



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
**MfeI (82)** **EcoNI (96)**  
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGTCCGCCTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

**Psp1406I (203)** **HindIII (245)** **Bsu36I (291)**  
**PvuII (239)** **EcoNI (287)**  
201 GTGAACGTTCTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCCTACCTGAGGCC  
301 GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

**KasI (535)** **AgeI (552)**  
501 TCTGTTTGTCCGCGCTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTAGGAGGCCACCATGGAATATCATCTGATTTAGAAAATTTG  
1 M E Y H P D L E N L

**KasI (697)**  
601 GATGAAGATGGATATACTCAATTACACTTCGACTCTCAAAGCAATACCAGGATAGCTGTTGTTTCAGAGAAAGGATCGTGTGCTGCATCTCCTCCTTGGC  
11 D E D G Y T Q L H F D S Q S N T R I A V V S E K G S C A A S P P W

**Acc65I (762)**  
701 GCCTCATTGCTGAATTTTGGGAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCTGGTACCATGGCTATTTGGAGATCCAATTCAGGAAGCAA  
44 R L I A V I L G I L C L V I L V I A V V L G T M A I W R S N S G S N  
801 CACATTGGAGAATGGCTACTTTTATCAAGAAATAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTCCTACCAAAGCTGTC  
77 T L E N G Y F L S R N K E N H S Q P T Q S S L E D S V T P T K A V

**SapI (953)**  
901 AAAACCACAGGGTCTTTCCAGCCTTGTCTCCTAATTGGATTATATATGAGAAGAGCTGTTATCTATTACAGCATGCTACTAAATTCCTGGGATGGAA  
111 K T T G V L S S P C P P N W I I Y E K S C Y L F S M S L N S W D G  
1001 GAAAAAGACAATGCTGGCAACTGGGCTTAATCTCCTAAAGATAGACAGCTCAAATGAATTGGGATTTATAGTAAAACAAGTGTCTTCCCAACTGATAA  
144 S K R Q C W Q L G S N L L K I D S S N E L G F I V K Q V S S Q P D N

**BstXI (1140)**  
1101 TTCATTTTGGATAGGCCTTTCTCGGCCAGACTGAGGTACCATGGCTCTGGGAGGATGGATCAACATTCTCTTCTAACTTATTTAGATCAGAACCACA  
177 S F W I G L S R P Q T E V P W L W E D G S T F S S N L F Q I R T T

**XcmI (1221)** **BbrPI (1239)**  
1201 GCTACCCAAGAAAACCCATCTCCAAATTGTGTATGGATTACGCTGTCAGTCATTATGACCAACTGTGTAGTGTGCCCTCATATAGTATTTGTGAGAAGA  
211 A T Q E N P S P N C V W I H V S V I Y D Q L C S V P S Y S I C E K

**MscI (1354)**  
1301 AGTTTTCAATGTAAGGGGAAGGGTGGAGAAGGAGAGAGAAATATGTGAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAA  
244 K F S M •

**HpaI (1486)** **MfeI (1497)**  
1401 CTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAAACAACAACAA

**EcoRI (1582)**  
1501 TTGCATTCATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTTAAAATACAGCA  
1601 TAGCAAACTTTAACCTCCTCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCT

**SapI (1764)**  
1701 GTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTCCCAAGGTTTGAAGTCTCTTCAATTTCTTTATGTTTTAAATGCACTGACCT

**SspI (1821)** **SwaI (1835)** **EcoO109I**  
1801 CCCACATTCCTTTTATGATAAATATTAGAAAATATTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGC  
1901 CCTTCATAATATCCCCAGTTTAGTGTGGACTTAGGGAACAAGAACCTTAAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCT  
141 • N R

**SacI (2096)**  
2001 GGTGACTTGGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAGCAGTCCAGGAGCATAGTCAGAGATGAGC  
138 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 A Y D S I L

**BstXI (2125)**  
2101 TCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCC  
104 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 T D F D K Q G

**StuI (2260)**  
2201 CGTTGCTCACAGCAGACCAATGGCAATGGCTTCCAGCACAGACAGTACCTGCCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTT  
71 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  
2301 GGTCTGATGGCCGCCCCGACATGGTGTCTTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCTGCTGAGAGATG  
38 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 L D Q Q S I

**BspHI (2410)** **XmnI (2402)** **AseI (2468)**  
2401 TTGAAGGCTTTCATGATGGCCCTCTATAGTGAGTCGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTC  
4 N F T K M

2501 CAGC T TATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGAC  
SacI (2525)

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2601 ATTTTGGAAAGTCCCGTTGATT**ACTAGT**CAAAACAACTCCCATTTGACGTCAATGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGTATCCAC  
SpeI (2623)

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2700 GCCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTG  
SnaBI (2751)

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2800 GGCATAATGCCAGGCGGGCCATTACCCTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTACCCT  
NdeI (2856)

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2900 AAATACTCCACCCATTGACGTCAATGAAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGGGGGGTTCGTTGGGCGGTC

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3000 AGCCAGGCGGGCCATTTACCCTAAGTTATGTAAC**CTGCAGTTAA**TTAAGAA**CA**TGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGG  
PstI (3035)
SdaI (3034)
PacI (3042)
BspLU11I (3052)

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3098 CCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAGAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAG  
SdaI (3034)
PacI (3042)
BspLU11I (3052)

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3198 ATACCAGGCGTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTG

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3298 GCGCTTTTCATAGCTCACGCTGTAGGTATCTCAGTTCGGGTGAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTAGCCCGACCGCT  
ApaLI (3366)

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3398 GCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTA

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3498 TGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTC

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3598 GGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGAT

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3698 CTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAA  
PacI (3782)
SwaI (3791)

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3798 ATC AGCGGCCGCAATAAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGA  
EagI (3802)
NotI (3801)

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3898 AACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAAGTGCCAGGTCAGAACATTTCTCTATCGAA