



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA **MfeI (82)**  
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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**Psp1406I (203)** 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACACGCGCCCGCCCTACCTGAGGCC  
**HindIII (245)**  
**PvuII (239)** 301 GCCATCCACGCGGTTGAGTGCAGTTCGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC  
**Bsu36I (291)**  
401 GGGCCTTTGTCCGGGCTCCCTTGAGCCTACCTAGACTACGCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

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**KasI (535)** 501 TCTGTTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTACCCATGGGGACCCGGGCAAGCAGCATCACCGCCCTCGCCTC  
**AgeI (552)** **BstEII (555)** **XmaI (569)** **SmaI (565)**  
601 TTGCAGCCGACCCGCGCAAGTCGGAGCCACGATGGTGCCTGCTCTTCTCTGCTGGATTCTCAGCACCATCACAGCTCAACCAGAACAAAAG  
13> C S R T A G Q V G A T M V A G S L L L L G F L S T I T A Q P E Q K  
1> M G T R A S S I T A L A S  
701 ACTCTGAGTCTCCCTGGCACCTACCGCCATGTTGACCGTACCCTGGCCAGGTGCTAACCTGCACAAGTGCCAGCAGGAACGTATGCTCCGAGCACT  
**MscI (744)**  
47> T L S L P G T Y R H V D R T T G Q V L T C D K C P A G T Y V S E H

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**BstAPI (824)** **SacII (836)** 801 GTACCAACATGAGCCTGCGAGTCTGCAGCAGCTGCCCGCGGGACCTTTACCAGGCACGAGAACGGCATAGAGAGATGCCATGACTGTAGTCAGCCATG  
**PshAI (883)** **BstXI (895)**  
80> C T N M S L R V C S S C P A G T F T R H E N G I E R C H D C S Q P C  
901 TCCATGGCCGATGATTGAGAGATTACCTTGTGCTGCTTACTGACCGAGAGTGCATCTGCCACCTGGAATGTATCAGTCTAATGGTACCTGCGCTCCC  
113> P W P M I E R L P C A A L T D R E C I C P P G M Y Q S N G T C A P  
1001 CATAAGTGTGCCCGTGGGCTGGGGTGTGCGGAAGAAAGGGACAGAGAATGAAGATGTGCGCTGTAAGCAGTGCCTCGGGTACCTTCTGACGTGC  
147> H T V C P V G W G V R K K G T E N E D V R C K Q C A R G T F S D V

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**Tth111I (1183)** **SphI (1196)** 1101 CTTCCAGTGTGATGAAGTGTAAAGCTCACACGGACTGTCTGGTGCAGAACCTGGAGGTGGTCAAGCCAGGACCAAGGAGACAGACAAGCTGTGGCAT  
180> P S S V M K C K A H T D C L G Q N L E V V K P G T K E T D N V C G M  
**NdeI (1264)**  
1201 GGCCTGTTCTTCTCCAGCACAAACCCACCTTCTCTGGCACAGTTACCTTTTCTCACCTGAGCATATGGAATCCCACGATGTCCTTCTCCACCTAT  
213> R L F F S S T N P P S S G T V T F S H P E H M E S H D V P S S T Y  
1301 GAGCCCAAGGCATGAACTCAACAGATTCCAACCTACTGCCTCTGTTAGAATTAAGTACCAAGTGGCATCGAGGAAGGACAGTGCCTGACAATACGA  
247> E P Q G M N S T D S N S T A S V R T K V P S G I E E G T V P D N T  
1401 GCTCAACAGTGGGAAGGAAAGGCACTAATAGGACCTTGCACAAACCCACACAAGTTACCACAGCAAGCCCAACAGACACATTCTGAAGCTGT  
280> S S T S G K E G T N R T L P N P P Q V T H Q Q A P H R H I L K L L

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**BstEII (1561)** 1501 GCCATCGTCCATGGAGGCCACGGGTGAGAAGTCCAGCACAGCCATCAAGGCCCAAGAGGGGTACCCACAGACAGAAGCTCACAAGCATTTGACATC  
313> P S S M E A T G E K S S T A I K A P K R G H P R Q N A H K H F D I  
**Bsp120I**  
1601 AACGAGCACTTGCCTTGGATGATCGTCTCTTCTTCTGCTGGTCTGGTGTGATAGTGGTGTGCGATATCCGAAAGAGCTCCAGGACTCTCAAAAAG  
347> N E H L P W M I V L F L L L V L V L I V V C S I R K S S R T L K K

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**XcmI (1715)**  
**BamHI (1710)** 1701 GGCCCCGGCAGGATCCCAGCGCCATAGTGGAAAAGCGGGGCTGAAGAAGTCCCTGACTCCCACCCAGAACCCGGGAGAAATGGATCTACTACCGCAACGG  
380> G P R Q D P S A I V E K A G L K K S L T P T Q N R E K W I Y Y R N G  
**HindIII (1819)**  
1801 CCATGGTATTGACATCTTGAAGCTTGTAGCAGCCAGGTGGGAAGCCAGTGGAAAGACATCTATCAGTTTCTTTCGACGCGAGGAGGGAGTGGCG  
413> H G I D I L K L V A A Q V G S Q W K D I Y Q F L C N A S E R E V A

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**Bsu36I (1972)** 1901 GCCTTCTCAATGGATACACTGCAGATCACGAACGGGCTACGCGGCTCTGCAGCACTGGACCATCCGTGGCCCTGAGGCCAGCCTTGCCAGCTCATT  
447> A F S N G Y T A D H E R A Y A A L Q H W T I R G P E A S L A Q L I  
**BbsI (2056)**  
2001 GCGCCTTGCAGCAGCACCAGCAATGATGTTGTGGAAAGATTCTGGGCTGATGGAAGACACTACACAGTTGGAAACAGACAAACTGGCTCTCCCAT  
480> S A L R Q H R R N D V V E K I R G L M E D T T Q L E T D K L A L P M

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**EcoRI (2154)** 2101 GAGCCCCAGTCCGCTGAGCCGAGCCCATCCCAGTCCCTAACGTGAAACTTGAAGATCCACTCTCTGACAGTGGAGCCCTCACCGCTGGACAAGAAC  
513> S P S P L S P S P I P S P N V K L E N S T L L T V E P S P L D K N  
2201 AAGTGCTTCTTCTGAGCAGTGCAGAGCCCTTCTGCTTGGACTCCACATCCAGTGGCTCTTCAAGTGCAGTGGAGCCCTCACCGCTGGACAAGAAC  
547> K C F F V D E S E P L L R C D S T S S G S S A L S R N G S F I T K  
2301 AAAAGAAGGACACAGTGTGCGGAGGTCGCTGACCCCTGTGACTTGACGCCCCTTGTGATGACATGCTGCATATCCTGAACCCCGAGGAGCTGCG  
580> E K K D T V L R Q V R L D P C D L Q P I F D D M L H I L N P E E L R

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**XmnI (2407)** 2401 GGTGATTGAAGAGATTCCCAGGCTGAGGACAACTGGACCGCTCTTCGAGATCATTGGGGTCAAGAGCCAAGAAGCCAGCCAGACCTCTTGGACTCT  
613> V I E E I P Q A E D K L D R L F E I I G V K S Q E A S Q T L L D S  
**MscI (2553)**  
**BsrGI (2501)** 2501 GTGTACAGTCATCTTCTGACCTATTGTAGAACACAGGGGCACTGCAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGACAAACCACAAC  
647> V Y S H L P D L L •

HpaI (2685) MfeI (2696)

2601 TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAAACAACAACAAT

EcoRI (2781)

2701 TGCATTCATTTTATGTTTCAGGTTACAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTCTAAAATACAGCAT

2801 AGCAAAACTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTG

2901 TTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGGTTTGAAGTACTCTTCATTCTTTTATGTTTTAAATGCACTGACCTC

SspI (3020) SwaI (3034)

3001 CCACATTCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCC

3101 CTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTCTG

3201 GTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCT

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

BstXI (3324)

3301 CTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCC

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

StuI (3459)

3401 GTTGCTCACAGCAGACCCAATGGCAATGGCTTCCAGCACAGACAGTACCCTGCAATGTAGCCCTCAATGTGGACAGCAGAGATGATCTCCCAAGTCTTG

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

3501 GTCCTGATGGCCGCCGACATGGTCTTGTGCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGT

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

BbsI (3605)

XmnI (3601)

AseI (3667)

3601 TGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCC

4 F T K M

3701 AGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCTACCGCCATTTCGCTCAATGGGGCGGAGTTGTTACGACA

SpeI (3822)

3801 TTTTGAAAGTCCCCTGTTGATTTACTAGTCAAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCTGAGTCAAACCGTATCCACGC

SnaBI (3950)

3901 CCATTGATGACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGG

NdeI (4055)

4001 CATAATGCCAGGCGGGCCATTTACCCTGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCCTAA

4101 ATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTCAG

PacI (4241)

SdaI (4233)

BspLU11I (4251)

4201 CCAGGCGGGCCATTTACCCTAAGTTATGTAACGCTGCAGGTTAATTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGC

4301 GTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATAC

4401 CAGGCGTTTTCCCCTGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGC

ApaLI (4565)

4501 TTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGTTCGTTCCGCTCCAAGTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGC

4601 CTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTA

4701 GGCGGTGTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAA

4801 AAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCA

PacI (4981) SwaI (4990)

4901 AGAAGATCCTTTGATCTTTTCTACGGGCTGACGCTCAGTGGAAACGAAAACCTACGTTAAGGGATTTGGTCATGGCTAGTTAATTAACATTTAAATC A

EagI (5001)

NotI (5000)

5001 GCGGCCGAATAAAATATCTTTATTTTTCATTACATCTGTGTGGTTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACA

5101 AAACAAACTAGCAAATAGGCTGTCCCAAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA