



**PvuI (7)**  
**SgfI (6)**  
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

**Psp1406I (203)** **HindIII (245)** **Bsu36I (291)**  
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCCGCCCTACCTGAGGCC  
301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCCGCTCCCGCTGTGGTGCCTCCTGAAGTCGCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGTCTTTGTTTCGTTT

**NcoI (560)**  
**BstEII (555)**  
**AgeI (552)**  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCCTACCTGAGATCACCGGTACCATTGGACAATATGTCTATTACGAATACACCAACAAGTAA  
1 M D N M S I T N T P T S N

**XcmI (636)**  
601 TGATGCCTGTCTGAGCATTGTGCATAGTTTGTGTCATAGTTTGTGTCATAGACAAGGTGGAGAGAGTAAACATTTGCAAAAAGAGCAATTGAAAGTTTGGTAAAGAAG  
13 D A C L S I V H S L M C H R Q G G E S E T F A K R A I E S L V K K  
701 CTGAAGGAGAAAAAGATGAATTGGATTCTTTAATAACAGCTATAACTACAAATGGAGCTCATCTAGTAAATGTGTACCATACAGAGAACATTGGATG  
47 L K E K K D E L D S L I T A I T T N G A H P S K C V T I Q R T L D

**SspI (899)**  
801 GGAGGCTTCAAGTGGCTGGTCCGAAAGGATTTCTCATGTGATCTATGCCGCTCTGGAGGTGGCTGATCTTCACAAAAATGAACTAAAACATGTTAA  
80 G R L Q V A G R K G F P H V I Y A R L W R W P D L H K N E L K H V K  
901 ATATTGTCAGTATGCGTTTGACTTAAAAATGTGATAGTGTCTGTGTGAATCCATATCACTACGAACGAGTTGTATCACCTGGAATTGATCTCTCAGGATTA  
113 Y C Q Y A F D L K C D S V C V N P Y H Y E R V V S P G I D L S G L  
1001 AACTGCAGAGTAATGCTCCATCAAGTATGATGGTGAAGGATGAATATGTGCATGCTTTGAGGGACAGCCATCGTTGCTCCACTGAAGGACATTCAATTC  
147 T L Q S N A P S S M M V K D E Y V H D F E G Q P S L S T E G H S I  
1101 AAACCATCCAGCATCCACCAAGTAAATCGTGCATCGACAGAGACATACAGCACCCAGCTCTGTTAGCCCCATCTGAGTCTAATGCTACCAGCACTGCCAA  
180 Q T I Q H P P S N R A S T E T Y S T P A L L A P S E S N A T S T A N

**XcmI (1205)** **Bst1107I (1241)** **BstXI (1238)**  
1201 CTTTCCCAACATTCTGTGGCTTCCACAAGTCAGCCTGCCAGTATACTGGGGGCGCCATAGTGAAGGACTGTTGCAGATAGCATCAGGGCCTCAGCCA  
213 F P N I P V A S T T S Q P A S I L G G S H S E G L L Q I A S G P Q P  
1301 GGACAGCAGCAGAATGGATTTACTGGTCAGCCAGCTACTTACCATATAACAGCATTACCCTGGACTGGAAGTAGGACTGCACCATACACACCTAAT  
247 G Q Q Q N G F T G Q P A T Y H H N S T T T W T G S R T A P Y T P N  
1401 TGCCTCACCAAAAACGGCCATCTTACGACACCACCGCCTATGCCGCCCATCCCGGACATTACTGGCTGTTCAAAATGAGCTTGCATTCCAGCCTCC  
280 L P H H Q N G H L Q H H P P M P P H P G H Y W P V H N E L A F Q P P  
1501 CATTTCAAATCATCTGCTCCTGAGTATTGGTGTTCATTGCTTACTTTGAAATGGATGTTCCAGGTAGGAGAGACATTTAAGGTTCCCTCAAGCTGCCCT  
313 I S N H P A P E Y W C S I A Y F E M D V Q V G E T F K V P S S C P  
1601 ATGTGTTACTGTTGATGGATAGCAGCCCTTCTGGAGGAGATCGCTTTTGGTTCAACTCCTCAATGTCCACAGGACAGAAGCCATTGAGAGAGCAA  
347 I V T V D G Y V D P S G G D R F C L G Q L S N V H R T E A I E R A

**BsrGI (1785)**  
1701 GGTTGCACATAGGCAAAGGTGTGCAGTTGGAATGTAAGGTGAAGGTGATGTTTGGGTCAGGTGCCTTAGTGACCACGCGGTCTTTGTACAGAGTTACTA  
380 R L H I G K G V Q L E C K G E G D V W V R C L S D H A V F V Q S Y Y

**ApaLI (1820)** **BglIII (1844)**  
1801 CTTAGACAGAGAAGCTGGGCGTGCACCTGGAGATGCTGTTTCATAAGATCTACCCAAGTGCATATATAAGGTCTTTGATTGCGTCAGTGTATCGACAG  
413 L D R E A G R A P G D A V H K I Y P S A Y I K V F D L R Q C H R Q  
1901 ATGCAGCAGCAGGCGGCTACTGCACAAGCTGCAGCAGCTGCCAGGCAGCAGCGTGGCAGGAAACATCCCTGGCCCAGGATCAGTAGGTGGAATAGCTC  
447 M Q Q Q A A T A Q A A A A A Q A A V A G N I P G P G S V G G I A

**PshAI (2041)** **NsiI (2055)**  
2001 CAGCTATCAGTCTGTGCTGCTGCTGGAATTGGTGTGATGACCTTCGTCGTTATGCATACTCAGGATGAGTTTTGTGAAAGGCTGGGACCGGATTA  
480 P A I S L S A A A G I G V D D L R R L C I L R M S F V K G W G P D Y

**ScaI (2175)**  
**XmnI (2173)**  
2101 CCCAAGACAGAGCATCAAAGAAACACCTTGTGGATTGAAATCACTTACACCGGCCCTCCAGCTCCTAGACGAAGTACTTTCATACCATGCCGATTGCA  
513 P R Q S I K E T P C W I E I H L H R A L Q L L D E V L H T M P I A

**MscI (2253)**  
**NheI (2247)**  
2201 GACCCACAACCTTTAGACTGAGGTCTTTTACCCTGGGCGCTTAAACGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAAC  
547 D P Q P L D •

**HpaI (2385)**  
2301 TAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAAT

**EcoRI (2481)**  
2401 TGCATTCAATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCAT  
2501 AGCAAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTTGCCAATGTGCATTAGCTG

**SapI (2663)**

2601 TTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCAAGGTTTGAAGTCTCTTCATTCTTTATGTTTTAAATGCACTGACCTC

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SspI (2720)      SmaI (2734)

2701 CCACATTCCCTTTTATAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCC

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2801 CTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGTG

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2901 GTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCT  
137 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 E

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BstXI (3024)

3001 CTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCC  
104 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

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StuI (3159)

3101 GTTGCTCACAGCAGACCAATGGCAATGGCTTACGACAGACAGTGCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTG  
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

3201 GTCCTGATGGCCGCCGACATGGTCTTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGT  
37 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 N

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BbsI (3305)

XmnI (3301)      AseI (3367)

3301 TGAAGTCTTCATGGTGGCCCTCTATAGTGGTCTGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCC  
4 F T K M

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3401 AGCTTATCTGACGGTTCATAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCTACCGCCATTGCGTCAATGGGGCGGAGTTGTTACGACA

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SpeI (3522)

3501 TTTTGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGCTATCCACGC

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SnaBI (3650)

3601 CCATTGATGACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCCATAAAGTCAAGTCAAGTACTGGG

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NdeI (3755)

3701 CATAATGCCAGGCGGGCATTACCGTCAATGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGACTGCCAAGTGGGCGAGTTTACCGTAA

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3801 ATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATATTGACGTCAATGGGCGGGGTCGTTGGGCGGTCAG

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PacI (3941)

SdaI (3933)      BspLU11I (3951)

3901 CCAGGCGGGCCATTACCGTAAGTATGTAACGCTGCAGGTTAATTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGC  
4001 GTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATAC

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4101 CAGGCGTTTTCCCTGGAAGTCCCTCGTGCCTCTCTGTTCCGACCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTGGGAAGCGTGGCGC

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ApaLI (4265)

4201 TTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGTTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTACGCCGACCGTCTGCGC

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4301 CTTATCCGGTAACTATCGTCTTGGTCCAAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTA

---

4401 GGCGGTGCTACAGAGTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAA

---

4501 AAAGAGTTGGTAGCTCTTATCCGCAAAACAAACACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCA

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4601 AGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACCTACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC A

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PacI (4681)      SmaI (4690)

EagI (4701)

NotI (4700)

4701 CGGGCGCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACA

4801 AAACAAACTAGCAAAATAGGCTGTCCCAAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA