



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
**MfeI (82)**  
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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**Psp1406I (203)** 201 GTGAACGTTCTTTTTTCGAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGGCCCGCCCTACCTGAGGCC  
**HindIII (245)**  
**Bsu36I (291)**  
301 GCCATCCACGCCGGTTGAGTCGGCTTTCGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTCGCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

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**NgoMIV (441)**  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTAGGAGGGCCAGCATGCCAACCTAGGCCAGCCAAGCCTATG  
**AgeI (552)** 1► M P N P R P A K P M  
**SphI (568)** 1► M P N P R P A K P M  
**AvrII (579)**

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601 GCTCCTTCCTTGCCCTTGCCCATCCCAAGGAGTCTTCCAAAGTGGAAAGTGCACCCAAGGGCTCAGAACTTCTAGGGACCAGGGGCTCTGGGGAC  
**SandI (695)**  
11► A P S L A L G P S P G V L P S W K T A P K G S E L L G T R G S G G

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701 CTTTCAAAGTGGGACCTGCGAAGTGGGGCCACACCTTCTTCTTGAACCCCTGCCACCATCCAGCTGCAGCTGCCTACAGTGGCCCTAGTCAT  
**PstI (771)**  
44► P F Q G R D L R S G A H T S S S L N P L P P S Q L Q L P T V P L V M

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801 GGTGGCACCGTCTGGGGCCGACTAGGTCCTCACCCACCTACAGGCCCTTCTCCAGGACAGACCACACTTCATGCATCAGCTCTCCACTGTGGATGCC  
**Tth111I (820)** 77► V A P S G A R L G P S P H L Q A L L Q D R P H F M H Q L S T V D A  
**NsiI (873)**  
901 CATGCCAGACCCCTGTGCTCCAAGTGGTCCACTGGACAACCAGCCATGATCAGCTCCACCACCTTCTGCTGCCACTGGGGTCTTCCCTCAAGG  
111► H A Q T P V L Q V R P L D N P A M I S L P P P S A A T G V F S L K  
1001 CCCGGCTGGCCTGCCACCTGGGATCAATGTGGCCAGTCTGGAATGGGTGCCAGGGAGCCAGCTCTACTCTGCACCTTCCCACGCTCGGGTACACCCAG  
144► A R P G L P P G I N V A S L E W V S R E P A L L C T F P R S G T P R

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**BamHI (1131)**  
1101 GAAAGACAGAACCTTTTGGCTGCACCCCAAGGATCCTACCCACTGCTGGCAAATGGAGTCTGCAAGTGGCCTGGTTGTGAGAAGGCTTCGAGGAGCCA  
177► K D S N L L A A P Q G S Y P L L A N G V C K W P G C E K V F E E P  
1201 GAAGAGTTTCTAAGCACTGCCAAGCAGATCATCTCCTGGATGAGAAAGGCAAGGCCAGTGCCTCCTCCAGAGAGAAGTGGTGCAGTCTCTGGAGCAGC  
211► E E F L K H C Q A D H L L D E K G K A Q C L L Q R E V V Q S L E Q  
1301 AGCTGGAGCTGAAAAGGAGAAGCTGGGAGCTATGCAGGCCACCTGGCTGGGAAGATGGCGTGGCCAAGGCTCCATCTGTGGCCTCAATGGACAAGAG  
244► Q L E L E K E K L G A M Q A H L A G K M A L A K A P S V A S M D K S

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**ScaI (1422)**  
1401 CTCTTGCTGCATCGTAGCCACAGTACTCAGGGCAGTGTGCTCCCGCCTGGTCTGCTCCTCGGGAGGCTCCAGACGGCGGCCTGTTTGCAGTGGGAGG  
277► S C C I V A T S T Q G S V L P A W S A P R E A P D G G L F A V R R

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**NcoI (1514)**  
1501 CACCTCTGGGGAAGCCATGGCAATAGTTCTTCCCAGAGTTCTTCCACAACATGGACTACTTCAAGTACCACAATATGCGACCCCTTTCACCTATGCCA  
311► H L W G S H G N S S F P E F F H N M D Y F K Y H N M R P P F T Y A  
1601 CCCTTATCCGATGGGCCATCCTGGAAGCCCCGAGAGGAGGACTCAATGAAATCTACCATTTGGTTTACTCGCATGTTCCGCTACTTCCAGAAACCA  
344► T L I R W A I L E A P E R Q R T L N E I Y H W F T R M F A Y F R N H  
1701 CCCCGCCACCTGGAAGAATGCCATCCGCCACAACCTGAGCCTGCACAAGTGTCTTGTGCGAGTGGAGAGCGAGAAGGGAGCAGTGTGGACCGTAGATGAA  
377► P A T W K N A I R H N L S L H K C F V R V E S E K G A V W T V D E

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**NheI (1860)**  
1801 TTTGAGTTTTCGAAAGAGGAGCAACGCCCAACAAGTGTCCAATCCCTGCCCTTGGAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTG  
411► F E F R K K R S Q R P N K C S N P C P •

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1901 GACAAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAACAAGT  
**HpaI (1998)**

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2001 TAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTC  
**MfeI (2009)** 2001  
**EcoRI (2094)** 2101 TAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAA

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2201 TGTGATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGTTTGAAGTACTGCTTTCATTTCTTTATGTTTTAA  
**SapI (2276)**

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2301 ATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCA  
**SspI (2333)** 2301  
**Swal (2347)** 2401 GATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAAGGAACCTTAAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTA

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2501 GCTTTAGTTCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAGCAGTCAGGAGCATAG  
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

2601 TCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAA  
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 (2772)

2701 AGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTACAGCACAGACAGTACCCTGCCAATGTAGGCCCTCAATGTGGACAGCAGAGATGAT  
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  
2801 CTCCCAGTCTTGGTCTGATGGCCGCCCCGACATGGTGCTTGTGTCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCC  
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  
AseI (2980)

2901 TGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGT  
8 Q Q S I N F T K M  
3001 GGATGGCGTCTCCAGCTTATCTGACGGTTCACATAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGG

SpeI (3135)

3101 AGTTGTTACGACATTTTGAAAGTCCCCTGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAA

SnaBI (3263)

3201 CCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAG

NdeI (3368)

3301 GTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGG  
3401 CAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTATTATTGACGTCAATGGCGGGGGTCC

PacI (3554)

PstI (3547)

SdaI (3546)

BspLU11I (3564)

3501 GTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACC  
3601 GTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGG  
3701 ACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCG

ApaLI (3878)

3801 GGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCCAGC  
3901 CCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAG  
4001 AGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCA  
4101 GTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAA  
PacI (4294)

4201 AAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATT

EagI (4314)

Swal (4303) NotI (4313)

4301 AACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAA  
4401 ACAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCGAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA