



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAGGTGGCGCGGGTAAACTGGAAAAGTGTCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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**Psp1406I (203)** 201 GTGAACGTTCTTTTTTCGAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACCGCGCCCGCCCTACCTGAGGCC

**HindIII (245)** 301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

**Bsu36I (291)** 401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

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**BstEII (555)**  
**AgeI (552)** 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCATGGGCGTCCCACGGCCCTGGAGGCCGGCAGCTGGCG

**SfiI (576)** 1▶ M G V P T A L E A G S W R

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**SapI (612)**  
**BamHI (604)** 601 CTGGGATCCCTGCTCTTCTGCTCTTCTGGTGGTCCCTAGTCCGGTGGCAGCCTTCAAGGTCGCCACGCCGATTCCCTGTATGTCTGTCGCCAG

**AvrII (639)** 13▶ W G S L L F A L F L A A S L G P V A A F K V A T P Y S L Y V C P E

**SdaI (719)** 701 GGCAGAACGTCACCCTACCTGCAGGCTCTTGGCCCTGTGGACAAAGGGCAGCATGTGACCTTCTACAAGAGCTGGTACCGCAGCTCGAGGGCGAGG

**Bsp120I (732)** 47▶ G Q N V T L T C R L L G P V D K G H D V T F Y K T W Y R S S R G E

**DraIII (751)** 801 TGCAGACCTGCTCAGAGCGCCGCCATCCGCAACCTCACGTTCCAGGACCTCACCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCAGCAGCT

**Acc65I (776)** 80▶ V Q T C S E R R P I R N L T F Q D L H L H H G G H Q A A N T S H D L

**XhoI (786)**

**XcmI (887)**

**FspI (959)** 901 GGCTCAGCGCCACGGGCTGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCCTGCTGGATAGCGGCCCTCTACTGCTGC

113▶ A Q R H G L E S A S D H H G N F S I T M R N L T L L D S G L Y C C

1001 CTGGTGGTGGAGATCAGGCACCACCTCGGAGCACAGGTTCCATGGTGCATGGAGTGCAGGTGCAGACAGGCAAAGATGCACCATCCAACCTGTGTGG

147▶ L V V E I R H H H S E H R V H G A M E L Q V Q T G K D A P S N C V

1101 TGTACCCATCCTCCTCCAGGAAGTAAACATCACGGTGCAGCCCTGGTACGGGTGCATCGTAGGAATCCTCTGCCTCCCCCTCATCTGCT

180▶ V Y P S S S Q D S E N I T A A A L A T G A C I V G I L C L P L I L L

1201 CCTGGTCTACAAGCAAAGGCAGGCGACCTCAACCGCCGTGCCAGGAGCTGGTGGGATGGACAGCAACATTCAAGGGATTGAAAACCCCGCTTTGAA

213▶ L V Y K Q R Q A A S N R R A Q E L V R M D S N I Q G I E N P G F E

1301 GCCTCACACCTGCCAGGGGATACCGAGGCCAAAGTCAGGCACCCCTGTCTATGTGGCCAGCGGCAGCCTTCTGAGTCTGGCGGCATCTGCTTT

247▶ A S P P A Q G I P E A K V R H P L S Y V A Q R Q P S E S G R H L L

**BbsI (1441)** 1401 CGGAGCCAGCACCCCTGTCTCTCCAGGCCCGGAGAGCTTCTTCCATCCCTGGACCCTGCTCCTGACTCTCAAACCTTTGAGGTACATAGCC

**Tth111I (1459)** 280▶ S E P S T P L S P P G P G D V F F P S L D P V P D S P N F E V I •

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**MscI (1512)**  
**NheI (1506)** 1501 CAGCTGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTAAAAAATGCTTTATTTGTGAAATTTGTG

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**HpaI (1644)** 1601 ATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAAACAACAACAAATGCATTCAATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGA

**MfeI (1655)**

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**EcoRI (1740)** 1701 GGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACCTTAACCTCCAAATCAAGCCTCTACTGAATCC

1801 TTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTTCATGGAGTTAAGATATAGTG

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**SapI (1922)** 1901 TATTTTCCAAGGTTTGAAGTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAAATAATTTAAA

**SspI (1979)** 2001 TACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAAC

**Swal (1993)** 2101 AAAGAACCTTTAATAGAAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGAC

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

**SacI (2254)** 2201 CAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTG

124▶ 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 R I S R

2301 TCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGA

90▶ 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 E A C V

**StuI (2418)** 2401 CAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCGAGTCTTGGTCTGATGGCCGCCCCGACATGGTGCTTGTGCTCATA

57▶ 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 N D E Y

BbsI (2564)  
**XmnI (2560)**

2501 GAGCATGGTGATCTTCTCAGTGGCGACCTCCACGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCCTATAGTGAGTCGTATTA  
24 L M T I K E T A V E V L E L D Q Q S I N F T K M ←

**AseI (2626)** SacI (2683)

2601 TACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAG  
←

**SpeI (2781)**

2701 ACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTACGACATTTTGAAAGTCCCGTTGATTTACTAGICAAAACAACTCC  
←

2801 CATTGACGTCAATGGGGTGGAGACTTGAAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGC  
←

**SnaBI (2909)**

2901 GATGACTAATACGTAGATGTACTIONGCAAGTAGGAAAGTCCATAAGGTCACTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATA  
←

**NdeI (3014)**

3001 GGGGGCGTACTTGGCATATGATACACTTGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGAAAAGTCCCTATTGGCG  
←

**SdaI (3192)**

3101 TTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTACGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGG  
←

**PacI (3200) BspLU11I (3210)**

3201 TTAATAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTCCATAGGCTCCGCCCCCTGACGAGC  
←

3301 ATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCCTCTGT  
←

3401 TCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAG  
←

**ApaLI (3524)**

3501 GTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGAC  
←

3601 ACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGTACAGAGTTCTGAAGTGGTGCCTAACTACGG  
←

3701 CTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCT  
←

3801 GGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTCTACGGGTCTGACGCTCAGT  
←

**EagI (3960)**

PacI (3940) SwaI (3949) **NotI (3959)**

3901 GGAACGAAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAATCAGCGGCCCAATAAAATATCTTTATTTTCATTACATCTGTGT  
←

4001 GTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGAAGTGCAG  
4101 GTGCCAGAACATTTCTCTATCGAA