



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

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**HindIII (245)**  
**Psp1406I (203)** 201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCCGCCGCTACCTGAGGCC  
**PvuII (239)**  
**Bsu36I (291)** 301 GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCTCCTGAAGTGCCTCCGCGCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

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**SphI (560)**  
**AgeI (552)** 501 TCTGTTCTGCGCGGTTACAGATCCAAGCTGTGACCGCGCGCTACCTGAGATCACCGGTCAGCATGCTTTTGGCCAGAATGCCTTCATGTCAGATCACT  
**XmnI (576)** 1▶ M L L S Q N A F I V R S L  
**NdeI (644)**  
**EcoRV (687)** 601 TAATTTGGTTCTCATGGTGTATATCAGCCTCGTGGTGGTATTTTCATATGATTCGCTGATTACAGATGAATCTTGCACTTTCAAGATATCATTGCCGA  
13▶ N L V L M V Y I S L V F G I S Y D S P D Y T D E S C T F K I S L R

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**BspHI (776)**  
**Bst1107I (768)** 701 AATTTCCGGTCCATCTTATCATGGGAATAAAAAACCCTCCATTGTACCAACTCACTATACATTGCTGTATACAATCATGAGTAAACCAGAAGATTGA  
47▶ N F R S I L S W E L K N H S I V P T H Y T L L Y T I M S K P E D L  
801 AGGTGGTTAAGAAGTGTGCAATACCACAAGATCATTTTGTGACCTCACAGATGAGTGGAGAAGCACACAGAGGCTATGTCACCGTCTAGAAGGATT  
80▶ K V V K N C A N T T R S F C D L T D E W R S T H E A Y V T V L E G F

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**Psp1406I (912)** 901 CAGCGGGAACACAACGTTGTTGCTCAGTGGCTCACACAATTTCTGGCTGGCCATAGACATGCTTTTGAACCACCAGAGTTTGGATTGTTGGTTTTACCAAC  
113▶ S G N T T L F S C S H N F W L A I D M S F E P P E F E I V G F T N  
**AseI (1003)**  
1001 CACATTAATGTGATGGTAAATTTCCATCTATTGTTGAGGAAGAATTACAGTTTGGTTTATCTCTCGTCATTGAAGAACAGTCAGAGGGAATTGTTAAGA  
147▶ H I N V M V K F P S I V E E L Q F D L S L V I E E Q S E G I V K  
1101 AGCATAAACCCGAAATAAAAGAAACATGAGTGGAAATTTACCTATATCATTGACAAGTTAATTCCAAACACGAACTACTGTGTATCTGTTTATTAGA  
180▶ K H K P E I K G N M S G N F T Y I I D K L I P N T N Y C V S V Y L E

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**BstAPI (1276)**  
1201 GCACAGTGTGAGCAAGCAGTAATAAAGTCTCCCTTAAATGACCCCTCTCCACCTGGCCAGGAATCAGAATCAGCAGAATCTGCCAAAATAGGAGGA  
213▶ H S D E Q A V I K S P L K C T L L P P G Q E S E S A E S A K I G G  
1301 ATAATTACTGTGTTTTGATAGCATTGGTCTTGACAAGCACCATAGTGACACTGAAATGGATTGGTTATATGCTTAAAGAAATAGCCTCCCAAGTCT  
247▶ I I T V F L I A L V L T S T I V T L K W I G Y I C L R N S L P K V

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**XcmI (1454)**  
**NcoI (1454)**  
**BstXI (1454)** 1401 TGAATTTTCATACTTTTAGCCTGGCCATTTCTAACCTGCCACCGTTGGAAGCCATGGATATGGTGGAGGTCATTTACATCAACAGAAAGAAGAAAGT  
280▶ L N F H N F L A W P F P N L P P L E A M D M V E V I Y I N R K K K V

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**NsiI (1576)**  
1501 GTGGGATTATAATTATGATGATGAAAGTATAGCATACTGAGGCAGCGCCAGGACAAGTGGCGGTGGCTATACCATGATGACTGCTGACGGCCT  
313▶ W D Y N Y D D E S D S D T E A A P R T S G G G Y T M H G L T V R P

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**Bsu36I (1672)**  
1601 CTGGGTCAGGCCTCTGCCACCTCTACAGAATCCAGTTGATAGACCCGGAGTCCGAGGAGGAGCCTGACCTGCCTGAGGTTGATGTGGAGCTCCCCACGA  
347▶ L G Q A S A T S T E S Q L I D P E S E E E P D L P E V D V E L P T

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**Bsp120I (1738)**  
1701 TGCCAAAGGACAGCCCTCAGCAGTTGGAAGTCTTGGTGGCCCTGTGAGAGGAGAAAGAGTCCACTCCAGGACCCTTTTCCGAAAGAGGACTACAGCTC  
380▶ M P K D S P Q Q L E L L S G P C E R R K S P L Q D P F P E E D Y S S  
1801 CACGGAGGGGCTGGGGGAGAATTACCTTCAATGTGGACTTAACTCTGTGTTTTGAGAGTCTTGTGATGACGAGGACAGTACGACTTAGAAGCCCT  
413▶ T E G S G G R I T F N V D L N S V F L R V L D D E D S D D L E A P

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**BamHI (1941)**  
1901 CTGATGCTATCGTCTCATCTGGAAGAGATGGTTGACCCAGAGGATCCTGATAATGTGCAATCAAACATTTGCTGGCCAGCGGGGAAGGGACACAGCCAA  
447▶ L M L S S H L E E M V D P E D P D N V Q S N H L L A S G E G T Q P  
2001 CCTTTCCAGCCCTCTCAGAGGGCCTGTGGTCCGAAGATGCTCCATCTGATCAAAGTACACTTCTGAGTCAAGTGTGACCTTGGGGATGGTTATAT  
480▶ T F P S P S S E G L W S E D A P S D Q S D T S E S D V D L G D G Y I

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**NheI (2128)**  
2101 AATGAGATGACTCCAAAATAT GAATGAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAACCACAAGTGAATGCAGTGAAGAAAAA  
513▶ M R •

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**HpaI (2266)** **MfeI (2277)**  
2201 TGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAACAAACAACATTGCAATTTTTATGTTTC

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**EcoRI (2362)**  
2301 AGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTTAAAATACAGCATAGCAAACTTTAACCTCCA  
2401 AATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCTCACCTTCT

**SapI (2544)**

2501 TCATGGAGTTTAAGATATAGTGTATTTTCCAAGGTTTGAAGTCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCCACATTCCTTTTATAGTA

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**SspI (2601)**      SwaI (2615)

2601 AATATTCAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGT

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2701 TTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTACTTGAGGGGGATGA

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2801 GTTCCTCAATGGTGGTTTTGACCAGCTTCCATTCACTCAATGAGCACAAGCAGTCAAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGG  
141 • N R T Y K L P I L

131 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 G C P

BstXI (2905)

2901 GCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCA  
98 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 A S G

3001 ATGGCAATGGCTTCAAGCAGACAGTACCCTGCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCAGTCTTGGTCTGATGGCCGCCCGA  
64 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 A G V

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**BbsI (3186)**

XmnI (3182)

3101 CATGGTGCTTGTTCCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGC  
31 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 M ←

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AseI (3248)

3201 CCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCAC

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3301 TAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCCTTGA

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**SpeI (3403)**

3401 TTTACTAGTCAAAACAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAA

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**SnaBI (3531)**

3501 ACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCCATAAGGTCATGTACTGGCATAATGCCAGGGGGCCA

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NdeI (3636)

3601 TTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCGATTTACCGTAAATACTCCACCCATTGACGT

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3701 CAATGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGGGGCCATTTACCG

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PacI (3822)

**PstI (3815)**

**SdaI (3814)**      BspLU11I (3832)

3801 TAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGGTGGCCTTTTCCAT  
←

3901 AGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAA

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4001 GTCCTCGTGCGCTCTCTGTTCCGACCTGCCGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTG

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**ApaLI (4146)**

4101 TAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCTTATCCGGTAACTATCGT

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4201 CTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGTTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTTCT

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4301 TGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTG

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4401 ATCCGGCAAAACAAACCCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTT

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**EagI (4582)**

PacI (4562)      SwaI (4571)      **NotI (4581)**

4501 TCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCCAATAAAATATC

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4601 TTTATTTTATTACATCTGTGTGTTGGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAAATAG

4701 GCTGTCCCAGTCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA