



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA **MfeI (82)**  
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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**HindIII (245)**  
**Psp1406I (203)** 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACACGCCGCCGCCCTACCTGAGGCC **PvuII (239)** **Bsu36I (291)**  
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

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**NcoI (560)**  
**BstEII (555)**  
**AgeI (552)** 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTCCACATGGACCTGGGAAACCAATGAAAAGCGTGCTGGTGGT  
601 GGCTCTCCTGTGCAATTTCCAGGTATGCCTGTGTCAAGATGAGGTCACGGACGATTACATCGGAGACAACACCACAGTGGACTACCTTTGTTCCGATCT  
130▶ A L L V I F Q V C L C Q D E V T D D Y I G D N T T V D Y T L F E S  
701 TTGTGCTCAAGAAGGACGTGCGGAACTTAAAGCCTGGTTCCTCCCTATCATGACTCCATCATTTGTTTCGTTGGCCCTACTGGCAATGGGCTGGTGC  
47▶ L C S K K D V R N F K A W F L P I M Y S I I C F V G L L G N G L V  
801 TGTTGACCTATATCTATTTCAAGAGGCTCAAGACCATGACCGATACCTACCTGCTCAACCTGGCGGTGGCAGACATCCTCTTCTCTGACCTTCCCTT  
80▶ V L T Y I Y F K R L K T M T D T Y L L N L A V A D I L F L L T L P F

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**SphI (989)**  
901 CTGGCCTACAGCGCGCAAGTCTGGGTCTTCGGTGTCCACTTTTGAAGCTCATCTTTGCCATCTACAAGATGAGCTTCTTCAAGTGGCATGCTCCTA  
113▶ W A Y S A A K S W V F G V H F C K L I F A I Y K M S F F S G M L L  
1001 CTTCTTTGCATCAGCATTGACCGCTACGTGGCCATCGTCCAGGCTGTCTCAGCTACCCGCCACCGTGGCCCGCTCTTCTCATCAGCAAGCTGCTCTGTG  
147▶ L L C I S I D R Y V A I V Q A V S A H R H R A R V L L I S K L S C

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**BsrGI (1145)** 1101 TGGGCATCTGGATACTAGCCACAGTGTCTCCATCCCAGAGCTCCTGTACAGTACCTCCAGAGGAGCAGCAGTGAGCAAGCGATGCGATGCTCTCAT  
180▶ V G I W I L A T V L S I P E L L Y S D L Q R S S S E Q A M R C S L I **BstAPI (1176)**  
1201 CACAGAGCATGTGGAGGCTTTATCACCATCCAGGTGGCCAGATGGTGATCGGCTTTCTGGTCCCCCTGCTGGCCATGAGCTTCTGTTACCTTGTGCATC  
213▶ T E H V E A F I T I Q V A Q M V I G F L V P L L A M S F C Y L V I

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**PvuII (1387)**  
1301 ATCCGCACCCTGCTCCAGGCACGCAACTTTGAGCGCAACAAGGCCATCAAGGTGATCATCGCTGTGGTGTGGTCTTTCATAGTCTTCCAGTGCCTTACA  
247▶ I R T L L Q A R N F E R N K A I K V I I A V V V V F I V F Q L P Y  
1401 ATGGGGTGGTCTGGCCAGACGGTGGCCAACTTCAACATCACCAGTAGCACCTGTGAGCTCAGTAAGCAACTCAACATCGCTACGACGTCACCTACAG  
280▶ N G V V L A Q T V A N F N I T S S T C E L S K Q L N I A Y D V T Y S

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**SapI (1578)** **EcoO109I (1586)**  
1501 CCTGGCCTGCGTCCGCTGCTGCGTCAACCTTTCTGTACGCCTTCATCGGCGTCAAGTTCGCAACGATCTCTTCAAGTCTTCAAGGACCTGGGCTGC  
313▶ L A C V R C C V N P F L Y A F I G V K F R N D L F K L F K D L G C  
1601 CTCAGCCAGGAGCAGCTCCGGCAGTGGTCTTCTGTGCGCACATCCGGCGCTCCTCATGAGTGTGGAGGCCGAGACCACCACCCTTCTCCCATAGG  
347▶ L S Q E Q L R Q W S S C R H I R R S S M S V E A E T T T T F S P •

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**NheI (1726)**  
1701 CGACTCTTCTGCCTGGACTAGAGGGAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATG

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**HpaI (1864)** **MfeI (1875)**  
1801 CTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTCATTTCATTTATGTTTCAG

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**EcoRI (1960)**  
1901 GTTCAGGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCCAAA  
2001 TCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCCTCACCTTCTTC

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**SapI (2142)** 2101 ATGGAGTTAAGATATAGTGATTTTTCCCAAGGTTTGAAGTGTCTTCTTTATGTTTAAATGCACTGACCTCCACATTCCCTTTTATGATAA **SspI (2199)**  
2201 ATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTT  
2301 AGTAGTTGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGT  
2401 TCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGC  
130▶ E E 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  
2501 TGACCACCTGATGGATCTGCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAAT  
97▶ V 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  
2601 GGCAATGGCTTACGACAGACAGTACCCTGCCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCCGGACA  
64▶ A I A 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

2701 TGGTGCTTGTTCCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCC  
 30 H H 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

2801 TCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTA  
 AseI (2846)

2901 AACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATT

3001 TACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAAC  
 SpeI (3001)

3101 CGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCACTGACTGGGCATAATGCCAGGCGGGCCATT  
 SnaBI (3129)

3201 TACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCA  
 NdeI (3234)

3301 ATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGGCGGGTCTGTTGGGCGGTCAGCCAGGCGGGCCATTACCCTA

3401 AGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCCTTTTCCATAG  
 PacI (3420)  
 PstI (3413)  
 SdaI (3412) BspLU11I (3430)

3501 GCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGC

3601 TCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCGCTTTTCTCCCTTCGGGAAGCGTGGCGCTTTTCTCATAGCTCACGCTGTA

3701 GGTATCTCAGTTCGGGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCT  
 ApaLI (3744)

3801 TGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTTCTTG

3901 AAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGAT

4001 CCGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTC

4101 TACGGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCAATAAAAATATCTT  
 PacI (4160) SmaI (4169) EagI (4180)  
 NotI (4179)

4201 TATTTTCATTACATCTGTGTGTTGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGC

4301 TGCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA