



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA **MfeI (82)**  
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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**Psp1406I (203)** 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTTCACGCGCCCGCCCTACCTGAGGCC **HindIII (245)** **Bsu36I (291)**  
301 GCCATCCACGCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCGCTCTAGGTAAGTTTAAAGTCAAGTGCAGACC

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401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGCTTTTGTTCGTTT **NgoMIV (441)**

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501 TCTGTTTGTGCGCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTACCATGGCCTCCAGCTCAGGCAGCAGTCTCGCCCGCCCC **AgeI (552)** **NcoI (560)**  
601 TGATGAGAATGAGTTTCCCTTTGGGTGCCCTCCACCCTGTGCCAGGACCCAAAGGAGCCAGGGCTCTCTGTGTGCAGGCTGTCTCTGAGAACCCG **1** M A S S S G S S P R P A P  
**13** D E N E F P F G C P P T V C Q D P K E P R A L C C A G C L S E N P

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701 AGGAATGGCGAGGATCAGATCTGCCCAATGCAGAGGGGAAGACCTCCAGTCTATAAGCCAGGAAGCCGTCTTCAACTCAGGAGAAGGCTCACCCCG **BglII (716)** **BstBI (773)**  
47 R N G E D Q I C P K C R G E D L Q S I S P G S R L R T Q E K A H P **Bsp119I (773)**  
801 AGGTGGCTGAGGCTGGAATTGGGTGCCCTTTGACAGTGTGGCTGCTCTTCAAGGGAAGCCACAGTCTGTGCAAGAGCATGAGGTCACTCCAGAC **80** E V A E A G I G C P F A G V G C S F K G S P Q S V Q E H E V T S Q T  
**NcoI (974)**  
**BstXI (974)**  
**Bsp120I (970)**

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901 CTCCACCTAAACCTGCTGTTGGGGTTCATGAAACAGTGAAGGCCCGCTGGGCTGTGGCCTGGAGTCTGGCCCATGGCCCTGGAGCAGAACCTGTCA **113** S H L N L L L G F M K Q W K A R L G C G L E S G P M A L E Q N L S  
1001 GACCTGCAGTGCAGGCAGCCGTGGAAGTGGCGGGGACCTGGAGTGCATTGCTACCGGCACCTGCTCCGAGAGCCAGGAGGAGTGGCCCTGCAGC **147** D L Q L Q A A V E V A G D L E V D C Y R A P C S E S Q E E L A L Q

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1101 ACTTCATGAAGGAGAAGCTTCTGGCTGAGCTGGAGGGGAAGCTGCGTGTGTTGAGAATTGTTGCTGCTCAACAAGGAGGTGGAGGCTCCACCT **HindIII (1114)**  
180 H F M K E K L L A E L E G K L R V F E N I V A V L N K E V E A S H L  
1201 GGCCTGGCCACCTCTATCCACCAGAGCCAGTGGACCTGAGCGCATCTGAGCTTGGAGCAGAGGGTGGTGGAGTTCAGCAGACCCTGGCCAGAAA **213** A L A T S I H Q S Q L D R E R I L S L E Q R V V E L Q Q T L A Q K

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1301 GACCAGGCCCTGGCAAGCTGGAGCAGAGCTTGGCCCTCATGGAGGAGCCTCCTTCGATGGCACTTTCTGTGGAAGATCACCATGTCAACAGGCGGT **BstAPI (1323)**  
247 D Q A L G K L E Q S L R L M E E A S F D G T F L W K I T N V T R R  
1401 GCCATGAGTGGCCCTGTGGCAGGACCTGAGCCTTCTCCCAAGCCTTCTACTGCAAGTATGGTACAAGTTGTGCTGCGGCTGTACCTGAATGG **280** C H E S A C G R T V S L F S P A F Y T A K Y G Y K L C L R L Y L N G

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1501 AGATGGCACTGGAAGAGAACCCATCTGCTCGCTTTCATCGTATCATGAGAGGGGATGATGCGCTGCTGCGGCTGGCCCTTCCGGAACAAGGTCAAC **SapI (1530)** **BspEI (1583)**  
313 D G T G K R T H L S L F I V I M R G E Y D A L L P W P F R N K V T  
1601 TTCATGCTGCTGGACCAGAACACCGTGAACGACGACCTTGGACGCTTCCGGCCTGACCTAAGCTCAGGCTCCTCCAGAGGCCAGAGTGAACCAACG **347** F M L L D Q N N R E H A I D A F R P D L S S A S F Q R P Q S E T N  
1701 TGGCAGTGGATGCCACTTCTTCCCTCAGCAAAGTGCAGTCAACCAAGCAGCCTACGTGAAGGACGACACAATGTTCTCAAGTGCATTGTGGA **380** V A S G C P L F F P L S K L Q S P K H A Y V K D D T M F L K C I V E

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1801 GACCAGCACTTAGGGTGGCGGGGCTCCTGAGGGAGCTCCAACCTAGCTAGTGGCCAGACATGATAAGATACATTGATGAGTTTGGCAAACCACAACT **Bsu36I (1826)** **NheI (1846)**  
413 T S T •

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1901 AGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATT **HpaI (1984)** **MfeI (1995)**

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2001 GCATTCATTTTATGTTTCAGGTTACAGGGGAGGTGTTGGGAGGTTTTTAAAGCAAGTAAACCTTACAAATGTGGTATGGAATCTAAAATACAGCATA **EcoRI (2080)**  
2101 GCAAACTTTAACCTCCAATCAAGCCTCTACTGAACTCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGCTGTTGCCAATGTGCATTAGCTGT

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2201 TTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGATTTTCCCAAGGTTTGAAGTCTTCTCATTTTATGTTTTAAATGCACTGACCTCC **SapI (2262)**

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2301 CACATTCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCC **SspI (2319)** **SwaI (2333)**  
2401 TTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGG **141** • N R T

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2501 TGTAAGTGGGGGATGAGTTTCTCAATGGTGGTTTTGACCAGCTTGCATTCATCTCAATGAGCACAAGCAGTCAAGGAGCAGTCAAGATGAGGCTC **137** 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 L E  
**BstXI (2623)**

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2601 TCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCG **104** 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 G

2701 TTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGG  
70 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 K T  
2801 TCCTGATGGCCGCCCGACATGGTGTCTTGTCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTT  
37 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 I N  
XmnI (2900) AseI (2966)  
2901 GAAGGCTTTCATGGTGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCA  
4 F T K M  
3001 GCTTATCTGACGGTTCACATAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACAT  
SpeI (3121)  
3101 TTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGCTATCCACGCC  
SnaBI (3249)  
3201 CATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGC  
NdeI (3354)  
3301 ATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAA  
3401 TACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCTGTTGGCGGTCAGC  
PacI (3540) SdaI (3532) BspLU11I (3550)  
3501 CAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAAATAAGAACATGTGAGCAAAAGGCCAGAAAAGGCCAGGAACCGTAAAAAGGCCGCG  
3601 TTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACC  
3701 AGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCT  
ApaLI (3864)  
3801 TTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTACGCCGACCGCTGCGCC  
3901 TTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAG  
4001 GCGGTGTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAA  
4101 AAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAA  
PacI (4280) SmaI (4289) NotI (4299)  
4201 GAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AG  
EagI (4300)  
4301 CGGCCGAATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAA  
4401 AACAAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA