



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGCAGAGCGCACATCGCCACAGTCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGTGCCTA **MfeI (82)**  
101 GAGAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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**Psp1406I (203)** 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTTCACGCGCCCGCCCTACCTGAGGCC  
**HindIII (245)**  
301 GCCATCCACGCGGTTGAGTCGCGTTTCTGCGCCCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGCTTTTGTTCGTTT  
**NgoMIV (441)**

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501 TCTGTTCTGCGCGCTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCATTGGCTGTGGATACAAGCTCAGCAGCTCCAAGGAGA  
**KasI (535)** **AgeI (552)** **NcoI (560)** **BstEII (555)**  
130 M A V W I Q A Q Q L Q G E  
**BglII (699)**

601 AGCCCTTCATCAGATGCAAGCGTTATATGGCCAGCATTTCCTATTGAGTGGCGCATTATTTATCCCAGTGGATTGAAAGCCAAGCATGGGACTCAGTA  
130 A L H Q M Q A L Y G Q H F P I E V R H Y L S Q W I E S Q A W D S V  
**BstAPI (756)** **DraIII (781)**

701 GATCTTGATAATCCACAGGAGAACATTAAGGCCACCCAGCTCCTGGAGGGCCTGGTGCAGGAGCTGCAGAAGAAGGCAGAGCACCAGGTGGGGGAAGATG  
470 D L D N P Q E N I K A T Q L L E G L V Q E L Q K K A E H Q V G E D  
**NcoI (866)** **BsrGI**

801 GGTTTTTACTGAAGATCAAGCTGGGGCACTATGCCACACAGCTCCAGAACACGTATGACCGCTGCCCATGGAGCTGGTCCGCTGCATCCGCCATATATT  
800 G F L L K I K L G H Y A T Q L Q N T Y D R C P M E L V R C I R H I L  
901 GTACAATGAACAGAGGTTGGTCCGAGAAGCCAACAATGGTAGCTCTCCAGCTGGAAGCCTTGCTGATGCCATGTCCAGAAACACCTCCAGATCAACCAG  
1130 Y N E Q R L V R E A N N G S S P A G S L A D A M S Q K H L Q I N Q  
**ScaI (1070)**

1001 ACGTTTGAGGAGCTGCAGCTGGTACCGCAGGACACAGAGAATGAGTTAAAAAGCTGCAGCAGACTCAGGAGTACTTCATCATCCAGTACCAGGAGAGCC  
1470 T F E E L R L V T Q D T E N E L K K L Q Q T Q E Y F I I Q Y Q E S

1101 TGAGGATCCAAGCTCAGTTTGCCCGCTGGCCAGCTGAGCCCCAGGAGCTGTGAGCCGGGAGACGGCCCTCCAGCAGAAGCAGGTGTCTCTGGAGGC  
1800 L R I Q A Q F G P L A Q L S P Q E R L S R E T A L Q Q K Q V S L E A  
**BamHI (1103)** **StuI (1196)**

1201 CTGGTTGCAGCGTGGGACAGACACTGCAGCAGTACCGCGTGGAGCTGGCCGAGAAGCACCAGAAGCCTGCAGCTGCTGGGAAGCAGCAGACCATC  
2130 W L Q R E A Q T L Q Q Y R V E L A E K H Q K T L Q L L R K Q Q T I  
**BstAPI (1272)**

1301 ATCCTGGATGACGAGCTGATCCAGTGGAAAGCGGCGCAGCAGCTGGCCGGAAAGCGGGGCCCCCGAGGGCAGCCTGGACGTGTACAGTCTGGTGTG  
2470 I L D D E L I Q W K R R Q Q L A G N G G P P E G S L D V L Q S W C  
1401 AGAAGTTGGCCGAGATCATCTGGCAGAACCAGCAGCAGTCCGAGGGCTGAGCACCTTGCAGCAGCTGCCATCCCCGGCCAGTGGAGGAGATGCT  
2800 E K L A E I I W Q N R Q Q I R A E H L C Q Q L P I P G P V E E M L  
**Bsp120I (1357)**

1501 GGCCGAGGTCAACGCCACCATCACGGACATTATCTCAGCCCTGGTACCAGCAGCTTCATCATTGAGAAGCAGCCTCCTCAGGTCTGAAGACCCAGACC  
3130 A E V N A T I T D I I S A L V T S T F I I E K Q P P Q V L K T Q T  
**BstEII (1542)**

1601 AAGTTTGAGCCACTGTGCGCCTGCTGGTGGGCGGAAGCTGAACGTGCACATGAACCCCCCAGGTGAAGGCCACCATCATCAGTGCAGCAGGCCA  
3470 K F A A T V R L L V G G K L N V H M N P P Q V K A T I I S E Q Q A  
**ApaLI (1645)**

1701 AGTCTCTGCTCAAGAACGAGAACACCCGCAATGATTACAGTGGCGAGATCTTGAACAACCTGCTGCGTCATGGAGTACCACCAAGCCACAGGCACCCTTAG  
3800 K S L L K N E N T R N D Y S G E I L N N C C V M E Y H Q A T G T L S  
1801 TGCCCACTTCAGGAATATGTCCCTGAAACGAATTAAGAGGTGAGACCGTCTGGGGCAGAGTCCGTGACAGAAGAAAAATTTACAATCCTGTTTGAATCC  
4130 A H F R N M S L K R I K R S D R R G A E S V T E E K F T I L F E S  
**BglII (1745)**

1901 CAGTTCAGTGTGGTGGAAATGAGCTGGTTTTTCAAGTCAAGACCCTGTCCCTGCCAGTGGTGGTGCATGTTTCATGGCAGCCAGGACAACAATGCGACGG  
4470 Q F S V G G N E L V F Q V K T L S L P V V V I V H G S Q D N N A T  
2001 CCACTGTTCTCTGGGACAATGCTTTTGACAGAGCCTGGCAGGGTGCATTTGCCGTGCCTGACAAAGTGTGTGGCCACAGCTGTGTGAGGCGCTCAACAT  
4800 A T V L W D N A F A E P G R V P F A V P D K V L W P Q L C E A L N M  
2101 GAAATTCAGGCCGAAGTGCAGAGCAACCGGGGCTGACCAAGGAGAACCCTGTTCTCTGGCCAGAAACTGTTCAACAACAGCAGCAGCCACCTGGAG  
5130 K F K A E V Q S N R G L T K E N L L V F L A Q K L F N N S S S H L E  
2201 GACTACAGTGGCCTGTCTGTCTGCTCCAGTTCAACAGGGAGAATTTACCAGGAGAAATTACACTTTCTGGCAATGGTTTGACGGTGTGATGGAAG  
5470 D Y S G L S V S W S Q F N R E N L P G R N Y T F W Q W F D G V M E  
2301 TGTTAAAAAACATCTCAAGCCTCATTGGAATGATGGGCGCATTGTTGGGTTTGTAAACAAGCAACAGGCCCATGACCTACTCATTAAACAGCCAGATGG  
5800 V L K K H L K P H W N D G A I L G F V N K Q Q A H D L L I N K P D G  
2401 GACCTTCTCCTGAGATTCAGTACTCAGAAATGGCGGCATCACCATTGCTTGAAGTTTGATTCTCAGGAAAGAAATGTTTTGGAATCTGATGCCTTTT  
6130 T F L L R F S D S E I G G I T I A W K F D S Q E R M F W N L M P F  
**Bst1107I (2593)**

2501 ACCACCAGAGACTTCTCCATTCCGTCCCTAGCCGACCGCTGGGAGACTTGAATTACCTTATCTACGTGTTTCTGATCGGCCAAAAGATGAAGTATACT  
6470 T T R D F S I R S L A D R L G D L N Y L I Y V F P D R P K D E V Y  
2601 CCAATACTACACACCAGTCCCTGCGAGTCTGCTACTGCTAAAGCTGTTGATGGATACGTGAAGCCACAGATCAAGCAAGTGGTCCCTGAGTTTGTGAA  
6800 S K Y Y T P V P C E S A T A K A V D G Y V K P Q I K Q V V P E F V N

2701 CGCATCTGCAGATGCCGGGGGGCAGCGCCACGTACATGGACCAGGCCCTCCAGCTGTGTGTCCAGGCTACTATAACATGTACCCACAGAAC  
 713▶ A S A D A G G G S A T Y M D Q A P S P A V C P Q A H Y N M Y P Q N  
 Tth111I (2803) BspLU11I (2783)  
 2801 CCTGACTCAGTCCTTGACACCGATGGGACTTCGATCTGGAGGACACAATGGACGTAGCGGGCGTGTGGAGGAGTCTCTGGCCGCAATGGACAGTC  
 747▶ P D S V L D T D G D F D L E D T M D V A R R V E E L L G R P M D S  
 BamHI (2903) NheI (2937)  
 2901 AGTGGATCCCGCAGCACAATCGTGACCCCGACCTGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAAC TAGAATGCAG  
 780▶ Q W I P H A Q S •  
 HpaI (3075) MfeI (3086)  
 3001 TGAATAAAATGCTTTATTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCAATTATAAGCTGCAATAAACAAAGTTAAACAACAATTGCATTTCATT  
 EcoRI (3171)  
 3101 TTATGTTTCAGGTTACAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATCTAAAATACAGCATAGCAAACCT  
 3201 TAACCTCCAAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTGCAGCCT  
 SapI (3353)  
 3301 CACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGGTTTGAAGTACTGCTCTTCATTCTTTATGTTTTAAATGCAGTACCTCCACATTCCC  
 SspI (3410) SmaI (3424)  
 3401 TTTTGTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATA  
 3501 TCCCCAGTTTAGTAGTTGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTCTGGTGTACTTGA  
 141▶ • N R T Y K L  
 3601 GGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACAT  
 134▶ 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 R C M  
 3701 GCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACA  
 101▶ 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 N S V  
 StuI (3849)  
 3801 GCAGACCAATGGCAATGGCTTCCAGCACAGACAGTACCCTGCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCAGTCTTGGTCTCTGATGG  
 67▶ 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 T R I A  
 3901 CCGCCCGACATGGTCTTGTGCTCATAGAGCATGGTGTCTTCTCAGTGGCAGCTCCACCAGTCCAGATCTGCTGAGAGATGTTGAAGTCTT  
 34▶ 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 F T K  
 AseI (4057)  
 4001 CATGGTGGCCCTCTATAGTGAGTCTGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTG  
 1▶ M  
 4101 ACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCTACCGCCATTTGCGTCAATGGGCGGAGTTGTTACGACATTTTGGAAAG  
 SpeI (4212)  
 4201 TCCCGTTGATTTACTAGTCAAACAACACTCCATTGACGTCAATGGGTTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGT  
 SnaBI (4340)  
 4301 ACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTCCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCA  
 NdeI (4445)  
 4401 GCGGGCCATTTACCGTCAATAGGGGGCGTACTTGGCATATGATACACTTGTACTGCAAGTGGGCGAGTTTACCGTAAATACTCCACC  
 4501 CATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTATTATTGACGTCAATGGGCGGGGCTGTTGGGCGGTGAGCCAGGCGGGC  
 PacI (4631) SdaI (4623) BspLU11I (4641)  
 4601 CATTACCGTAAGTTATGTAACGCTGCAAGTTAAATAAGAACATGTGAGCAAAAGGCCAGGAACCGTAAAAAGCCGCTTGTGCGG  
 4701 TTTTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAAGTCAAGGTTGGCGAAACCCGACAGGACTATAAAGATACCAGGCTTTC  
 4801 CCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTCTCATAG  
 ApaLI (4955)  
 4901 CTCACGCTGTAGGTATCTCAGTTCGGTGTAGTCTGCTCCAGCTGGGCTGTGTGCACGAACCCCCGTTGAGCCGACCGCTGCGCTTATCCGGT  
 5001 AACTATCGTCTTGAAGTCCAAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTA  
 5101 CAGAGTCTTGAAGTGGTGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGG  
 5201 TAGCTCTTGTATCCGCAAAACACCCGCTGGTAGCGGTGGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCT  
 EagI (5391)  
 5301 TTGATCTTTTCTACGGGCTGACGCTCAGTGGAAACGAAAACCTACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAA  
 PacI (5371) SmaI (5380) NotI (5390)  
 5401 TAAAAATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTGTGTAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTA  
 5501 GCAAAATAGGCTGTCCCGAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA