



**PvuI (7)**  
**SgfI (6)**
**MfeI (82)**

1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
 101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTGCTGTACTGGCTCCGCTTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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**HindIII (245)**
**Bsu36I (291)**

**Psp1406I (203)**
**PvuII (239)**
**Bsu36I (291)**

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCGCCCTACCTGAGGCC  
 301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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**NgoMIV (441)**

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGGCTGACCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

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**BstEII (555)**

**AgeI (552)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCACCATGGCAGAGGCACCAGCCTCCCCGGTCCCGTCTCTCC  
1▶ M A E A P A S P V P L S P

601 GCTCGAAGTGGAGCTGGACCCAGAGTTCGAGCCACAGAGTCGGCCACGCTCCTGTACGTGGCCCTGCAGAGCCGGAGCTGCAGGCGAGCCCGCCAAAG  
 13▶ L E V E L D P E F E P Q S R P R S C T W P L Q R P E L Q A S P A K

**BbsI (751)**

701 CCCTCGGGGAGACGGCCGAGACTCCATGATCCCCGAGGAGACGACGATGAAGACGACGAGGACGGCGGGCCGAGCCAGCTCGGCCATGGTGATCG  
 47▶ P S G E T A A D S M I P E E D D E D D E D G G R A S S A M V I

**XhoI (838)**

801 GTGGCGCGTGAGCAGCAGCTGGGTTCCGGGCTGCTCCTCGAGGATTCGGCCATGCTGCTGGCTCCAGGAGGCAGGACCTCGGGTCCGGGGCCAGCGTC  
 80▶ G G G V S S T L G S G L L L E D S A M L L A P G G Q D L G S G P A S

**PvuII (934)**
**BstAPI (948)**

901 CGCCGAGGCGCTCTGAGTGGGGCACGCCGACGCTGCAGCCTCAGCAGCCTGCCACAGCCGAGCCGGGGCGGCTGGGGGCTCTGGGAACCA  
 113▶ A A G A L S G G T P T Q L Q P Q Q P L P Q P Q P G A A G G S G Q P  
 1001 AGGAAATGCTCCTCGCGCGAATGCCTGGGGAACTGTCTATGCCGACCTGATCACCCGCGCCATCGAGAGCTCCCCGGACAAACGGCTCACTTTGT  
 147▶ R K C S S R R N A W G N L S Y A D L I T R A I E S S P D K R L T L

**BglII (1103)**

1101 CCCAGATCTACGAGTGGATGGTGCCTGTGTGCCCTACTTCAAGGATAAGGGCGACAGCAACAGCTCTGCGGGCTGGAAGAACTCCATCCGGCACAACCT  
 180▶ S Q I Y E W M V R C V P Y F K D K G D S N S S A G W K N S I R H N L  
 1201 GTCCTGCACAGCCGTTTCATGCGGTTTCAAGTGAAGGCACGGGCAAGAGCTCTTGGTGGATCATCAACCCCGATGGGGAAAGAGCGGGAAGGCCCCC  
 213▶ S L H S R F M R V Q N E G T G K S S W W I I N P D G G K S G K A P

**SdaI (1377)**

1301 CGGCGCGTGGGCTTCCATGGACAACAGCAACAAGTACACCAAGAGCCGAGGCGGGGAGCCAAAGAAGAAGCGGCCCTGCAGGCTGCCCCAGAGTCGG  
 247▶ R R R A V S M D N S N K Y T K S R G R A A K K K A A L Q A A P E S  
 1401 CAGACGACAGTCTTCCAGCTTCCAAGTGGCTGGCAGCCACGTCGCCGACGAGCAGGAGCTGGATGCGTGGACCGACTTCCGCTCGCGCACCAA  
 280▶ A D D S P S Q L S K W P G S P T S R S S D E L D A W T D F R S R T N

**NotI (1520)**
**BsrGI (1598)**

1501 TTCCAACGCCAGCACCGTGGCGCCGCTGTGCGCCATCCTGGCAAGCACGGAGCTGGATGACGTCACAGGATGATGATGGACCCCTGTCCCCATGCTG  
 313▶ S N A S T V S G R L S P I L A S T E L D D V Q D D D G P L S P M L

**SacII (1657)**
**NgoMIV (1675)**

1601 TACAGCAGCTCTGCCAGCCTGTGCGCCCTCCGTGAGCAAGCCGTGACTGTGGAGCTTCCGCGGCTGACGGACATGGCCGGCACCATGAATCTGAATGATG  
 347▶ Y S S S A S L S P S V S K P C T V E L P R L T D M A G T M N L N D  
 1701 GGCTGGCCGAGAACCCTCATGGACGACCTGTGGATAACATCGCGCTCCCGCCATCGCAGCCATCGCCTCCTGGCGGGCTTATGAGCGGGGCTCCAGCTT  
 380▶ G L A E N L M D L L D N I A L P P S Q P S P P G G L M Q R G S S F  
 1801 CCCATATACCCCAAGAGCTCCGGCCTGGGCTCCCCAACCCTCCTTCAACAGTACCGTGTGGACCTTCTGACCTTCTGAACCTTGCCTCAGTCAACC  
 413▶ P Y T A K S S G L G S P T G S F N S T V F G P S S L N S L R Q S P  
 1901 ATGCAGACTATCCAGGAGAACAGACCAGCCACCTTCTTCCGTGTCACTACGGAACAGACACTCCAAGACCTGCTTGCCTCAGACTCACTCAGCC  
 447▶ M Q T I Q E N R P A T F S S V S H Y G N Q T L Q D L L A S D S L S

**Tth111I (2016)**

**BspHI (2009)**
**NheI (2044)**

2001 ACAGCGAGCTCATGATGACCCAGTCCGACCCCTTGATGTCTCAGGCTAGCAGCCGCGTGTCCGCCAGAATGCCCGCCGAACGTGATGCTTCGCAACGA  
 480▶ H S D V M M T Q S D P L M S Q A S T A V S A Q N A R R N V M L R N D  
 2101 TCCAATGATGTCTTTGCTGCCAGCCTACCCAGGGAGTTTGGTCAATCAGAACTTGTCTCCACCACCAGCACCACCCAGGGCGCTTGTGGTGGCAGC  
 513▶ P M M S F A A Q P T Q G S L V N Q N L L H H Q H Q T Q G A L G G S  
 2201 CGTGCCTTGTCAAATTCTGTGACCAACATGGGCTTGTGACTCCAGCAGCCTTGGCTCAGCCAAACACCAGCAGCAGTCTCCCGCCAGCCAGTCTATGC  
 547▶ R A L S N S V S N M G L S D S S S L G S A K H Q Q Q S P A S Q S M

**BspLU11**

2301 AAACCCTCTCGACTCTCTCAGGCTCCTCACTGTATTAGCTAGTGCAAACTTCCGTCATGGGCCAGGATAAGTCCCCAGTGACTTGGACCTGGA  
 580▶ Q T L S D S L S G S S L Y S A S A N L P V M G H D K F P S D L D L D  
 2401 CATGTTCAATGGGAGCTTGAATGTGACATGGAGTCCATCATCCGTAGTGAACCTCATGGATGCTGACGGGTTGGATTTAACTTTGACTCCCTCATCTCC  
 613▶ M F N G S L E C D M E S I I R S E L M D A D G L D F N F D S L I S

Psp1406I (2506) StuI (2549) Acc65I (2568)  
 2501 ACACAGAACGTTGTTGGTTTGAATGTGGGGAACCTCACTGGTGCTAAGCAGGCCTCATCTCAAAGCTGGGTACCAGGCTGAAGGATCACTGAGGAAAGGG  
 647▶ T Q N V V G L N V G N F T G A K Q A S S Q S W V P G •  
 AvrII (2604) MscI (2616)  
 2601 GAAACCTAGGACTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAAT

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HpaI (2748) MfeI (2759)  
 2701 TGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAAACAAGTTAAACAACAACAATTGCATTTCATTTTATGTTTCAGGTTCAAGGGGAGGTGT

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EcoRI (2844)  
 2801 GGGAGGTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGA  
 2901 ATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATAT

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SspI (3026) SspI (3083) SmaI (3097)  
 3001 AGTGTATTTTCCAAGGTTTGAAGTCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCCACATTCCTTTTATAGTAAATATTCAGAAATAATT  
 3101 TAAATACATCATTGCAATGAAAAATAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGG  
 3201 GAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTT  
 141◀ • N R T Y K L P I L E E I T T K  
 3301 TGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGA  
 125◀ V L K G N M E I L V F C D P A Y D S I L E R C M G C P S V V R I S  
 3401 TCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCAAATGGTGTCAAAGTCTTCTGCCCGTGTCTACAGCAGACCCAAATGGCAATGGCTTCAGCA  
 92◀ R D V E D S Y P H R V A V I T D F D K Q G N S V A S G I A I A E A  
 StuI (3522)  
 3501 CAGACAGTGACCCTGCCAATGTAGGCCCTCAATGTGGACAGCAGAGATGATCTCCCGAGTCTTGGTCTGATGGCCGCCCGACATGGTCTTGTGCTCT  
 58◀ 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 A G V H H K N D E  
 BbsI (3668)  
 XmnI (3664)  
 3601 CATAGAGCATGGTATCTTCTCAGTGGCAGCTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCTATAGTGAGTCGT  
 25◀ Y L M T I K E T A V E V L E L D Q Q S I N F T K M ◀

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AseI (3730)  
 3701 ATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTAT

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SpeI (3885)  
 3801 ATAGACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCCTGATTTACTAGTCAAAAACAAA  
 3901 CTCCCATTGACGTC AATGGGGTGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTA CTGCAAACCGCATCATCATGGTAA

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SnaBI (4013)  
 4001 TAGCGGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAAGTCACTGACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTC

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NdeI (4118)  
 4101 AATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCGAGTTTACCGTAAATACTCCACCATTGACGTC AATGGAAAGTCCCTATT

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SdaI (4296)  
 4201 GCGTACTATGGGAACATACGTCATTATTGACGTC AATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAACGCTG

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PacI (4304) BspLU11I (4314)  
 4301 CAGGTTAATTAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGGTGGCGTTTTTTCATAGGCTCCGCCCTGAC  
 4401 GAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTC  
 4501 CTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTTCCCTTCGGGAAGCGTGGCGCTTTTTCATAGCTCACGCTGTAGGTATCTCAGTTCCGGT

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ApaLI (4628)  
 4601 GTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTGAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTA  
 4701 AGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAAGTGGTGGCTAACT  
 4801 ACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCAC  
 4901 CGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCT

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PacI (5044) SmaI (5053) NotI (5063)  
 5001 CAGTGAACGAAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGAATAAAAATATCTTTATTTTATTACATCT  
 5101 GTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCGAGTGAAGT  
 5201 GCAGGTGCCAGAACATTTCTCTATCGAA