



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGCGCAATTGAACGGGTGCCTA  
**MfeI (82)**  
101 GAGAAGGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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**Psp1406I (203)** 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTCACGCGCCGCCCTACCTGAGGCC  
**HindIII (245)**  
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

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**BstEII (555)**  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTACCATGGCGTCGCTCACCGTGAAGGCCTACCTTCTGGGCAA  
**AgeI (552)** **NcoI (560)** **StuI (581)**  
1▶ M A S L T V K A Y L L G K

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**BssHII (610)** 601 GGAGGACGCGGCGCGAGATTGCGCGCTTCACTTCTGCTGCAGCCCCGAGCCTGAGCGGAAGCCGAGGCTGCGGCGGGTCCGGGACCCTGCGAGCGG  
13▶ E D A A R E I R R F S F C C S P E P E A E A E A A A G P G P C E R  
701 CTGCTGAGCCGGTGGCCGCCCTGTTCCCCGCTGCGGCCTGGCGGCTTCCAGGCGCACTACCGCGATGAGGACGGGACTTGGTTGCCTTTTCCAGTG  
47▶ L L S R V A A L F P A L R P G G F Q A H Y R D E D G D L V A F S S

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801 ACGAGGAATTGACAATGGCCATGTCCTACGTGAAGGATGACATCTTCCGAATCTACATTAAGAGAAAAAGAGTGGCCGGGACCACCGCCACCACTG  
80▶ D E E L T M A M S Y V K D D I F R I Y I K E K K E C R R D H R P P C  
**NgoMIV (875)** **DraIII (893)**

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901 TGCTCAGGAGGCGCCCCGCAACATGGTGACCCCAATGTGATCTGCGATGGCTGCAATGGGCCTGTGGTAGGAACCCGCTACAAGTGCAGCGTCTGCCCA  
113▶ A Q E A P R N M V H P N V I C D G C N G P V V G T R Y K C S V C P  
1001 GACTACGACTTGTGTAGCGTCTGCGAGGGAAAGGCTTGACCGGGGGCACACCAAGCTCGCATTCCCAGCCCCTTCGGGCACCTGTCTGAGGGCTTCT  
147▶ D Y D L C S V C E G K G L H R G H T K L A F P S P F G H L S E G F  
**ApaLI (925)** **BstAPI (986)**

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1101 CGCACAGCCGCTGGCTCCGGAAGGTGAAACACGGACACTTCGGGTGGCAGGATGGGAAATGGGTCCACCAGGAACTGGAGCCACGTCCTCCTCGTGC  
180▶ S H S R W L R K V K H G H F G W P G W E M G P P G N W S P R P P R A  
**BstXI (1168)**

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1201 AGGGGAGGCCCGCCTGGCCCCACGGCAGAATCAGCTTCTGGTCCATCGGAGGATCCGAGTGTGAATTTCTGAAGAACGTTGGGAGAGTGTGGCAGCT  
213▶ G E A R P G P T A E S A S G P S E D P S V N F L K N V G E S V A A  
**BamHI (1251)** **Psp1406I (1276)**

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1301 GCCCTTAGCCCTCTGGGCATTGAAGTTGATATCGATGTGGAGCACGGAGGGAAAAGAGCCGCTGACCCCGTCTCTCCAGAGAGTTCAGCACAGAGG  
247▶ A L S P L G I E V D I D V E H G G K R S R L T P V S P E S S S T E  
**SapI (1401)** **BstAPI (1421)**

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1401 AGAAGAGCAGCTCACAGCCAAGCAGCTGCTGCTGACCCAGCAAGCCGGTGGGAATGTTGAGGGGCCACGCAGTCTCTGGCGGAGCAGATGAGGAA  
280▶ E K S S S Q P S S C C S D P S K P G G N V E G A T Q S L A E Q M R K  
**BbsI (1584)**

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1501 GATCGCCTTGAGTCCGAGGGGCGCCCTGAGGAACAGATGGAGTCGGATAACTGTTACAGGAGGAGATGACTGGACCCATCTGTCTTCAAAGAAGTG  
313▶ I A L E S E G R P E E Q M E S D N C S G G D D D W T H L S S K E V  
**SandI (1677)**

