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAAC  
 4201 GAAACAAAACAACTAGCAAAATAGGCTGTCCCAAGTCAAGTGACAGGTGCCAGAACATTTCTCTATCGAA