



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

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**Psp1406I (203)** 201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACGCGCCCGCCGCTACCTGAGGCC **HindIII (245)** **Bsu36I (291)**  
301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCGCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT **NgoMIV (441)**

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501 TCTGTTCTGCGCGCTTACAGATCCAAGCTGTGACCGCGCGCTACCTGAGATCACCGGTACCATTGGCCCAACCTGTGGTCTATCTGGGGCTCCTGGC **NcoI (560)**  
**BstEII (555)** 1▶ M A A N L W L I L G L L A  
**KasI (535)** **AgeI (552)**

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601 ATCCCACTCTTCAGATCTGGCTGCGGTCCGTGAGGCTCCACCCACTGCTGTGACCACGCCATCCAGAACCCTGCATATCGACCCCGCCACTACACACTG **BglII (612)** **RsrII (623)**  
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  
**SmaI (704)** 701 AGCTGGGACCCCGCCCGGGCGCTGACATCACGACAGGGGCTTTTGCAGGAAGGGCAGGGACATCTTGTCTGGGCTGACCCCGGGCTTGCCCGCTGCT **XmaI (781)**  
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  
**BamHI (871)** 801 CATTCCAGTCGCTCTCCCTCTGCCATGTGACCAACTTCACCGTCTTCTGGGGAAGGACAGGGCTGTGGCAGGATCCATCCAGTTCACCCAGATGATGG **BsrBI (970)** **ApaLI (997)**  
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  
901 TGGCGACCACGAGCCGACGCCAGCCAGGACCTGCGCTGCTGGGTGCATGAGGGGAGCTGAGCTGCAATGGGAGCGGGTCCGAAAGCAACGGGTGACGTG **BstEII (1182)**  
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 **Tth11II (1168)**  
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  
1101 CTCATGGTGGCCATGAAGCTGCACCCTTGACCTCGACACTGTCTGGCTCCACCCCAACAGCCCTGACCTTGCCCCAGGTCCACCATCACCGTCAA **Tth11II (1168)** **BstEII (1182)**  
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)** 1201 CGGCAGTGGCCGCTGGCCCGTGCCTGCATGGACAACACTGTGGACCTGCAGCGCGCAGAGGTCTGGCCCGCCACGTTGACAGTGGAGTGCAAC **BssHIII (1254)** **XcmI (1277)**  
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)** 1301 GGCTCTGAGGCCATGCCCGATGGGTCGCGCGGAACAGATTCCACCATGGCCTCCTTGGGTACACCCTGCAGGTCAACCAGAGCTCCCGCTCAGAGCCAC **XmnI (1332)** **NcoI (1344)** **SdaI (1365)** **BsrBI (1386)**  
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 AGGAATACAATGTCTCCATCCCCACTTCTGGGTCACCAACGCCGGTGCATCTCCTTCCGGGTCAAGTGCAGGTGAGAGTTTACCCTCGGAAGCTCAG **XcmI (1344)**  
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 **SgrAI (1440)**  
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 GTGGCAGCTGGGCTCCTGCTGTGGTGGAGGAAGTGCCTGCTACCAGCTGTGCCACCACTTCCACGCTGCGCCTGCCCTTGGCAGGGGAGATGGTCG **MscI (1768)**  
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  
**NheI (1762)** 1701 TGTGGAAACCAGCTCTTGAAGACTGCGAGGTGACGCTGTGACAGACGCTGAGAAGTGTGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTT **MscI (1768)**  
380▶ V W E P A L E D C E V T P V T D A •  
1801 TGGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAA

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**HpaI (1900)** **MfeI (1911)** 1901 GTTAACAACAACAATTGCATTCTTTTATGTTTCAGGTTCAAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAAT **EcoRI (1996)**  
2001 TCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCC  
2101 AATGTGCATTAGCTGTTGACGCTCACCTTCTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGTTTGAAGTACTAGCTCTTCATTTCTTTATGTTTT

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2201 AAATGCACCTGACCTCCACATTCCTTTTTAGTAAAATATTGAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATC **SspI (2235)** **SwaI (2249)**  
2301 CAGATGCTCAAGGCCCTTATAATATCCCCAGTTAGTAGTTGACTTAGGGAACAAAGAACCTTTAATAGAAATGGACAGCAAGAAAGCGAGCTTC  
2401 TAGCTTTAGTTCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTATCTCAATGAGCACAAAGCAGTCAGGAGCAT  
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 C D P A Y  
**BstXI (2539)** 2501 AGTCAGAGATGAGCTCTGACATGCCACAGGGGCTGACCACTGATGGATGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTG  
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 CGGAGTTGTTACGACATTTTGAAAGTCCCCTGATTACTAGTCAAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCTGAGT

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**SnaBI (3165)**

3099 CAAACCGCTATCCACGCCATTGATGACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCCA

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**NdeI (3270)**

3199 TAAGGTCATGACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGACTGCCAAG  
3299 TGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGG

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

3399 GGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAACGCCTGCAGGTTAA TTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCA  
3497 GGAACCGTAAAAAGCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAGAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCC  
3597 GACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCTGTTCCGACCTGCGGCTTACCGGATACCTGTCCGCTTTTCTC

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**ApaLI (3780)**

3697 CCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCGG  
3797 TTCAGCCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGTAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGAT  
3897 TAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTG  
3997 AAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGTATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGC  
4097 GCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGGCTAG

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

4197 TTAATTAACATTTAAATC AGCGGCCGCAATAAAAATATCTTTATTTTTCATTACATCTGTGTGTTGTTTTTTTGTGTGAATCGTAACTAACATACGCTCTCC  
4297 ATCAAAAACAAAACGAAACAAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAAGTGCCAGAACATTTCTCTATCGAA