



PvuI (7)  
SgfI (6) MfeI (82)  
1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCCGCAATTGAACGGGTGCCTA  
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGTGCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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Psp1406I (203)  
201 GTGAACGTTCTTTTTTCGAACGGGTTTCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACCGCCCGCCCTACCTGAGGCC  
301 GCCATCCACGCCGGTTGAGTCGGTTCGCGCCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

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BstEII (555)  
AgeI (552) NcoI (560)  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCATGGTCTGACGCTGCTTCTCCGCCACAACTGTG  
1 M V L T L L F S A Y K L C  
PvuI (636) RsrII (654) NcoI (682)  
601 CCGCTTCTACCATGTCCAGGCCACGGCCGGCGCCGATCGGCTGACAGTGCCTGGACCGGATCGGAGTGGTGGCGCCAGCCATGGTGGGCTGCGGGC  
13 R F F T M S G P R P G A D R L T V P G P D R S G G A S P W W A A G  
NruI (711)  
701 GGTGCGGGTCTCGCAAGTGTGCGCCGAGTGGGCACTGAGGIGCAAGGCGCCCTGGAGCGTTCGCTGCCTGAGCTGCAGCAGGCGCTGTCCGAGCTGA  
47 G R G S R E V S P G V G T E V Q G A L E R S L P E L Q Q A L S E L  
80 AACAGGCAAGCGCGCGGGCTGTGGCGCGGCTCTCGCCAGGCTTCCAGCTGGTAGAGGAAGCTGGTGTCCGCGCGTGGCCGAGGTTGGC  
80 K Q A S A A R A V G A G L A E V F Q L V E E A W L L P A V G R E V A  
90 CCAAGGTCTATGCGATGTATACGTCTGGACGGTGGCCTCGACTTGTGTTGCGGCTGCTCAGGCACCGGAGCTAGAGACCCGTGTGACGGCCGCGCGC  
113 Q G L C D A I R L D G G L D L L R L L Q A P E L E T R V Q A A R  
1001 TTGCTGGAGCAGATCCTGGTGGCTGAGAACCGGACCGTGGCGCGCATCGTCTAGGCGTATCTTGAACCTGGCAAGGAGCGCGAGCCTGTGGAAC  
147 L L E Q I L V A E N R D R V A R I G L G V I L N L A K E R E P V E  
BspLU11I (1130) StuI (1179)  
1101 TGGCAGCAAGCGTGGCGGCATCTTGGAGCACATGTTCAAGCACTCGGAGGAGACGTGCCAGCGGCTGGTGGCGCCGAGGCTCGACGCGGTGCTGTA  
180 L A R S V A G I L E H M F K H S E E T C Q R L V A A G G L V A G L D A V L Y  
1201 CTGGTGCCCGCACAGACCCGGCGCTGCTGCGCCACTGCGCTTTCGCTGGCGAAGTGCAGCGTGCACGGGGCCAGACGGTGCAGCGGTGCATGGTG  
213 W C R R T D P A L L R H C A L A L A N C A L H G G Q T V Q R C M V  
1301 GAGAAGCGCGCCCGAGTGGCTTCCCGCTCGCTTCTCCAAGGAGGACGAGCTGTGCGGCTGCACGCGCTGCCTGGCGGTGGCGGTGTTGGCTACCA  
247 E K R A A E W L F P L A F S K E D E L L R L H A C L A V A V L A T  
1401 ACAAGGAGGTGGAACGCGAGGTCGAGCATTCTGGCACATTGGCGCTTGTGAGCCGCTCGTGGCATCGCTGGACCCCGGCGCTTCCGCCGCTGCCTGGT  
280 N K E V E R E V E H S G T L A L V E P L V A S L D P G R F A R C L L V  
1501 GGATGCCAGTGACACAAGCCAGGTCGTGGACCAGACCTGCAGAGCCTGGTGTGCTCGATTCGTCGCGTGGAGGCTCAGTGCATAGGAGCA  
313 D A S D T S Q G R G P D D L Q S L V L L L D S S R L E A Q C I G A  
BstAPI (1612)  
FspI (1609)  
1601 TTCTACCTGTGCGCAGAGGCTGCCATCAAGAGCCTACAGGAAAGACCAAGGTGTTACGCGACATCGGCGCTATCCAGAGCCTGAAACGCTGGTTTCTT  
347 F Y L C A E A A I K S L Q G K T K V F S D I G A I Q S L K R L V S  
1701 ACTCTACGAATGGCACCACGTCGGCGCTGGCCAAGCGCGCTGCGCTATTGGCGAGGAGGTGCCAAGCGCATCCTGCCCTGCGTGGCCAGCTGGAA  
380 Y S T N G T T S A L A K R A L R L L G E E V P R R I L P C V A S W K  
ScaI (1844) BstEII (1879)  
1801 GGAAGCTGAGGTCAGACCTGGTACAGCAGATCGGCTTCTCCAGTACTGCGAGAATTTCCGGAGCAGCAGGTAGATGGTGACCTGCTTCTAAGACTC  
413 E A E V Q T W L Q Q I G F S Q Y C E N F R E Q Q V D G D L L L R L  
AvrII (1923)  
1901 ACAGATGAAGAACTCCAGACAGACCTAGGCATGAAATCAAGCATCACCCGCAAGAGGTTCTTTAGGGAGCTCACAGAGCTCAAGACCTTCGCCAGCTACG  
447 T D E E L Q T D L G M K S S I T R K R F F R E L T E L K T F A S Y  
BamHI (2043)  
2001 CTACTTGCACCCGAGCAACCTAGCGGACTGGCTGGGAGCCTGGATCCTCGCTTCCGCCAGTACACCTATGGCTGGTCACTGCGGTGTTGGACCGCTC  
480 A T C D R S N L A D W L G S L D P R F R Q Y T Y G L V S C G L D R S  
DraIII (2107)  
2101 CCTGCTGCACCGCTGTGAGCAGCAGCTCCTGGAGGACTGTGGCATCCGCTGGGAGTGCACCGCACGCGCATCCTCTGACGCCAGAGgtcacttt  
513 L L H R V S E Q Q L L E D C G I R L G V H R T R I L S A A R G H F  
Tth111I (2228)  
2201 gccagactggcctgagaagcttgaggagaccaagtctccacgatgatggaccccgatagaagcagtggggaagaccacccctcacctccatgtctcttt  
547 A Q T G L R S L R R P S L H D D G P R D K Q W G R A T L T S M S L  
SandI (2398)  
EcoO109I  
2301 ccttggctccagAAATGCTACATCCCCGCTGCCTGTACTGGAGGCAAGCTCAGTGGGGACACCCAGATGTCTTTATCAGTTACCGGAGGAACTCAGG  
580 S L A P E M L H S P L P C T G G K L S G D T P D V F I S Y R R N S G  
2401 GTCCAGCTGGCCAGCCTCCTGAAGGTGCACCTGCAGCTTACGGCTTCCAGGCTTCCATCGACGTGGAGAAGCTGGAAGCCGCAAAATTCGAGGACAAG  
613 S Q L A S L L K V H L Q L H G F S V F I D V E K L E A G K F E D K

**SphI (2567)**

2501 CTTATCCAAAGCGTCATAGCGGCTCGCAATTTTGTCTGGTGTGTCTGCTGGGGCGCTGGATAAGTGCATGCAGGACCATGACTGCAAGGACTGGGTGC  
647▶ L I Q S V I A A R N F V L V L S A G A L D K C M Q D H D C K D W V  
2601 ACAAGGAGATTGTGACTGCTTTAAGCTGTGGCAAGAACATTGTGCCATCATTGATGGCTTTGAGTGGCCTGAGCCTCAGGCGCTGCCTGAGGATATGCA  
680▶ H K E I V T A L S C G K N I V P I I D G F E W P E P Q A L P E D M Q  
2701 GGCTGTACTCACCTTCAACGGCATCAAATGGTCCCATGAGTACCAGGAGGCCACCATCGAGAAGATCATCCGCTTCCCTACAGGGCCGCCCTCTCAGGAC  
713▶ A V L T F N G I K W S H E Y Q E A T I E K I I R F L Q G R P S Q D

**NheI (2875)**

2801 TCCTCTGCCGGATCGGATACCAGTTTGGAGGGAGCTACGCCAATGGGTCTGCCTAACCTGTCCCCAGTTCCTCGTCTAGTGGCCAGACATGATAAGAT  
747▶ S S A G S D T S L E G A T P M G L P •

2901 ACATTGATGAGTTTGGACAAACCACAACCTAGAAATGCAGTGAACAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATATAAG

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**HpaI (3013) MfeI (3024)**

3001 CTGCAATAAAACAAGTTAAACAACAACAATTGCATTTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTTAAAGCAAGTAAACCTCTACAAA

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**EcoRI (3109)**

3101 TGTGGTATGGAATTCTAAAATACAGCATAGCAAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATC  
3201 AGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCAAGGTTTGAAGTACTGCTTTCAT

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**SspI (3348) SmaI (3362)**

3301 TTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTT

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**EcoO109I (3423)**

3401 ATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAA  
3501 GAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAG  
141▶ • N R T Y K L P I L E E I T T K V L K G N M E I L V F  
3601 CAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAG  
113▶ 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 H R V A

**StuI (3787)**

3701 CCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAAATGGCAATGGCTTTCAGCACAGACAGTACCCTGCCAATGTAGGCCCTCAATGTG  
80▶ 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 A E I H  
3801 GACAGCAGAGATGATCTCCCGTCTTGGTCTGATGGCCGCCGACATGGTCTTGTCTCATAGAGCATGGTATCTTCTCAGTGGCAGCTCC  
47▶ 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 A V E

**XmnI (3929) AseI (3995)**

3901 ACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCTATAGTGAATGCTATTATACTATGCCGATATACTATGCCGATGATTA  
13▶ V L E L D Q Q S I N F T K M  
4001 TTGTCAAACAGCGTGGATGGCTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCTACCGCCATT

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**SpeI (4150)**

4101 GCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATGACGTCAATGGGGTGAGACTTGGAAA

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**SnaBI (4278)**

4201 TCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTA

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**NdeI (4383)**

4301 GGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCATTACCCTGATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGT  
4401 GTACTGCCAAGTGGGCGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGT

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**PacI (4569)**

**SdaI (4561) BspLU11I (4579)**

4501 CAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTACCCTAAGTTATGTAACGCTGCGAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGC  
4601 AAAAGGCCAGGAACCGTAAAAAGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTG  
4701 GCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCC  
4801 GCCTTTCTCCCTCGGGAAGCGTGGCGCTTTCATAGCTCACGCTGTAGGTATCTAGTTCCGTTGAGTTCGTTCCGCTCCAAGCTGGGCTGTGTGCAG  
4901 AACCCCCGTTACGCCCAGCGCTGCGCCTTATCCGGTAACTATCGTCTTGTGTTGAGTCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGG  
5001 TAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGC  
5101 GCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGTATCCGGCAACAAACCACCGCTGGTAGCGGTGTTTTTTGTTTGAAGCAGC  
5201 AGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGCTGACGCTCAGTGAACGAAAACTCACGTTAAGGGATTTTGGT

PacI (5309) SmaI (5318) **NotI (5328)**

5301 CATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTGTGTGAATCGTAACTAACAT

5401 ACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCGAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA