



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
**MfeI (82)**  
101 GAGAAGTGGCGCGGGTAAACTGGAAAGTGATGCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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**HindIII (245)**  
**Psp1406I (203)** 201 GTGAACGTTCTTTTTCGCAACGGGTTTCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCCGCCCTACCTGAGGCC  
**PvuII (239)**  
**Bsu36I (291)**  
301 GCCATCCACGCGGTTGAGTGCCTTCTGCCGCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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**NgoMIV (441)**  
**NaeI (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

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**NcoI (560)**  
**BstEII (555)**  
501 TCTGTTCTGCGCGGTTACAGATCCAAGCTGTGACCGCGCGCTACCTGAGATCACCGGTCCACCATGGAACCAACTTCTCCATTCTCTGAATGAAACTGA  
**KasI (535)** 1▶ M E T N F S I P L N E T E  
**AgeI (552)**  
601 GGAGGTGCTCCCTGAGCCTGCTGGCCACACCGTCTGTGGATCTTCTCATTGCTAGTCCACGGAGTCACTTTGTCTTCCGGGGTCTGGGCAATGGGCTT  
13▶ E V L P E P A G H T V L W I F S L L V H G V T F V F G V L G N G L

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**BspEI (719)**  
701 GTGATCTGGTGGCTGGATTCCGGATGACACGCACAGTCAACACCATCTGTTACCTGAACCTGGCCCTAGCTGACTTCTTTTTCAGTCCATCCTACCAT  
47▶ V I W V A G F R M T R T V N T I C Y L N L A L A D F S F S A I L P

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**BsaBI (873)**  
801 TCCGAATGGTCTCAGTCGCCATGAGAGAAAAATGGCCTTTTGGCTCATTCTATGTAAGTTAGTTCATGTTATGATAGACATCAACCTGTTTGTCAAGTGT  
80▶ F R M V S V A M R E K W P F G S F L C K L V H V M I D I N L F V S V

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**XcmI (911)**  
**BsaBI (906)** 901 CTACCTGATCACCATCATTGCTCTGGACCGCTGTATTTGTGCTCTGCATCCAGCTGGGCCAGAACCATCGCACCATGAGTCTGGCCAGAGGGTGATG  
113▶ Y L I T I I A L D R C I C V L H P A W A Q N H R T M S L A K R V M  
**Bsp120I (956)**

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**ScaI (1063)**  
1001 ACGGGACTCTGGATTTTACCATAGTCTTACCTTACCAAATTCATCTTCTGGACTACAATAAGTACTACGAATGGGGACACATACTGTATTTTCAACT  
147▶ T G L W I F T I V L T L P N F I F W T T I S T T N G D T Y C I F N

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**XmnI (1134)** 1101 TTGCATTCTGGGGTGACACTGCTGTAGAGAGTTGAACGTGTTACCATGCCCCAAGTCTTCTGATCCCTCACTTCACTTATTGGCTTCAGCGTGCC  
180▶ F A F W G D T A V E R L N V F I T M A K V F L I L H F I I G F S V P  
**NcoI (1148)**  
1201 TATGTCCATCATCACAGTCTGCTATGGGATCATCGCTGCCAAAATTCACAGAAACCATGATTAAATCCAGCCGTCCTTACGTGCTTTCGCTGCTGTG  
213▶ M S I I T V C Y G I I A A K I H R N H M I K S S R P L R V F A A V  
**XcmI (1173)**  
1301 GTGGCTTCTTTTTCATCTGTTGGTCCCTTATGAACCTAATGGCAGTCTGAGTCAAAGAGATGTTGTTAAATGGCAAATACAAAATCA  
247▶ V A S F F I C W F P Y E L I G I L M A V W L K E M L L N G K Y K I

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**PvuII (1443)**  
1401 TTCTTGTCTGATTAACCAACAAGCTCCTTGGCCTTTTTTAAACAGTGCCTCAACCAATTCTCTACGCTTTATGGGTGCGTAACCTCCAAGAAAGACT  
280▶ I L V L I N P T S S L A F F N S C L N P I L Y V F M G R N F Q E R L

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**PshAI (1536)**  
**SpeI (1516)** 1501 GATTGCTCTTTGCCACTAGTGGAGAGGGCCCTGACTGAGGTCCCTGACTCAGCCAGACCAGCAACACAGACACCCTTCTGCTTACCTCCTGAG  
313▶ I R S L P T S L E R A L T E V P D S A Q T S N T D T T S A S P P E  
**Bsp120I (1529)**  
1601 GAGACGGAGTTACAAGCAATGTGAGGTCGGGATATTTTCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATG  
347▶ E T E L Q A M •

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**HpaI (1778)** 1701 CAGTGAATAAAGCTGCAATAAACAAGTTAAACAACAACCTGATTC  
**MfeI (1789)**

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**EcoRI (1874)**  
1801 ATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAAA  
1901 CTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAG  
2001 CCTCACCTCTTTTTCATGGAGTTTAAAGATATAGTATTTTCCCAAGTGTGAAGTCTTCTTCTTTATGTTTTAAATGCACTGACCTCCACATT

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**SspI (2113)** 2101 CCCTTTTATAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATA  
**SwaI (2127)**  
2201 ATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAAGGAACCTTAAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACT  
141▶ N R T Y K  
**SacI (2388)**

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2301 TGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAGCAGTCAAGGAGCATAGTCAGAGATGAGCTCTCTGCA  
135▶ 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 R C  
2401 CATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTC  
102▶ 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 N S

**StuI (2552)**

2501 ACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGA  
 68 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 R I

XmnI (2694)

2601 TGGCCGCCCCGCATGGTGTCTTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGT  
 35 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 F T

**BspHI (2702)** **AseI (2760)**

2701 CTT**CATGATGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAA**ACAGCGTGGATGGCGTCTCCAGCTTA  
 2 K M

SacI (2817)

2800 TCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCCACCCTACACGCCTACCGCCATTTGCGTCAATGGGCGGAGTTGTTACGACATTTTGG

SpeI (2915)

2900 AAAGTCCCGTTGATTT**ACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGAGACTTGAAATCCCCGTGAGTCAAACCGTATCCACGCCATT**

**SnaBI (3043)**

2999 GATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTATGTACTGGGCATAA

**NdeI (3148)**

3099 TGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCGAGTTTACCGTAAATACT

3199 CCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCTGTTGGCGGTCAGCCAGG

**PstI (3327)** **SdaI (3326)** **PacI (3334)** **BspLU11I (3344)**

3299 CGGGCCATTTACCGTAAGTTATGTAACGCC**CTG C A G G T T A A T T A A G A A C A T G T G A G C A A A A G G C C A G A A A A G G C C A G A A A A G G C C G G T T**

3397 GCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACAG

3497 GCGTTTTCCCGTGGAAAGCTCCCTCGTGGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTT

**ApaLI (3658)**

3597 CTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGGTCCCAAGCTGGGCTGTGTGCACGAACCCCGGTTAGCCCGACCGCTGCGCCTT

3697 ATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGC

3797 GGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAACAAA

3897 GAGTTGGTAGCTCTTGATCCGGCAAACAACCCCGCTGGTAGCGGTGGTTTTTTTGTGGTTCGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGA

**EagI (4094)**

PacI (4074) SwaI (4083) **NotI (4093)**

3997 AGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGC

4096 GGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAA

4196 ACAAACCTAGCAAAATAGGCTGTCCCCAGTGCAAGTGCAAGTGCCAGAACATTTCTCTATCGAA