



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA **MfeI (82)**

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

**HindIII (245)**  
**Psp1406I (203)** 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCGCCCTACCTGAGGCC **PvuII (239)** **Bsu36I (291)**

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTGGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT **NgoMIV (441)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCCCTACCTGAGATCACCGGTCACCATGGGCAAAGGAGATCCTAAGAAGCCGAGAGGCAAAAT **NcoI (560)** **BstEII (555)** **AgeI (552)**  
1 M G K G D P K K P R G K M

**NsiI (608)**  
**NdeI (605)** 601 GTCATCATATGCATTTTTTGTGCAAACTTGTCCGGAGGAGCATAAGAAGAAGCACCCAGATGCTTCAGTCAACTTCTCAGAGTTTTCTAAGAAGTGCTCA  
13 S S Y A F F V Q T C R E E H K K K H P D A S V N F S E F S K K C S

**Tth111I (711)**  
**BbsI (708)** 701 GAGAGGTGAAGACCATGTCTGCTAAAGAGAAAAGAAAATTTGAAGATATGGCAAAGCGGACAAGGCCGTTATGAAAGAGAAATGAAAACCTATATCC  
47 E R W K T M S A K E K G K F E D M A K A D K A R Y E R E M K T Y I

801 CTCCCAAAGGGGAGACAAAAAAGAGTTCAAGGATCCCAATGCACCCAAAGGCTCCTTCGGCCTTCTTCTCTTCTGCTCTGAGTATCGCCAAAAAT **BamHI (831)** **StuI (850)**  
80 P P K G E T K K K F K D P N A P K R P P S A F F L F C S E Y R P K I

901 CAAAGGAGAACATCCTGGCCTGTCCATTGGTGATGTTGCGAAGAACTGGGAGAGATGTGAATAAACTGCTGCAGATGACAAGCAGCCTTATGAAAAG **PstI (971)**  
113 K G E H P G L S I G D V A K K L G E M W N N T A A D D K Q P Y E K

1001 AAGGCTGCGAAGCTGAAGGAAAAATACGAAAAGGATATTGCTGCATATCGAGCTAAAGGAAAGCCTGATGCAGCAAAAAAGGGAGTTGTCAAGGCTGAAA  
147 K A A K L K E K Y E K D I A A Y R A K G K P D A A K K G V V K A E

1101 AAAGCAAGAAAAAGAGGAAAGAGGAAAGATGAGGAAGATGAAGAGGATGAGGAGGAGGAGGAAAGATGAAGAAGATGAAGATGAAGAAGAAGATGATGA  
180 K S K K K K E E E E D E E D E E E E E E D E E D E E E D D D

**MscI (1231)**  
**NheI (1225)** 1201 TGATGAATAAGTTGGTTCTAGCGCAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGACAAACCACAAC TAGAATGCAGTGAAAAAATGC  
213 D E •

1301 TTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAAACAAGTTAAACAACAATTGCATTCATTTTATGTTTCAGG **HpaI (1363)** **MfeI (1374)**

1401 TTCAGGGGAGGTGTGGGAGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTTCTAAAATACAGCATAGCAAACTTTAACCTCCAAT **EcoRI (1459)**

1501 CAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCTCACCTTCTTTCA

1601 TGGAGTTAAGATATAGTGATTTTCCCAAGGTTGAACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTATAGTAAA **SapI (1641)** **SspI (1698)**

1701 TATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTA **SwaI (1712)** **EcoO109I (1773)**

1801 GTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTT  
141 • N R T Y K L P I L E

1901 CCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCT **SacI (1973)**  
130 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 M G C P S

2001 GACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATG **BstXI (2002)**  
97 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 V A S G I

2101 GCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCCTCAATGTGGACAGCAGAGATGATCTCCCGAGTCTTGGTCTGATGGCCGCCCGACAT **StuI (2137)**  
63 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 A A G V H

2201 GGTGCTTGTTCCTCATAGAGCATGGTATCTTCTAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTTCATGATGGCCCT **BspHI (2287)** **BbsI (2283)** **XmnI (2279)**  
30 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 K M

2301 CCTATAGTGAGTCGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACATA **AseI (2345)**

SacI (2402)  
2401 ACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCC GTTGATTT

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SpeI (2500)  
2501 **ACTAGT**CAAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAC

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SnaBI (2628)  
2600 CGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTATGTACTGGGCATAATGCCAGGCGGGCCATT

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NdeI (2733)  
2700 TACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGTACTGCCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCA  
2800 ATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCTGTTGGCGGTGACGCCAGGCGGGCCATTACCGTA

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PstI (2912)  
SdaI (2911) PacI (2919) BspLU11I (2929)  
2900 AGTTATGTAACGCC**TGCAGGTTAA**TTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTCTGCGCTTTTCCAT

←

2998 AGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAA  
3098 GCTCCCTCGTGGCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTG

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ApaLI (3243)  
3198 TAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCCAGCCGACCCTGCGCCTTATCCGGTAACTATCGT  
3298 CTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCT  
3398 TGAAGTGGTGGCCTAACTACGGTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTG  
3498 ATCCGGCAAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTT

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PacI (3659) SmaI (3668) EagI (3679) NotI (3678)  
3598 TCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATC

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3698 TTTATTTTCATTACATCTGTGTGGTTTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAG  
3798 GCTGTCCCGAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA