



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA **MfeI (82)**

101 GAGAAAGTGGCGGGGTAACGGAAAGTGATGCTGTACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

**Psp1406I (203)** **HindIII (245)** **Bsu36I (291)**  
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACGCGCCCGCCCTACCTGAGGCC

301 GCCATCCACGCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCGCTAGGTAAGTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

**NcoI (560)**  
**BstEII (555)**  
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCGCTACCTGAGATCACCGGTACCATTGGCCCAACCTGTGGTCTATCTGGGGCTCCTGGC **1▶ M A A N L W L I L G L L A**

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

601 ATCCCACTCTTCAGATCTGGCTGCGGTCCGTGAGGCTCCACCCACTGCTGTGACCACGCCATCCAGAACCCTGCATATCGACCCCGCCACTACACACTG **13▶ S H S S D L A A V R E A P P T A V T T P I Q N L H I D P A H Y T L**

**BglII (612)** **RsrII (623)**

701 AGCTGGGACCCCGCCCGGGCGCTGACATCACGACAGGGGCTTTTGCAGGAAGGGCAGGGACATCTTGTCTGGGCTGACCCCGGGCTTGCCCGCTGCT **47▶ S W D P A P G A D I T T G A F C R K G R D I F V W A D P G L A R C**

**SmaI (704)** **XmaI (781)**

801 CATTCCAGTCGCTCTCCCTCTGCCATGTGACCAACTTACCCTCTTCTGGGGAAGGACAGGGCTGTGGCAGGATCCATCCAGTTCCCCCGAGATGATGG **80▶ S F Q S L S L C H V T N F T V F L G K D R A V A G S I Q F P P D D G**

**BamHI (871)** **BsrBI (970)** **ApaLI (997)**

901 TGGCGACCACGAGCCGACGCCAGCCAGGACCTGCGCTGCTGGGTGCATGAGGGGAGCTGAGCTGCAATGGGAGCGGGTCCGAAAGCAACGGGTGACGTG **113▶ G D H E A A A Q D L R C W V H E G Q L S C Q W E R G P K A T G D V**

1001 CACTACCGGATGTTCTGGCGTGATGTGCGGCTCGGTCTGCCACAACCGGAGTGTCCACACTACCACAGCCTTGATGTCAACACCGCTGGCCCGGCC **147▶ H Y R M F W R D V R L G P A H N R E C P H Y H S L D V N T A G P A**

**MscI (1107)** **Tth111I (1135)** **Tth111I (1168)** **BstEII (1182)**

1101 CTCATGGTGGCCATGAAGCTGCACCCTGACCTCGACACTGTCTGGCTCCACCCCAACAGCCTGTGACCTTGTCCCCAGGTCCACCATCACCGTCAA **180▶ P H G G H E G C T L D L D T V L G S T P N S P D L V P Q V T I T V N**

**SfiI (1207)** **BssHIII (1254)** **XcmI (1277)**

1201 CGGCAGTGGCCGCTGGCCCGTGCCTGCATGGACAACACTGTGGACCTGCAGCGCGCAGAGGTCTGGCCCGCCACGTTGACAGTGGAGTGCAAC **213▶ G S G R A G P V P C M D N T V D L Q R A E V L A P P T L T V E C N**

**XcmI (1344)** **XmnI (1332)** **NcoI (1344)** **SdaI (1365)** **BsrBI (1386)**

1301 GGCTCTGAGGCCATGCCCGATGGGTCGCGCGGAACAGATTCCACCATGGCCTCCTTGGGTACACCCTGCAGGTCAACCAGAGCTCCCGCTCAGAGCCAC **247▶ G S E A H A R W V A R N R F H H G L L G Y T L Q V N Q S S R S E P**

**SmaI (1430)** **SgrAI (1440)**

1401 AGGAATACAATGTCTCCATCCCCACTTCTGGGTCCCCAACGCCGGTGCATCTCCTTCCGGGTCAAGTGCAGGTGAGGTTTACCCTCGGAAGCTCAG **280▶ Q E Y N V S I P H F W V P N A G A I S F R V K S R S E V Y P R K L S**

1501 CAGCTGGAGCGAAGCCTGGGCTCGTCTGCCCGCAGAGGTGATGCCTGTGAAGACAGCCTTGGTGACTTCACTGAGTGGTACGGTGTGGGGCAGGGCTC **313▶ S W S E A W G L V C P P E V M P K T A L V T S V A T V L G A G L**

1601 GTGGCAGCTGGGCTCCTGCTGTGGTGGAGGAAGTGCCTGCTTACCCTGTGCCACCCATTCCAGCCTGCGCCTGCCCTTGGCAGGGGAGATGGTCG **347▶ V A A G L L L W W R K S L L Y R L C P P I P R L R L P L A G E M V**

**MscI (1768)** **NheI (1762)**

1701 TGTGGAAACCAGCTCTTGAAGACTGCGAGGTGACGCTGTGACAGACGCTGAGAAGTGTGTCTAGCTGGCCAGACATGATAAGATACATTGATGAGTT **380▶ V W E P A L E D C E V T P V T D A •**

1801 TGGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAA

**HpaI (1900)** **MfeI (1911)** **EcoRI (1996)**

1901 GTTAACAACAACAATTGCATTCTTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAAT

2001 TCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCC

2101 AATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGTTTGAAGTACTAGCTCTTCATTTCTTTATGTTTT

**SspI (2235)** **SwaI (2249)**

2201 AAATGCACCTGACCTCCACATTCCTTTTTAGTAAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTATTAGGCAGAATC

2301 CAGATGCTCAAGGCCCTTATAATATCCCCAGTTTGTAGTGGACTTAGGGAACAAAGAACCTTTAATAGAAATGGACAGCAAGAAAGCGAGCTTC

2401 TAGCTTTAGTTCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAAGCAGTCAGGAGCAT **441▶ • 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 C D P A Y**

**BstXI (2539)**

2501 AGTCAGAGATGAGCTCTGACATGCCACAGGGGCTGACCCCTGATGGATGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTG **109▶ 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 V I T D**

2601 AAAGTCCTTCTGCCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCCTCAATGTGGACAGCAGAGATG  
76 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 V A S I  
2701 ATCTCCCAGTCTTGGTCCTGATGGCCGCCCGACATGGTGCTTGTTCCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGAT  
42 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 V L E L D

**StuI (2674)**

**BspHI (2824)**

XmnI (2816) AseI (2882)

2801 CCTGCTGAGAGATGTTGAAGGTCTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGC  
9 Q Q S I N F T K M  
2901 GTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGG

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**SpeI (3037)**

3000 CGGAGTTGTTACGACATTTTGAAAAGTCCCCTGATTACTAGTCAAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAAATCCCCTGAGT

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**SnaBI (3165)**

3099 CAAACCGCTATCCACGCCATTGATGTAAGTCCGATCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTCCGAAAGTCCCA

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**NdeI (3270)**

3199 TAAGGTCATGTAAGTCCGATCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTCCGAAAGTCCCA

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3299 TGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGG

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SdaI (3448) PacI (3456) **BspLU11I (3466)**

3399 GGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAAGTATGTAACGCCTGCAGGTTAA TTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCA  
3497 GGAACCGTAAAAAGGCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAGCAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCC  
3597 GACAGGACTATAAAGATACAGGCGTTTTCCCTGGAAGCTCCCTCGTGCGCTCTCTGTTCCGACCTGCGGCTTACCGGATACCTGTCCGCTTTTCTC

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**ApaLI (3780)**

3697 CCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCGG  
3797 TTCAGCCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGTAGTCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGAT  
3897 TAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTG  
3997 AAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGTATCCGGCAAAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGC  
4097 GCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACACTCACGTTAAGGGATTTTGGTCATGGCTAG

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**EagI (4216)**  
PacI (4196) SwaI (4205) **NotI (4215)**

4197 TTAATTAACATTTAAATC AGCGGCCGCAATAAAAATATCTTTATTTTTCATTACATCTGTGTGTTGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCC  
4297 ATCAAAAACAAAACGAAAACAAAACAAACTAGCAAAATAGGCTGTCCCGAGTCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA