



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

1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGCGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTGTGCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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**HindIII (245)**

**Psp1406I (203)**
**PvuII (239)**
**Bsu36I (291)**

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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**NgoMIV (441)**

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

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**BstEII (555)**

**AgeI (552)**
**NcoI (560)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCATGGGAAACAAGTGTACAACGTGGTGGTCATTGTGCT

1▶ M G N N C Y N V V V I V L

**BstAPI (692)**

601 GCTGCTAGTGGGCTGTGAGAAGTGGGAGCCGTGCAGAACTCCTGTGATAACTGTCAGCCTGGTACTTTCTGCAGAAAATACAATCCAGTCTGCAAGAGC

13▶ L L V G C E K V G A V Q N S C D N C Q P G T F C R K Y N P V C K S

701 TGCCCTCAAGTACCTTCTCCAGCATAGGTGGACAGCCGAAGTGAACATCTGCAGAGTGTGTGCAGGCTATTTCAAGTTCAGAAGTTTTGCTCCTCTA

47▶ C P P S T F S S I G G Q P N C N I C R V C A G Y F R F K K F C S S

**MscI (882)**

801 CCCACAACGCGGAGTGTGAGTGCATTGAAGATTCCATTGCTTGGGGCCACAGTGCACCAGATGTGAAAAGGACTGCAGGCCTGGCCAGGAGCTAACGAA

80▶ T H N A E C E C I E G F H C L G P Q C T R C E K D C R P G Q E L T K

**XcmI (939)**
**SalI (959)**
**XbaI (981)**

901 GCAGGTTGCAAAACCTGTAGCTTGGGAACATTTAATGACCAGAACGGTACTGGCGTCTGCGACCCTGGACGAACTGCTCTAGACGGAAGTCTGTG

113▶ Q G C K T C S L G T F N D Q N G T G V C R P W T N C S L D G R S V

1001 CTTAAGACCGGGACCACGGAGAAGGACGTGGTGTGGACCCCTGTGGTGTGAGCTTCTCTCCAGTACCACCATTTCTGTGACTCCAGAGGGAGGACCAG

147▶ L K T G T T E K D V V C G P P V V S F S P S T T I S V T P E G G P

**BstAPI (1104)**
**EcoO109I (1115)**

1101 GAGGGCACTCCTTGCAGGTCCTTACCTTGTCTGGCGCTGACATCGGCTTTGCTGTGGCCCTGATCTTCATTACTCTCCTGTTCTCTGTGCTCAAATG

180▶ G G H S L Q V L T L F L A L T S A L L L A L I F I T L L F S V L K W

**XmnI (1206)**
**BbsI (1242)**

1201 GATCAGGAAAAAATTCCCCACATATTTCAAGCAACCATTTAAGAAGACCACTGGAGCAGCTCAAGAGGAAGATGCTTGTAGTGCAGTGTCCACAGGAA

213▶ I R K K F P H I F K Q P F K K T T G A A Q E E D A C S C R C P Q E

**MscI (1342)**

**NheI (1336)**

1301 GAAGAAGGAGGAGGAGGAGGCTATGAGCTGTGATGTGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAAGTGAATGCAGT

247▶ E E G G G G G Y E L •

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**HpaI (1474)**
**MfeI (1485)**

1401 GAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTGCATTCA

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**EcoRI (1570)**

1501 TATGTTTCAGGTTTCAAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTTACAAATGTGGTATGGAATTCAAAATACAGCATAGCAAAC

1601 AACCTCAAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTC

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**SapI (1752)**

1701 ACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCAAGTTTGAAGTACTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCT

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**SspI (1809)**
**SwaI (1823)**
**EcoO109I (1884)**

1801 TTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAAT

1901 CCCCCAGTTTAGTGTGACTTAGGGAACAAAGAACCTTTAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAG

141◀ • N R T Y K L

**SacI (2084)**

2001 GGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATG

134◀ 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 D S I L E R C M

**BstXI (2113)**

2101 CCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAG

100◀ 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 F D K Q G N S V A

**StuI (2248)**

2201 CAGACCAATGGCAATGGCTTCAACACAGACAGTACCTGCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGC

67◀ S G I 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

BbsI (2394)  
XmnI (2390)

2301 CGCCCCGACATGGTGCTTGTTCCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTC  
34 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 Q Q S I N F T K

AseI (2456)

2401 ATGGTGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGA  
0 M

SacI (2513)

2501 CGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAAGT

SpeI (2611)

2601 CCCGTTGATTTACTAGTCAAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTA

SnaBI (2739)

2701 CTGCCAAAACCGCATCATCATGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAAGTCATGTACTGGGCATAATGCCAG

NdeI (2844)

2801 GCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCC

2901 ATTGACGTCAATGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCTGTTGGGCGGTACGCCAGGGGGCC

PacI (3030)

SdaI (3022)      BspLU11I (3040)

3001 ATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGT  
3101 TTTCCATAGGCTCCGCCCCCTGACGAGCATCAGAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCC  
3201 CCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGTTTCTCATAGC

ApaLI (3354)

3301 TCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCAGCCCAGCCGCTGCGCCTTATCCGGTA  
3401 ACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTAC  
3501 AGAGTTCTTGAAGTGGTGCCTAACTACGGTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGT  
3601 AGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTT

EagI (3790)  
PacI (3770)    SwaI (3779)    NotI (3789)

3701 TGATCTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAATCAGCGGCCCAAT  
3801 AAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAG  
3901 CAAAATAGGCTGTCCCAAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA