



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGACAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
**MfeI (82)** **EcoNI (96)**  
101 GAGAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

**Psp1406I (203)** **HindIII (245)** **Bsu36I (291)**  
**EcoNI (287)** 201 GTGAACGTTCTTTTTCGCAACGGGTTTGGCCGACAGACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCCGCCCTACCTGAGGCC  
301 GCCATCCACGCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

**NgoMIV (441)** 401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGTTGCTCAACTCTACGTCTTTGTTTCGTTT

**NcoI (560)** **BstEII (555)**  
**KasI (535)** **AgeI (552)** 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCTACCTGAGATCACCGGTCCACATGGACCAAAGAGAAATCTGCAGCAACTACTGAAAGA  
601 AGCCAGAAAAAGAACTCAACAGTGAAGGAGTTTCCAGTGAATTTCTGAAGCTGAAAAGGCAATCCACCAAGTACAAGGCCGCAAAAATCTATCTACA  
13▶ A Q K K K L N S E E F A S E F L K L K R Q S T K Y K A D K I Y P T

**HpaI (786)** 701 ACTGTGGCTCAGAGGCCAAGAATATCAAGAAAAACAGATACAAGGATATTTTGCCTATGATCACAGCCTGGTAGAGCTGTCTGTTAACTCCGATG  
47▶ T V A Q R P K N I K K N R Y K D I L P Y D H S L V E L S L T S D  
801 AGGATCCAGTTATATCAATGCCAGCTTTATTAAGGGTGTCTATGGACCAAGGCTTATATTGCTACCCAGGGTCTTTATCTACAACCTCTCCGACTT  
80▶ E D S S Y I N A S F I K G V Y G P K A Y I A T Q G P L S T T L L D F  
901 CTGGAGGATGATCGGGAGTACCGCATCTGGTCATTGTCATGGCATGTATGGAGTTTGAATGGGAAAGAAAAATGTGAGCGTTATTGGGCCGAGCCA  
113▶ W R M I W E Y R I L V I V M A C M E F E M G K K K C E R Y W A E P  
1001 GGAAACCGCAGCTGCAATTTGGCCCTTTTCTATATCTGTAAGCTGAGAAAAAGAAATCTGATTAAAAATCAGGACTCTGAAGGCCAAGTTCAATA  
147▶ G E T Q L Q F G P F S I S C E A E K K K S D Y K I R T L K A K F N

**MscI (1138)** 1101 ATGAAACTCGAATATTTTACCAGTTTCATTATAAGAATTTGGCCAGACCATGATGTGCCTTCATCTATAGACCCTATTCTCAGCTCATCTGGGATATCGC  
180▶ N E T R I I Y Q F H Y K N W P D H D V P S S I D P I L Q L I W D M R

**BstAPI (1232)** **NsiI (1230)** **NgoMIV (1246)** **PshAI (1260)** 1201 TTGTTACCAAGAAGATGACTGTGTTCTATATGCACTTCTGAGTGGCGGCTGCGGAAGGACAGGTGCATTTGTGCTGTTGATTATACATGGATGCTG  
213▶ C Y Q E D D C V P I C I H C S A G C G R T G V I C A V D Y T W M L

**StuI (1366)** 1301 CTGAAAGATGGGATAATTCTAAGAAGTTCAGTGTTTTAAATTTGATTGAGGATGCGAACACAGAGGCTTCGCTAGTTCAAACCTCAGGAACAGTACG  
247▶ L K D G I I P K N F S V F N L I Q E M R T Q R P S L V Q T Q E Q Y  
1401 AACTGGTCTACAGTGTGTTAGAGCTGTTTAAAGGGCACATGGATGTTATCTGATAATCACCTTGAAGAGAGATTCAAGCACAATGCTCAATTC  
280▶ E L V Y S A V L E L F K R H M D V I S D N H L G R E I Q A Q C S I P

**PshAI (1525)** 1501 TGAACAGAGCCTCACGATAGAAGCTGACTCTTGCTCTGGATTTACCAAAAAACGCCATGAGGGATGTGAAAACGACAAACAGCATAGCAAACAGGG  
313▶ E Q S L T I E A D S C P L D L P K N A M R D V K T T N Q H S K Q G

**BbsI (1623)** **Bsu36I (1635)** 1601 GCTGAAGCGGAGAGCACTGGAGGCTTCCCTTGGCCTTAGGACTTCTACGATGAATGCCGAGGAAGAGTTGGTTTTGCACTCGGCTAAATCAAGCCCTT  
347▶ A E A E S T G G S S L G L R T S T M N A E E E L V L H S A K S S P  
1701 CTTTTAACTGTTTAGAGCTAAACTGCGGGTGAACAACAAGGCTGTGATAACAGGAACGGCAGGCAAGGGCTTCTCCAGTCGTTGGGAGAGCCCTTCA  
380▶ S F N C L E L N C G C N N K A V I T R N G Q A R A S P V V G E P L Q  
1801 GAAGTATCAAAGTCTGGATTTCCGGTCCATGTTGTTGGGTCTGTCTAGTGTCTGCCATAAACACAGCGGACAGGTATCACAATCAAAGGGGCCG  
413▶ K Y Q S L D F G S M L F G S C P S A L P I N T A D R Y H N S K G P  
1901 GTAACAGGACCAACTCACTCCCTTGAAGTACTGATCAGCAGAGAAAAACAAATGACTTGGCCGTGGGAGACGGTTTTTCATGCTGGAATCTCAGCTGC  
447▶ V K R T K S T P F E L I Q Q R K T N D L A V G D G F S C L E S Q L  
2001 ATGAGCATTACAGTCTCAGGAGCTGCAGTGCAGAGAGTGGCCATGTTTCTCAGAAGAGCTGAATTATTCAGTGCCTGGTGCCTGTGATGCGTCGTG  
480▶ H E H Y S L R E L Q V Q R V A H V S S E E L N Y S L P G A C D A S C

**BsrGI (2138)** 2101 TGTCCCCGACAGCCCCGCGCTTTGAGAGTGCATCTGTACACATCTTTAGCGGAAGATCCTATTTTTTCATCATCCCTCCGAATAGTGTGATTCA  
513▶ V P R H S P G A L R V H L Y T S L A E D P Y F S S S P P N S A D S  
2201 AAGATGCTTTTGTATCTGCTGAGAAACAGGATGGAGCACTTCCCTGGCGCTCTATTGCCAGCCTTCTACAACTCCTTCTTTTATAGCAACCCAC  
547▶ K M S F D L P E K Q D G A T S P G A L L P A S S T T S F F Y S N P  
2301 ACGACTCCCTAGTGTGAACACTCTGACCAGCTTTTCCCACCGTTAAACCAAGAGACAGCTGAGAAGCTCCTTCTCGGAGGACAGATGAAATCCC  
580▶ H D S L V M N T L T S F S P P L N Q E T A V E A P S R R T D D E I P

**BbrPI (2465)** **DraIII (2462)** 2401 CCCGCCACTCCCTGAACGGACACCCGAGTCTTTTATTGTGGTTGAGGAAGCCGAGAGCCCTCACCAGTGTACCAGTCTTACCTCTGGTGGTAACA  
613▶ P P L P E R T P E S F I V V E E A G E P S P R V T E S L P L V V T  
2501 TTTGGAGCATCACCAGAATGCAGTGGGACATCTGAAATGAAGAGCCATGACTCTGTAGGGTTTACACCAAGCAAGAATGTGAAACTCCGAAGTCCCAAT  
647▶ F G A S P E C S G T S E M K S H D S V G F T P S K N V K L R S P K

**BsaBI (2602)** **XbaI (2649)** **Bst1107I (2681)** 2601 CAGATCGACATCAGGATGGTTCTCTCCACCTCTCTCCAGAAAGAAGTCTAGAGTCTTCTTCTTCTGCTGATGAGGACTGTATACAGGCAACCCGCT  
680▶ S D R H Q D G S P P P P L P E R T L E S F F L A D E D C I Q A Q Q A V  
2701 GCAAACCTTCTACTAGCTATCTGAAACACAGAGAACTCCACATCTTCTAAACAACATTGAGGACCCCTGGAAAAAGTTTCAAGGAGTAAGAGT  
713▶ Q T S S T S Y P E T T E N S T S S K Q T L R T P G K S F T R S K S

**BstBI (2810)**  
**Bsp119I (2810)**  
 2801 TTGAAGATTTTTCGAAATATGAAAAAAGTGTGTTGTAATTCCTCTACCAAGCAAGCCTACAGAACGTGTTAGCCAAAAAATCCAGCTCCTTTCTGA  
 747▶ L K I F R N M K K S V C N S S S P S K P T E R V Q P K N S S S F L

MscI (2992)  
**BstXI (2950)** **NheI (2986)**  
 2901 ATTTTGGTTTCGAAATCGTTTTTCAAACCCAAAGGACCAAGGAACCCGCCATCAGCTTGGAAATATGTAACGCACCTCTGGATTTGCTAGCTGGCCAGA  
 780▶ N F G F G N R F S K P K G P R N P P S A W N M •

3001 CATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTA

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HpaI (3124) MfeI (3135)  
 3101 ACCATTATAAGCTGCAATAACAAGTTAACAACAACAATTGCATTTCATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAA

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**EcoRI (3220)**  
 3201 ACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAG  
 3301 GCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTATTTCCTCAAGGTTTGAAC

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**SspI (3459)** SmaI (3473)  
 3401 TAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTGTAGAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAAT  
 3501 AAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAA  
 3601 TTGCACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTTCCTCAATGGTGGTTTTGACCAGCTTGCATTTCATCTCAA

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SacI (3734) **BstXI (3763)**  
 3701 TGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGG  
 117▶ 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 R D V E D S Y P

StuI (3898)  
 3801 GTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGCACCTGCCAATGTAG  
 84▶ 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 C V T V R G I Y  
 3901 GCCTCAATGTGGACAGCAGAGATGATCTCCCGAGTCTTGGTCTGATGGCCGCCCGACATGGTGTCTTGTCTCATAGAGCATGGTATCTTCTCAG  
 50▶ 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 Y L M T I K E T

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**BbsI (4044)**  
 4001 TGGCAGCTCCACCAGTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATG  
 17▶ A V E V L E L D Q Q S I N F T K M

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**AseI (4106)** SacI (4163)  
 4101 CCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCATAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCT

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**SpeI (4261)**  
 4201 ACCGCCCATTTGCGTCAATGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGG

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**SnaBI (4389)**  
 4301 AGACTTGAAATCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGT

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**NdeI (4494)**  
 4401 ACTGCCAAGTAGGAAAGTCCATAAGGTGATGACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATG  
 4501 ATACACTTGATGACTGCCAAGTGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTC

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PacI (4680) **SdaI (4672)** **BspLU11I (4690)**  
 4601 ATTATTGACGTCAATGGGCGGGGTCGTTGGGCGTCCAGCCAGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGC  
 4701 AAAAGGCCAGAAAAGCCAGGAACCGTAAAAGGCCGCGTGTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAGAAAATCGACGCTCA  
 4801 AGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCTGCCGTTACCG  
 4901 GATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGG

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**ApaLI (5004)**  
 5001 CTGTGTGCACGAACCCCGTTCCAGCCGACCGCTGCGCTTATCCGTAACATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCA  
 5101 GCAGCCACTGTTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGATTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTAT  
 5201 TTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGCAACAAACACCGCTGGTAGCGGTGTTTTTTTGT  
 5301 TTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGCTGACGCTCAGTGAACGAAAACACGTTAA

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**EagI (5440)**  
 PacI (5420) SmaI (5429) **NotI (5439)**  
 5401 GGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCCAATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTGTGTAATC  
 5501 GTAACAAACATACGCTCTCCATCAAACAAACGAAACAAACAAACTAGCAAATAGGCTGTCCCGAGTGCAAGTGCAGGTGCCAGAACATTTCTCTAT  
 5601 CGAA