



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGCAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCCGCAATTGAACGGGTGCCTA

MfeI (82)  
101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTGTGCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

301 GCCATCCACGCCGGTTGAGTCGGCTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCCGCTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCAGCTTTGCTGACCTGCTTCTCAACTCTACGCTTTGTTTCGTTT

**AgeI (552)** 501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCTACCTGAGATCACCGTCAACATGTCTGAAGAAGTTACTTATGCAGATCTTCAATTCCA  
**BglII (585)**  
1 M S E E V T Y A D L Q F Q

601 GAACTCCAGTGAGATGGAAAAATCCCAGAAATGGCAAATTTGGGAAAAAGCACCTCCAGCTCCCTCTCATGTATGGCGTCCAGCAGCCTGTTTCTG  
13 N S S E M E K I P E I G K F G E K A P P A P S H V W R P A A L F L  
701 ACTCTTCTGTGCCTTCTGTTGCTCATTGGATTGGGAGTCTGGCAAGCATGTTTCAGTAACCTTGAAGATAGAAATGAAAAAATGAACAACTACAAA  
47 T L L C L L L L I G L G V L A S M F H V T L K I E M K K M N K L Q

**SapI (808)** 801 ACATCAGTGAAGAGCTCCAGAGAAATATTTCTCACTGATGAGTAACATGAATATCTCCAACAAGATCAGGAACCTCTCCACCACACTGCAAACAT  
**XmnI (821)**  
80 N I S E E L Q R N I S L Q L M S N M N I S N K I R N L S T T L Q T I

901 AGCCACAAATATGTGCTGAGCTATATAGCAAAGAACAAGAGCACAAATGTAAGCCTTGCCAAGGAGATGGATTTGGCATAAGGACAGCTGTTATTTCC  
113 A T K L C R E L Y S K E Q E H K C K P C P R R W I W H K D S C Y F

**NsiI (1085)**  
1001 CTAAGTGTGATGTCCAACATGGCAGGAGAGTAAATGGCCTGTGCTGCTCAGAATGCCAGCCTGTTGAAGATAAACAAACAAAATGCATTGGAATTTA  
147 L S D D V Q T W Q E S K M A C A A Q N A S L L K I N N K N A L E F

**NdeI (1118)**  
1101 TAAATCCAGAGTAGATCATATGACTATTGGCTGGGATTATCTCCTGAAGAAGATCCACTCGTGGTATGAGAGTGGATAATATAATCAACTCCTCTGC  
180 I K S Q S R S Y D Y W L G L S P E E D S T R G M R V D N I I N S S A  
1201 CTGGTTATAAGAAACGCACCTGACTTAAATAACATGTATTGTGGATATATAAATAGACTATATGTTCAATATTACTGCACTTATAAAACAAGAAATG  
213 W V I R N A P D L N N M Y C G Y I N R L Y V Q Y Y H C T Y K Q R M

**MscI (1313)** 1301 ATATGTGAGAAGATGGCCAAATCCAGTGCAGCTTGGTTCTACATATTTAGGGAGGCATGAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTG  
**NheI (1360)**  
247 I C E K M A N P V Q L G S T Y F R E A •

**MscI (1366)**  
1401 GACAAACCACAAC TAGAATGCAGTGA AAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGT

**HpaI (1498)**

**MfeI (1509)** 1501 TAACAACA AATTGCATTCA TTTTATGTTTCAGGTT CAGGGGAGGTGTGGGAGT TTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTC  
**EcoRI (1594)**

1601 TAAAATACAGCATAGCAAAC TTAACCTCAAATCAAGCCTCTACTTGAATC TTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAA

**SapI (1776)**  
1701 TGTGCATTAGCTGTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTCCCAAGTTTGAAGTACTGCTTCTTCTTATGTTTTAA

**SwaI (1847)**  
1801 ATGCACTGACCTCCACATTCCCTTTTTAGTAAATATTCAGAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCA

**EcoO109I (1908)**  
1901 GATGCTCAAGGCCCTTATAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAAGAACCTTAAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTA

2001 GCTTTAGTTCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAG  
141 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 A Y  
2101 TCAGAGATGAGCTCTCTGCACATGCCACAGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAA  
108 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 T D F

**StuI (2272)**  
2201 AGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCCAGCAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGAT  
75 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 S I I  
2301 CTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGTGTTGCTCATAGAGCATGGTGTCTTCTCAGTGGCAGCTCCACCAGCTCCAGATCC  
42 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 L D

**BbsI (2418)**  
 XmnI (2414) **AseI (2480)**  
 2401 TGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGT  
 8 Q Q S I N F T K M ←  
 2501 GGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGG

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**SpeI (2635)**  
 2601 AGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCGTGAGTCAAA

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**SnaBI (2763)**  
 2701 CCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAG

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**NdeI (2868)**  
 2801 GTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACTTGTACTGCCAAGTGGG  
 2901 CAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTC

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**PacI (3054)**  
**PstI (3047)**  
**SdaI (3046)**  
 3001 GTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACC  
 3101 GTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAAGGTTGGCGAAACCCGACAGG  
 3201 ACTATAAAGATACCAGGCGTTTTCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCG

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**ApaLI (3378)**  
 3301 GGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCCAGC  
 3401 CCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGTAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAG  
 3501 AGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCA  
 3601 GTTACCTTCGAAAAAGATTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAA

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**PacI (3794)**  
 3701 AAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATT

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**EagI (3814)**  
 SwaI (3803) **NotI (3813)**  
 3801 AACATTTAAATCAGCGGCGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAA  
 3901 ACAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCGAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA