



**PvuI (7)**  
**SgfI (6)** **MfeI (82)**  
1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGCGCAATTGAACGGGTGCCTA  
101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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**Psp1406I (203)**
**HindIII (245)**  
**PvuII (239)** **Bsu36I (291)**  
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCCGCCGCTACCTGAGGGCC  
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCCGCTTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

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**BstEII (555)**  
**AgeI (552)** **XmaI (573)** **EagI (583)** **Bsp120I (598)**  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCATGGAGCGGCCCGGGGCTGCGGCCGGCGGGCGGCGG  
1▶ M E R P P G L R P G A G G

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**SgrAI (627)**  
601 GCCTGGGAGATGCGGGAGCGGCTGGGCACCGCGGCTTCGGGAACGTCTGTCTGTACCAGCATCGGGAACCTGATCTCAAAATAGCAATTAAGTCTTGT  
13▶ P W E M R E R L G T G G F G N V C L Y Q H R E L D L K I A I K S C  
701 GCCTAGAGCTAAGTACAAAACAGAGAACGATGGTCCATGAAATCCAGATTATGAAGAAGTTGAACCATGCCAATGTTGTAAAGCCTGTGATGTTCC  
47▶ R L E L S T K N R E R W C H E I Q I M K K L N H A N V V K A C D V

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**SspI (811)**  
801 CTGAAGAATTGAATTTTTGATTCATGATGTGCCTCTTCTAGCAATGGAATACTGTTCTGGAGGAGATCTCCGAAAGCTGCTCAACAAACCAGAAAATTG  
80▶ P E E L N I L I H D V P L L A M E Y C S G G D L R K L L N K P E N C  
901 TTGTGGACTTAAAGAAAGCCAGATACTTTCTTACTAAGTGATATAGGGTCTGGGATTCGATATTTGCATGAAAACAAAATTATACATCGAGATCTAAAA  
113▶ C G L K E S Q I L S L L S D I G S G I R Y L H E N K I I H R D L K

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**BsaBI (1072)**  
1001 CCTGAAAACATAGTTCTTCAGGATGTTGGTGGAAAAGATAATACATAAAAATAATTGATCTGGGATATGCCAAAAGATGTTGATCAAGGAAGTCTGTGTACAT  
147▶ P E N I V L Q D V G G K I I H K I I D L G Y A K D V D Q G S L C T  
1101 CTTTTGTGGAACTGACGATCTGGCCCCAGAGCTCTTTGAGAATAAGCCTTACACAGCCACTGTTGATTATTGGAGCTTTGGACCATGGTATTTGA  
180▶ S F V G T L Q Y L A P E L F E N K P Y T A T V D Y W S F G T M V F E

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**BstAPI (1227)** **BstXI (1240)**  
1201 ATGTATTGCTGGATATAGCCCTTTTTGCATCATCTGCAGCCPTTTACCTGGCATGAGAAGATTAAGAAGAAGGATCCAAAGTGTATATTTGCATGTGAA  
213▶ C I A G Y R P F L H H L Q P F T T W H E K I K K K D P K C I F A C E  
1301 GAGATGTCAGGAGAAGTTCGGTTTAGTAGCCATTACCTCAACCAAATAGCCTTTGTAGTTAATAGTAGAACCCATGAAAACCTGGCTACAGTTGATGT  
247▶ E M S G E V R F S S H L P Q P N S L C S L I V E P M E N W L Q L M

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**SmaI (1406)** **AseI (1467)**  
1401 TGAATTGGGACCTCAGCAGAGAGGAGGACCTGTTGACCTACTTTGAAGCAGCAAGATGTTTTGTATTAATGGATCACATTTGAATTTGAAGATAGT  
280▶ L N W D P Q Q R G G P V D L T L K Q P R C F V L M D H I L N L K I V

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**XmnI (1555)**  
1501 ACACATCCTAAATATGACTTCTGCAAAGATAATTTCTTTCTGTTACCACCTGATGAAAGTCTTCATTCACTACAGTCTCGTATTGAGCGTAAAAGTGA  
313▶ H I L N M T S A K I I S F L L P P D E S L H S L Q S R I E R E T G

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**XbaI (1677)**  
1601 ATAAACTGTTCTCAAGAACTCTTTTCAGAGACAGGAATTTCTCTGGATCCTCGGAAACCAGCCTCTCAATGTGTTCTAGATGGAGTTAGAGGCTGTG  
347▶ I N T G S Q E L L S E T G I S L D P R K P A S Q C V L D G V R G C  
1701 ATAGCTATATGTTTATTTGTTGATAAAAAGTAAAAGTGTATATGAAGGGCCATTTGCTTCCAGAAGTTTATCTGATTGTGTAATATATTTGACAGGA  
380▶ D S Y M V Y L F D K S K T V Y E G P F A S R S L S D C V N Y I V Q D

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**PvuII (1825)** **DraIII (1855)**  
1801 CAGCAAAATACAGCTTCCAATTATACAGCTGCGTAAAGTGTGGCTGAAGCAGTGCATATGTGTCTGGACTAAAAGAAGACTATAGCAGGCTCTTTTCAG  
413▶ S K I Q L P I I Q L R K V W A E A V H Y V S G L K E D Y S R L F Q  
1901 GGACAAAGGGCAGCAATGTTAAGTCTTCTAGATATAATGCTAACTTAACAAAATGAAGAACACTTTGATCTCAGCATCACAAACACTGAAAGCTAAAT  
447▶ G Q R A A M L S L L R Y N A N L T K M K N T L I S A S Q Q L K A K

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**EcoRV (2064)**  
2001 TGGAGTTTTTTCACAAAAGCATTGACCTGAGAGATACAGGAGCAGATGACGTATGGGATATCTTCAGAAAAAATGCTAAAAGCATGGAAGA  
480▶ L E F F H K S I Q L D L E R Y S E Q M T Y G I S S E K M L K A W K E

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**SphI (2172)** **SapI (2196)**  
2101 AATGGAAGAAAAGCCATCCACTATGCTGAGGTTGGTGTCTTGGATACCTGGAGGATCAGATTATGCTTTGCGATGCTGAAATCATGGAGCTACAGAAG  
513▶ M E E K A I H Y A E V G V I G Y L E D Q I M S L H A E I M E L Q K  
2201 AGCCCCTATGGAAGAGCTCAGGGAGACTTGTGGAATCTCTGGAACAGCGTGCATTGATCTATATAAGCAGTTAAAACACAGACCTTCAGATCACTCCT  
547▶ S P Y G R R Q G D L M E S L E Q R A I D L Y K Q L K H R P S D H S

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**DraIII (2335)**  
**BstAPI (2334)**  
2301 ACAGTGACAGCACAGAGATGGTAAAATCATTGTGCACACTGTGCAGAGTCCGACCGTGTGCTCAAGGAGCTGTTTGGTCATTTGAGCAAGTTGTTGG  
580▶ Y S D S T E M V K I I V H T V Q S Q D R V L K E L F G H L S K L L G

2401 CTGTAAGCAGAAGATTATTGATCTACTCCCTAAGGTGGAAAGTGGCCCTCAGTAATATCAAAGAAGCTGACAATACTGTTCATGTCAGGGAAAAAGG  
613▶ C K Q K I I D L L P K V E V A L S N I K E A D N T V M F M Q G K R

2501 CAGAAAGAAATATGGCATCTCCTTAAAATTGCCTGTACACAGAGTTCTGCCCGTCCCTTGTAGGATCCAGTCTAGAAGGTGCAGTAACCCCTCAGACAT  
647▶ Q K E I W H L L K I A C T Q S S A R S L V G S S L E G A V T P Q T

2601 CAGCATGGCTGCCCCGACTTCAGCAGAACATGATCATTCTGTGCATGTGTGTAACCTCCTCAAGATGGGGAGACTTCAGCACAAATGATAGAAGAAAA  
680▶ S A W L P P T S A E H D H S L S C V V T P Q D G E T S A Q M I E E N

2701 TTTGAACCTGCCTTGGCCATTTAAGCACTATTATTTCATGAGGCAATGAGGAACAGGGCAATAGTATGATGAATCTTGATTGGAGTTGGTTAACAGAAGGA  
713▶ L N C L G H L S T I I H E A N E E Q G N S M M N L D W S W L T E G

2801 TCCTATCCCTATGATGTGCCAGACTATGCTGGCTATCCATATGATGTTCTGATTATGCTGGATACCCTTATGATGTGCCAGACTATGCTAAAGCTAGC  
747▶ S Y P Y D V P D Y A G Y P Y D V P D Y A G Y P Y D V P D Y A •

2901 TGGCCAGACATGATAAGATACATTGATGAGTTTGGACAACCACTAGAAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTT

3001 TATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAACCAACAACAAATTGCATTCTTTATGTTTCAGGTTCCAGGGGAGGTGTGGGAGGTTTTTAAAG

3101 CAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGA

3201 TGAATAAGGCATAGGCATCAGGGGCTGTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTCTTTCATGGAGTTAAGATATAGTGATTTTTCCCAAG

3301 GTTTGAACCTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCA

3401 ATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTT

3501 AATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATT  
141◀ • N R T Y K L P I L E E I T T K V L K G N

3601 CATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCA  
120◀ 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 R D V E D

3701 GAGTAGGGGTGCCTGACAGCCAAATGGTGTCAAAGTCTTCTGCCCGTGTCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTACCCTGC  
86◀ 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 C V T V R G

3801 CAATGTAGCCTCAATGTGGACAGCAGATGATCTCCCAGTCTTGGTCTGTAGGCGCCCGACATGGTCTTGTGTCTCATAGAGCATGGTGAT  
53◀ 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 Y L M T I

3901 CTTCTCAGTGGGACCTCCACCAGTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGAT  
20◀ K E T A V E V L E L D Q Q S I N F T K M

4001 ATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCATAACGAGCTCTGCTTATATAGACCTCCACCCT

4101 ACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCATTGACGTCAA

4201 TGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATAC

4301 GTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTATGACTGGGCATAATGCCAGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTT

4401 GGCATATGATACACTTGTACTGCAAGTGGGCGAGTTTACCCTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAA

4501 CATACGTATTATTGACGTCAATGGGCGGGTCTGTTGGGCGTCCAGCAGCGGGCCATTTACCCTAAGTTATGTAACGCCTGAGGTTAATTAAGAAC  
PacI (4588) SdaI (4580) BspLU111

4601 ATGTGAGCAAAGGCCAGCAAAGGCCAGGAACGTAAGGCGCGTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATC

4701 GACGCTCAAGTCAGAGGTGGCAAACCCGACAGGACTATAAGATACCAGGCTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCC

4801 GCTTACCGGATACCTGTCCGCTTTCTCCCTCGGGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCC

4901 AAGCTGGGCTGTGTGCACGAACCCCGTTCAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGTAGTCAACCCGGTAAGACACGACTTATCGC

5001 CACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAG

5101 AACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGT

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5201 TTTTTTGTGGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGAACGAAAAC

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EagI (5348)

PacI (5328) SmaI (5337) NotI (5347)

5301 CACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTG

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5401 TGTGAATCGTAACATAACATACGCTCTCCATCAAACAAAACGAAACAAAACAAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACAT

5501 TTCTCTATCGAA