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1601 GACCCGCTACAGGTGAAGTCCAGTCCCTACAGATGCCAGAATCCGAAGGGCCAAGCTCTCTGGACCCCTCCAGGAGGGACCCACAGGGCTGAAGGAAG  
347▶ D P S T G E L Q S L Q M P E S E G P S S L D P S Q G E G P T G L K E  
**SacII (1735)** **NcoI (1769)**

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1701 CTGCCTTGATCCACATCTCCCGCCAGAGGCTGACCCGCGGCTGATTGAGTCCCTCTCCAGATGCTGTCATGGGCTTCTCTGATGAAGCGGCTGGCT  
380▶ A A L Y P H L P P E A D P R L I E S L S Q M L S M G F S D E G G W L  
**BsrBI (1835)**

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1801 CACCAGGCTCCTGCAGACCAAGAATATGACATCGGAGCGGCTCTGGACACCATCCAGTATTCAAAGCATCCCCGCCGTTGTGACCACTTTTGGCCACC  
413▶ T R L L Q T K N Y D I G A A L D T I Q Y S K H P P P L •  
**NheI (1906)**

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1901 TCTTCTGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAACCACAAGTGAAGTGAAGGAAATGCTTTATTTGTGAAATTTGTG

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2001 ATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAAACAACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGA  
**HpaI (2044)** **MfeI (2055)**

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2101 GGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCTCTACTGAAATCC  
**EcoRI (2140)**

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2201 TTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTCATGGAGTTAAGATATAGTG

2301 **SapI (2322)** TATTTTCCAAGTTTGAAGTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCCACATTCCCTTTTATGAAAATATTAGAAAATAATTTAAA  
**SspI (2379)** **SwaI (2393)**  
 2401 TACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAAC  
 2501 AAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTACTTGAGGGGATGAGTTTCCTCAATGGTGGTTTTGAC  
 141 • N R T Y K L P I L E E I T T K V  
**SacI (2654)** **BstXI (2683)**  
 2601 CAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTG  
 124 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 V R I S R  
 2701 TCCACCTCATCAGAGTAGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGA  
 90 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 I A E A C V  
**StuI (2818)**  
 2801 CAGTGACCCTGCCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGCTTGTGTCTCATA  
 57 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 H K N D E Y  
**BbsI (2964)** **XmnI (2960)**  
 2901 GAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCCTATAGTGAGTCGTATTA  
 24 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 (3026)** **SacI (3083)**  
 3001 TACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCCACAGCTTATCTGACGGTTCATAAACGAGCTCTGCTTATATAG  
**SpeI (3181)**  
 3101 ACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGCGGAGTTGTTACGACATTTTGAAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCC  
 3201 CATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGC  
**SnaBI (3309)**  
 3301 GATGACTAATACGTAGATGTAAGTCCATAAGGTGCAATGACTGGGCATAATGCCAGGCGGGCCATTTACCGTCAATTGACGTCAATA  
**NdeI (3414)**  
 3401 GGGGGCGTACTTGGCATATGATACACTTGTACTGCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATGAAAAGTCCCTATTGGCG  
**SdaI (3592)**  
 3501 TTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGC  
**PacI (3600)** **BspLU11I (3610)**  
 3601 TTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGC  
 3701 ATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCTCGGAAGCTCCCTCGTGCGCTCTCTGT  
 3801 TCCGACCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAG  
**ApaLI (3924)**  
 3901 GTCGTTGCTCCAAGCTGGGCTGTGTGACGCAACCCCGTTGAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAAGTCCAAACCGGTAAGAC  
 4001 ACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGG  
 4101 CTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGTATCCGCAAAACAAACCACCGCT  
 4201 GGTAGCGGTGGTTTTTTTGTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGT  
**EagI (4360)**  
**PacI (4340)** **SwaI (4349)** **NotI (4359)**  
 4301 GGAACGAAAACCTCACGTTAAGGGATTTTGGTATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTATTACATCTGTGT  
 4401 GTTGGTTTTTTGTGTAATCGTAACATAACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCAGTGCAAGTGCAG  
 4501 GTGCCAGAACATTTCTCTATCGAA