



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

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

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**NgoMIV (441)**  
401 GGGCCTTTGTCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGTCTCAACTCTACGCTTTGTTTCGTTT

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**BstEII (555)**  
**AgeI (552)** 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCATGGGGCTCCCTGGGCTGTTCTGCTTGGCCGTGCTGGC  
**NcoI (560)** 1 M G L P G L F C L A V L A  
601 TGCCAGCAGCTTCTCAAGGCACGGGAGGAAGAATTACCCCTGTGGTCTCCATTGCCTACAAAGCTTGGAAAGTTTTCCCAAAGGCCGCTGGGTGCTC  
13 A S S F S K A R E E E I T P V V S I A Y K V L E V F P K G R W V L

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**ApaLI (710)** 701 ATAACTGCTGTGCACCCAGCCACCACCGCCCATCACCTATTCCCTCTGTGGAACCAAGAACATCAAGGTGCCAAGAAGTGGTGAAGACCACAGAGC  
47 I T C C A P Q P P P P I T Y S L C G T K N I K V A K K V V K T H E  
**BstXI (773)**  
801 CGGCTCCTTCAACCTCAACGTCACTCAAGTCCAGTCCAGACTGCTCACCTACTTCTGCTGGGCTCCTCCACCTCAGGTGCCATGTGGACAGTGC  
80 P A S F N L N V T L K S S P D L L T Y F C W A S S T S G A H V D S A  
901 CAGGCTACAGATGCACTGGGAGCTGTGGTCCAAGCCAGTGTCTGAGCTGCGGGCAACTTCACTCTGCAGGACAGAGGGGAGGCCCCAGGGTGGAGATG  
113 R L Q M H W E L W S K P V S E L R A N F T L Q D R G A G P R V E M  
1001 ATCTGCCAGGCTCCTCGGGCAGCCACCTATCACCAACAGCCTGATCGGGAAGGATGGGCGAGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTG  
147 I C Q A S S G S P P I T N S L I G K D G Q V H L Q Q R P C H R Q P  
1101 CCAACTTCTCCTTCTGCCGAGCCAGACATCGGACTGGTCTGGTGCAGGCTGCAACAACGCCAATGTCCAGCAGCAGCCCTCACAGTGGTGCCCC  
180 A N F S F L P S Q T S D W F W C Q A A N N A N V Q H S A L T V V P P

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**BstEII (1204)** 1201 AGTGGTGACCAGAAGATGGAGGACTGGCAGGGTCCCTGGAGAGCCCATCCTTGCCTTGGCGCTCTACAGGAGCACCCGCGTCTGAGTGAAGAGGAG  
213 G G D Q K M E D W Q G P L E S P I L A L P L Y R S T R R L S E E E  
**SmaI (1230)**  
**BsrBI (1261)**  
1301 TTTGGGGGTTTCAAGATAGGGAATGGGGAGGTCAGAGGACGCAAAGCAGCAGCCATGTAGAATGAACCGCTAGCTGGCCAGACATGATAAGATACATTGA  
247 F G G F R I G N G E V R G R K A A A M •  
1401 TGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAGAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAAT

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**HpaI (1506)** 1501 AAACAAGTAAACAACAACAAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTA  
**MfeI (1517)**

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**EcoRI (1602)** 1601 TGGAAATCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCT

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**SapI (1784)** 1701 GTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGAGTAAAGATATAGTGTATTTTCCCAAGGTTTGAAGTCTTTCATTTCTTTA

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**SspI (1841)** 1801 TGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAAAATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGC  
**SwaI (1855)**  
1901 AGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAAGAACCTTTAATAGAAATGGACAGCAAGAAAGCG  
2001 AGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAGCAGTCAG  
144 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

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**SacI (2116)** 2101 GAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAAT  
111 A Y D S I 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  
**BstXI (2145)**  
2201 GGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCCAGCAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCA  
78 T D F D K 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  
2301 GAGATGATCTCCAGCTTGGTCTGTAGGGCCCGCCGACATGGTGTCTGTTGCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCT  
44 S I I E G 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

BbsI (2426)  
**XmnI (2422)** **AseI (2488)**

2401 CCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAA  
11 L D Q Q S I N F T K M

SacI (2545)

2501 AACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAA

SpeI (2643)

2601 TGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGT

SnaBI (2771)

2701 GAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGT

NdeI (2876)

2801 CCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGC

2901 CAAGTGGGCGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGG

PacI (3062)  
**SdaI (3054)** **BspLU11I (3072)**

3001 CGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATAAGAACATGTGAGCAAAAGGCCAGCAAAGGC

3101 CAGGAACCGTAAAAAGGCCGCTTGGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAAC

3201 CCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTC

ApaLI (3386)

3301 TCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCC

3401 CGTTCAGCCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGG

3501 ATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGC

3601 TGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTAC

3701 GCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCT

**EagI (3822)**  
PacI (3802) **SwaI (3811)** **NotI (3821)**

3801 AGTTAATTAACATTTAAATCAGCGGCCGAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCT

3901 CCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA