



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
**MfeI (82)**  
101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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**Psp1406I (203)** 201 GTGAACGTTCTTTTTTCGAACGGGTTTCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTCACGGCCCGCCCTACCTGAGGCC  
**HindIII (245)**  
**Bsu36I (291)**  
301 GCCATCCACGCCGGTTGAGTCGGTTCGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

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501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTATCATGAAGCTCTCCCCAGCCTTCATGTGTTAACCTGGG  
**AgeI (552)** **BspHI (560)** **HpaI (589)**  
601 GATGATGTGGACCTGGGCACTGTGGATGCTCCCITCACTCTGCAAAATTCAGCCTGGCAGCTCTGCCAGCTAAGCCTGAGAACATTTCCGTGTCTACTAC  
130 M M W T W A L W M L P S L C K F S L A A L P A K P E N I S C V Y Y  
701 TATAGGAAAAATTTAACCTGCACCTGGAGTCCAGGAAAGGAAACAGTTATACCCAGTACACAGTTAAGAGAATTACGCTTTTGGAGAAAAACATGATA  
470 Y R K N L T C T W S P G K E T S Y T Q Y T V K R T Y A F G E K H D

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**BsrGI (802)**  
801 ATTGTACAACCAATAGTCTACAAGTGAAAATCGTGCTTCGTGCTTTTTTCCCTTCCAAGAATAACGATCCCAGATAATTATACCATTGAGGTGGAAGC  
80 N C T T N S S T S E N R A S C S F F L P R I T I P D N Y T I E V E A  
901 TGAAAATGGAGTGGTGAATTAATTAATCTCATATGACATACTGGAGATTAGAGAACATAGCGAAAATGAACCACCTAAGATTTTCCGTGTGAAACAGTT  
113 E N G D G V I K S H M T Y W R L E N I A K T E P P K I F R V K P V  
1001 TTGGGCATCAAACGAATGATTCAAATGAATGGATAAAGCCTGAGTTGGCGCTGTTTCATCTGATTTAAAATACACACTTCGATTGAGGACAGTCAACA  
147 L G I K R M I Q I E W I K P E L A P V S S D L K Y T L R F R T V N

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**PstI (1171)**  
1101 GTACCAGCTGGATGGAAGTCAACTTCGCTAAGAACCCTAAGGATAAAAAACCAACCTGACACCTCACGGGCTGCAGCCTTTTACAGAATATGTCATAGC  
180 S T S W M E V N F A K N R K D K N Q T Y N L T G L Q P F T E Y V I A  
1201 TCTGCGATGTGCGGTCAAGGAGTCAAAGTTCTGGAGTACTGGAGCNAAGAAAAAATGGGAATGACTGAGGAAGAAGCTCCATGTGGCCTGGAACCTGTGG  
213 L R C A V K E S K F W S D W S Q E K M G M T E E E A P C G L E L W  
1301 AGAGTCTGAAACAGCTGAGGCGGATGGAAGAAGGCCAGTGCAGTTGTTATGGAAGAAGGCAAGAGGAGCCAGTCTAGAGAAAACACTTGCTACA  
247 R V L K P A E A D G R R P V R L L W K K A R G A P V L E K T L G Y  
1401 ACATATGTTACTATCCAGAAAGCAACTAACCTCACAGAAACAACTAACACTACTAACAGCAGCTTGAAGTGCATCTGGGAGGCGAGAGCTTTGGGT  
280 N I W Y Y P E S N T N L T E T M N T T N Q Q L E L H L G G E S F W V

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**Bsu36I (1545)**  
1501 GTCTATGATTTCTTATAATTCTCTTGGGAAGTCTCCAGTGGCCACCTGAGGATCCAGCTATTCAAGAAAAATCATTTCAGTGCATTGAGGTGCATGCAG  
313 S M I S Y N S L G K S P V A T L R I P A I Q E K S F Q C I E V M Q

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**XbaI (1647)** **BspEI (1680)**  
1601 GCCTGCGTTGCTGAGGACCAGCTAGTGGTGAAGTGGCAAAGCTCTGCTCTAGACGTGAACACTTGATGATTGAATGGTTTCCGGATGTGGACTCAGAGC  
347 A C V A E D Q L V V K W Q S S A L D V N T W M I E W F P D V D S E  
1701 CCACCACCTTTCTGGGAATCTGTGTCTCAGGCCAGAACTGGAGATCCAGCAAGATAAATTTAAACCTTTCTGGTGTCTATAACATCTCTGTGTATCC  
380 P T T L S W E S V S Q A T N W T I Q Q D K L K P F W C Y N I S V Y P  
1801 AATGTTGCATGACAAAGTTGGGAGCCATATCCATCCAGGCTTATGCCAAAGAAGGCTTCATCAGAAGTCTGAGACCAAGGTGGAGAACATTGGC  
413 M L H D K V G E P Y S I Q A Y A K E G V P S E G P E T K V E N I G

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**XcmI (1980)**  
1901 GTGAAGACGGTACGATCACATGAAAAGAGATCCCAAGAGTGAAGAAAAGGGTATCATCTGCAACTACACCATCTTTTACCAAGCTGAAGGTGAAAAAG  
447 V K T V T I T W K E I P K S E R K G I I C N Y T I F Y Q A E G G K  
2001 GATTCTCAAGACAGTCAATCCAGCATCTTGCAGTACGGCCTGGAGTCCCTGAAACGAAAGACCTTTACATTGTTGAGGTCATGGCCAACCACAGTGC  
480 G F S K T V N S S I L Q Y G L E S L K R K T S Y I V Q V M A N T S A

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**Tth11I (2133)**  
2101 TGGGGAAACCAACGGGACCAGCATAAATTTCAAGACATTGTCAATTCAGTGTCTTTGAGATTATCCTCATAACTTCTGATTGGTGGAGGCCCTTCTTATT  
513 G G T N G T S I N F K T L S F S V F E I I L I T S L I G G G L L I  
2201 CTCATTATCCTGACAGTGGCATATGGTCTCAAAAAACCAACAAATTGACTCATCTGTGTTGGCCACCGTTCCCAACCTGCTGAAAGTAGTATAGCCA  
547 L I I L T V A Y G L K K P N K L T H L C W P T V P N P A E S S I A

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**XcmI (2396)**  
2301 CATGGCATGGAGATGATTTCAAGGATAAGCTAAACCTGAAGGAGTCTGATGACTCTGTGAACACAGAAGACAGATCTTAAAAACCATGTTCCACCCAG  
580 T W H G D D F K D K L N L K E S D D S V N T E D R I L K P C S T P S  
2401 TGACAAGTTGGTATTGACAAGTTGGTGGTGAACCTTTGGGAATGTTCTGCAAGAAATTTTACAGATGAAGCCAGAACGGGTGAGAAAAACAATTTAGGA  
613 D K L V I D K L V V N F G N V L Q E I F T D E A R T G Q E N N L G  
2501 GGGAAAAAAGTGGTATGTGACCTGCCCTTACGGCCTGATTGTCCCCTGGGAAAAAGTTTGGAGAGTCCAGTTTACCTGAGATTCCGCCAGAA  
647 G E K N G Y V T C P F R P D C P L G K S F E E L P V S P E I P P R

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**SandI (2632)**  
2601 AATCCCAATACCTACGTTTCGAGGATGCCAGAGGGACCCGACCAAGCAAGAGCAGCTTCTCTTTCTGTTCAAAGTTTAGTACCAGATCATCTGTG  
680 K S Q Y L R S R M P E G T R P E A K E Q L L F S G Q S L V P D H L C  
2701 TGAGGAAGGAGCCCAATCCATATTTGAAAAATTCAGTGACAGCCAGGGAATTTCTGTGTCTGAAAAACTCCAGAGCACACCAAGGGAGAAGTCTAA  
713 E E G A P N P Y L K N S V T A R E F L V S E K L P E H T K G E V •

2801 ATGCGACCATAGCATGAGACCGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTA  
**NheI (2821)**

2901 TTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACCAAGTTAACAAACAACAATTGCATTCATTTTATGTTTCAGTTCA  
HpaI (2959) MfeI (2970)

3001 GGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCCAAATCAAG  
**EcoRI (3055)**

3101 CCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGA

3201 GTTTAAGATATAGTGATTTTTCCAAGGTTTGAAGTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTATGAAAAATTT  
**SapI (3237)** **SspI (3294)**

3301 CAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAG  
SwaI (3308)

3401 TTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTAGCTTTAGTTCTGGTGTACTTGAGGGGATGAGTTCTCT  
141 • N R T Y K L P I L E E

3501 AATGGTGGTTTTGACCAGCTTGCATTCATCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACC  
129 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 S V

3601 ACCCTGATGGATCTGCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAA  
95 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 I A I

3701 TGGCTTCAGCACAGACAGTGACCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTG  
62 A E A C V T V R G I Y A E I H V A S I E G T K T R I A A G V H H

3801 CTTGTTGCTCATAGAGCATGGTGTCTCTCAGTGGCGACTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCCTA  
29 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

3901 TAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGA  
**AseI (3941)**

4001 GCTCTGTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGCGGAGTTGTTACGACATTTTGAAAGTCCCCTTGATTTACTA  
**SpeI (4096)**

4101 GTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCAAAACCGCAT

4201 CATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCCATAAGGTCATGACTGGGCATAATGCCAGGCGGGCCATTTACCG  
**SnaBI (4224)**

4301 TCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGACTGCCAAGTGGGCGATTTACCGTAAATACTCCACCCATTGACGTCAATGGA

4401 AAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTACGCCAGGCGGGCCATTTACCGTAAGTTA

4501 TGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGTTGCTGGCGTTTTTCCATAGGCTCC  
PacI (4515) PstI (4508) SdaI (4507) BspLU11I (4525)

4601 GCCCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGTACCAGGCGTTTCCCCCTGGAAGCTCCCT

4701 CGTGCGCTCTCCTGTTCCGACCTGCCGTTACCGGATACCTGTCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTAT

4801 CTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCCGTTCCAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGT  
**ApaLI (4839)**

4901 CCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGATTCTTGAAGTG

5001 GTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGC

5101 AAACAAACCACCGCTGGTAGCGGTGGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTCTACGG

5201 GGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTT  
**EagI (5275)** Pacl (5255) SwaI (5264) NotI (5274)

5301 TCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCC

5401 CCAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA