



**PvuI (7)**  
**SgfI (6)**
**MfeI (82)** **EcoNI (96)**

1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
 101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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**Psp1406I (203)**
**Bsu36I (291)**

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACAGCGCCCGCCGCTACCTGAGGCC  
 301 GCCATCCACGCGGTTGAGTGCAGTCTGCCGCTCCCGCCTGTGGTGCCTCTGAACTGCGTCCGCGCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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**NgoMIV (441)**
**NaeI (441)**

401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGTCTTTGTTTCGTTT

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**KasI (535)**
**AgeI (552)**

501 TCTGTTCTGGCGGTTACAGATCCAAGCTGTGACCGCGGCTACCTGAGATCACCGGTCAACATGTGCCTCTCTCCGGTTAAAGGCGCAAAGCTCATCCT  
1▶ M C L S P V K G A K L I L

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**AvrII (612)**
**Ppu10I (632)**
**NsiI (632)**

601 GATCTTTCTGTTCTAGGAGCGGTTAGTCCAATGCATTGATAGTAAATTTGACAGATTCAAAGGTAAGTTCCTTTATGCGAATGGGAGATGAATTT  
13▶ I F L F L G A V Q S N A L I V N L T D S K G T C L Y A E W E M N F

**NdeI (707)**

701 ACAATAACATATGAAACTACAAACCAAACAAATAAACTATAACATTGCAGTACCTGACAAGGCGACACACGATGGAAGCAGTTGTGGGATGACCGGA  
47▶ T I T Y E T T N Q T N K T I T I A V P D K A T H D G S S C G D D R

**BspHI (882)**

801 ATAGTGCCAAAATAATGATACAATTTGGATTTCGTCTCTTTGGGCTGTGAATTTTACCAAGGAAGCATCTCATTATTCAATTCATGACATCGTGCTTTC  
80▶ N S A K I M I Q F G F A V S W A V N F T K E A S H Y S I H D I V L S

**SpeI (907)**

901 CTACAACACTAGTGATAGCACAGTATTTCTGGTGTGTAGCTAAAGGAGTTCATACTGTTAAAAATCCTGAGAATTTCAAAGTTCATTGGATGTCATC  
113▶ Y N T S D S T V F P G A V A K G V H T V K N P E N F K V P L D V I

**PshAI (1032)**
**SspI (1049)**
**HindIII (1070)**

1001 TTTAAGTGAATAGTGTTTTAACTTACAACCTGACTCTGTGTTTCAGAAATATTGGGTATTACCTGCAAGCTTTTGTCCAAAATGGTACAGTGAGTA  
147▶ F K C N S V L T Y N L T P V V Q K Y W G I H L Q A F V Q N G T V S

**SalI (1170)**

1101 AAAATGAACAAGTGTGTGAAGAAGACAAAACCTCCACCCTGTGGCACCCATCATTACACCCTGCCCCGTCGACTACAACCTACTCACTCAACTTC  
180▶ K N E Q V C E E D Q T P T T V A P I I H T T A P S T T T T L T P T S

**NcoI (1283)**

1201 AACACCCACTCCAACCTCCAACCTCCAACCTCCAACCGTTGGAAACTACAGCATTAGAAATGGCAATACTACTGTCTGCTGGCTACCATGGGGCTGCAGCTG  
213▶ T P T P T P T P T P T V G N Y S I R N G N T T C L L A T M G L Q L

1301 AACATCACTGAGGAGAAGGTGCCTTTTCAATTTTAAACATCAACCTGCCACAACCAACTTCACCGGCAGCTGTCAACCTCAAAGTGTCAAATAGGCTGA  
247▶ N I T E E K V P F I F N I N P A T T N F T G S C Q A F Q S A Q L R L

1401 ACAACAGCCAAATTAAGTATCTTGACTTTATCTTTGCTGTGAAAAATGAAAAACGGTTCATCTGAAGGAAGTGAATGTACATGTATTTGGCTAATGG  
280▶ N N S Q I K Y L D F I F A V K N E K R F Y L K E V N V Y M Y L A N G

**XbaI (1594)**

1501 CTCAGCTTTCAACATTTCCAACAAGAACCTTAGCTTCTGGGATGCCCTCTGGGAAGTCTTATATGTGCAACAAGAGCAGGTGCTTCTGTGTCTAGA  
313▶ S A F A N I S N K N L S F W D A P L G S S Y M C N K E Q V L S V S R

1601 GCGTTTCAGATCAACACCTTTAACTTAAAGGTGCAACCTTTTAAATGTGACAAAAGGACAGTATTCTACAGCTCAAGACTGCAGTGCAGATGAAGACAAC  
347▶ A F Q I N T F N L K V Q P F N V T K G Q Y S T A Q D C S A D E D N

**ScaI (1737)**

1701 TCCTTGTCATAGCGGTGGGAGCAGCTCTGGGAGGAGTACTTATTCTAGTGTGCTGGCTTATTTTATTGGTCTCAAGCGCCATCATACTGGATATGA  
380▶ F L V P I A V G A A L G G V L I L V L L A Y F I G L K R H H T G Y E

**MscI (1824)**

**NheI (1818)**

1801 GCAATTTAGTAAGTGCAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTT  
413▶ Q F •

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**HpaI (1956)**
**MfeI (1967)**

1901 GTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCAATTTATGTTTCAGGTTTCAGGG

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**EcoRI (2052)**

2001 GGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAAATCTAAAATACAGCATAGCAAACCTTTAACCTCCAATCAAGCCT  
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2101 CTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGAGCCTCACCTTCTTTCATGGAGTT

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**SspI (2291)**

2201 TAAGATATAGTGTATTTTCCAAGGTTTGAAGTCTCTTCAATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTATGTAATAATATTACAG

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**SwaI (2305)**
**EcoO109I (2366)**

2301 AAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTG

2401 GACTTAGGGAACAAGGAACCTTTAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAAT  
141▶ • N R T Y K L P I L E E I

2501 GGTGGTTTTGACCAGTTGCCATTTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACC  
128 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 V  
2601 CTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCCGTTGCTCACAGCAGACCCAATGGCAATGG  
94 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 A

**SacI (2566)**

2701 CTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGCTT  
61 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 H H K

**StuI (2730)**

2801 GTTGTCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTTCATGATGGCCCTCCTATAG  
28 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

**XmnI (2872)**

**BspHI (2880)**

2901 TGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCT  
A A C A G C G T G G A T G G C G T C C C A G C T T A T C T G A C G G T T C A C T A A A C G A G C T

**AseI (2938)**

**SacI (2995)**

3001 CTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAAGTCCCGTTGATTTACTAGT  
C T G C T T A T A T A G A C C T C C C A C G T A C A C G C C T A C C G C C A T T T G C G T C A A T G G G G C G G A G T T G T T A C G A C A T T T T G A A A G T C C C G T T G A T T T A C T A G T

**SpeI (3093)**

3100 CAAAAAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCA  
C A A A A A A A C T C C A T T G A C G T C A A T G G G G T G G A G A C T T G A A A T C C C G T G A G T C A A A C C G C T A T C C A C G C C A T T G A T G T A C T G C C A A A A C C G C A T C A

**SnaBI (3221)**

3200 TCATGGTAATAGCGATGACTAATACGTAGATGTAAGTCCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTC  
T C A T G G T A A T A G C G A T G A C T A A T A C G T A G A T G T A C T G C C A A G T A G G A A A G T C C C A T A A G G T C A T G T A C T G G G C A T A A T G C C A G G C G G G C C A T T T A C C G T C

**NdeI (3326)**

3300 ATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATGGAAA  
A T T G A C G T C A A T A G G G G G C T A C T T G G C A T A T G A T A C A C T T G A T G T A C T G C C A A G T G G C A G T T T A C C G T A A A T A C T C C A C C C A T T G A C G T C A A T G G A A A

3400 GTCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGCTGTTGGGCGGTACAGCCAGGCGGGCCATTTACCCTAAGTTATG  
G T C C T A T T G G C G T T A C T A T G G G A A C A T A C G T C A T T A T T G A C G T C A A T G G G C G G G G C T G T T G G G C G G T C A G C C A G G C G G G C C A T T T A C C G T A A G T T A T G

**SdaI (3504)** **PacI (3512)**

3500 TAACGCCCTGCAGGTTAA TTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCC  
T A A C G C C T G C A G G T T A A T T A A G A A C A T G T G A G C A A A G G C C A G C A A A G G C C A G G A A C C G T A A A A A G G C C G G T T G C T G G C G T T T T T C C A T A G G C T C C

3598 GCCCCCTGACGAGCATCAGAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTTGGAAGCTCCCT  
G C C C C C T G A C G A G C A T C A G A A A A T C G A C G C T C A A G T C A G A G G T G G C G A A A C C C G A C A G G A C T A T A A A G A T A C C A G G C G T T T C C C C T G G A A G C T C C C T

3698 CGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTTCCCTTCGGGAAGCGTGGCGCTTTTTCATAGCTCACGCTGTAGGTAT  
C G T G C G C T C T C C T G T T C C G A C C C T G C C G C T T A C C G G A T A C C T G T C C G C T T T T C C C T T C G G G A A G C G T G G C G C T T T T C A T A G C T C A C G C T G T A G G T A T

**ApaLI (3836)**

3798 CTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACAGCCGACCGCTGCGCCTTATCCGTAACATATCGTCTTGTAGT  
C T C A G T T C G G T G T A G G T C G T T C C G C T C C A A G C T G G G C T G T G T G C A C G A A C C C C C G T T A C A G C C C G A C C G C T G C G C C T T A T C C G T A A C A T A T C G T C T T G A G T

3898 CCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTG  
C C A A C C C G G T A A G A C A C G A C T T A T C G C C A C T G G C A G C A G C C A C T G G T A A C A G G A T T A G C A G A G C G A G G T A T G T A G G C G G T G C T A C A G A G T T C T T G A A G T G

3998 GTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGC  
G T G G C C T A A C T A C G G C T A C A C T A G A A G A A C A G T A T T T G G T A T C T G C G C T C T G C T G A A G C C A G T T A C C T T C G A A A A A G A G T T G G T A G C T C T T G A T C C G G C

4098 AAACAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGG  
A A A C A A C C A C C G C T G G T A G C G G T G T T T T T T T G T T T G A A G C A G C A G A T T A C G C G C A G A A A A A A G G A T C T C A A G A A G A T C C T T T G A T C T T T T C T A C G G

**EagI (4272)**

**PacI (4252)** **SwaI (4261)** **NotI (4271)**

4198 GGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCCAATAAAAATATCTTTATTT  
G G T C T G A C G C T C A G T G A A C G A A A A C C T C A C G T T A A G G G A T T T T G G T C A T G G C T A G T T A A T T A A C A T T T A A A T C A G C G G C C A A T A A A A T A T C T T T A T T T

4298 TCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCC  
C C A G T G C A A G T G C A G G T G C C A G A A C A T T T C T A T C G A A

4398