



**PvuI (7)**  
**SgfI (6)**
**MfeI (82)**

1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
 101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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**HindIII (245)**
**PvuII (239)**
**Bsu36I (291)**

201 GTGAACGTTCTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACCGCGCCCGCCGCTACCTGAGGCC  
 301 GCCATCCACGCGGTTGAGTGCAGTTCGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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**NgoMIV (441)**

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

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**KasI (535)**
**AgeI (552)**
**NcoI (560)**
**BstEII (555)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTCCACATGGAGGAAATGCCTTTGAGAGAATCAAGTCCTCAAAG  
 601 GGCAGAGAGGTGCAAGAAGTCATGGCTCTTGTGCATAGTGGCTCTGTTACTGATGTTGCTCTGTTCTTTGGGTACACTGATCTACTTCACTCAAGCCA  
 13▶ A E R C K K S W L L C I V A L L L M L L C S L G T L I Y T S L K P

**DraIII (772)**

701 ACTGCCATCGAGTCTGCATGGTAAAGTTTGAACATATCATCTCAAATGGCACATGACATCTCCAAACCTCACTGTGTGAATACGACATCTGATGGGA  
 47▶ T A I E S C M V K F E L S S S K W H M T S P K P H C V N T T S D G

**PstI (811)**

801 AGCTGAAGATACTGCAGAGTGGCACATATTTAATCTACGGCCAAGTGATTCTGTGGATAAGAAATACATAAAAGACAATGCCCCCTTCGTAGTACAGAT  
 80▶ K L K I L Q S G T Y L I Y G Q V I P V D K K Y I K D N A P F V V Q I

**SphI (975)**

901 ATATAAAAAGAAATGATGCTCTACAACTCTAATGAATGATTTTCAAATCTTGCCTATAGGAGGGTTTATGAACCTGCATGCTGGAGATAACATATATCTG  
 113▶ Y K K N D V L Q T L M N D F Q I L P I G G V Y E L H A G D N I Y L  
 1001 AAGTTCAACTCTAAAGACCATATTCAGAAAACAAACATACTGGGGATCATCTTAATGCCTGATCTACCATTATCTCTTAGAGATTGGGTTTGGTCT  
 147▶ K F N S K D H I Q K T N T Y W G I I L M P D L P F I S •

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**MscI (1116)**
**NheI (1110)**

1101 CCTCATCTTCGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACAGATAAGTGAATAAATGCTTTATTTGTGAAATT

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**HpaI (1248)**
**MfeI (1259)**

1201 TGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACAAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGT

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**EcoRI (1344)**

1301 GGGAGGTTTTTTAAAGCAAGTAAACCTCTACAAATGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGA  
 1401 ATCCTTTTCTGAGGGATGAATAAGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTTCATGGAGTTTAAAGATAT

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**SapI (1526)**
**SspI (1583)**
**SwaI (1597)**

1501 AGTGTATTTTCCCAAGGTTTGAAGTCTCTTCAATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTCTAGTAAATATTCAGAAAATAATT

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**EcoO109I (1658)**

1601 TAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGG  
 1701 GAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTT  
 141▶ • N R T Y K L P I L E E I T T K

**SacI (1858)**
**BstXI (1887)**

1801 TGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCATGCCACAGGGGCTGACCACCCTGATGGA  
 125▶ V 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  
 1901 TCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCA  
 92▶ R 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

**StuI (2022)**

2001 CAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAAGTCTTGGTCTGATGGCCGCCCGACATGGTGTGTTGTCTCT  
 58▶ C V 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

**BbsI (2168)**
**XmnI (2164)**

2101 CATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGT  
 25▶ Y L M T I K E T A V E V L E L D Q Q S I N F T K M

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**AseI (2230)**
**SacI (2287)**

2201 ATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTAT

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**SpeI (2385)**

2301 ATAGACCTCCCACGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAAAA  
 2401 CTCCCATGACGTCAATGGGGTGGAGACTTGGAAATCCCGTGGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCCAAACCGCATCATGTTAA

2501 TAGCGATGACTAATACGTAGATGTAAGTACTGCCAAGTAGGAAAAGTCCATAAAGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTC

**SnaBI (2513)**

2601 AATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATT

**NdeI (2618)**

PstI (2797)

2701 GGCCTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTG

**SdaI (2796)**

PacI (2804) **BspLU11I (2814)**

2801 CAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGAC

2901 GAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCCTGGAAGCTCCCTCGTGCCTC

3001 CTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTCTCCCTTCGGAAAGCGTGGCGCTTTCATAGCTCACGCTGTAGGTATCTCAGTTGGT

**ApaLI (3128)**

3101 GTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAAGTCCAAACCCGGTA

3201 AGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACT

3301 ACGGCTACTAGAAAGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCAC

3401 CGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCT

**EagI (3564)**

PacI (3544) SwaI (3553) **NotI (3563)**

3501 CAGTGAACGAAAACACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACTTTAAATCAGCGGCCGCAATAAATATCTTTATTTTCATTACATCT

3601 GTGTGTTGGTTTTTTTGTGTAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGT

3701 GCAGGTGCCAGAACATTTCTCTATCGAA