



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

1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGCGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTATGTCGTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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**HindIII (245)**

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

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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**NgoMIV (441)**

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

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**BbsI (564)**

**AgeI (552)** **BspHI (560)**
**XbaI (591)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACTCTGAGATCACCGGTCATCATGAAGACCTTCAACATCTCCAGCAGGATCTAGAATT

1 M K T F N I S Q Q D L E L

**BsrBI (659)** **BsiWI (670)**

601 AGTAGAAGTAGCGACAGAGAAGATTACAATGCTTTATGAGGATAATAAACATCATGTGGGAGCGGCAATTCGTACGAAAACAGGAGAAATCATTTCGGCA

13 V E V A T E K I T M L Y E D N K H H V G A A I R T K T G E I I S A

**BstBI (768)**

701 GTACATATTGAAGCGTATATAGGACGAGTAAGTGTGGTGCAGAAAGCCATTGCGATTGGTAGTGCAGTTTCGAATGGACAAAAGGATTTTGACACGATTG

47 V H I E A Y I G R V T V C A E A I A I G S A V S N G Q K D F D T I

801 TAGCTGTTAGACACCTTATTCTGACGAAGTAGATAGAAGTATTGAGTGGTAAGTCTTGTGGTATGTGTAGGGAGTTGATTCAGACTATGCACCAGA

80 V A V R H P Y S D E V D R S I R V V S P C G M C R E L I S D Y A P D

**NheI (993)**

**EcoRI (987)** **MscI (999)**

901 TTGTTTTGTGTTAATAGAAATGAATGGCAAGTTAGTCAAACTACGATTGAAGAACTATTCCACTCAAATATACCCGAAATTAAGAATTCGCTAGCT

113 C F V L I E M N G K L V K T T I E E L I P L K Y T R N •

1001 GGCCAGACATGATAAGATACATTGATGAGTTTGACAAACCACAACACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTT

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**HpaI (1131)** **MfeI (1142)**

1101 ATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGC

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**EcoRI (1227)**

1201 AAGTAAACCTCTACAAATGTGGTATGGAATTCATAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGAT

1301 GAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCTCACCTTCTTTCATGGAGTTTAAAGATATAGTGTATTTCCCAAGG

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**SapI (1409)**
**SspI (1466)**
**SwaI (1480)**

1401 TTTGAAGTACTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAAATTCAGAAATAATTTAAATACATCATTGCAA

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**EcoO109I (1541)**

1501 TGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAGGAACCTTTA

1601 ATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTC

141 N R T Y K L P I L E E I T T K V L K G N

**SacI (1741)** **BstXI (1770)**

1701 ATCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAG

119 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 D V E D S

1801 AGTAGGGTGCCGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCCAGCAGACAGTACCCTGCC

86 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 T V R G

**StuI (1905)**

1901 AATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCGTCTTGGTCTGATGGCCGCCGACATGGTGTCTGTTGCTCCTCATAGAGCATGGTGATC

53 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 L M T I

**BbsI (2051)**

2001 TTCTCAGTGGCGACTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATA

19 K E T A V E V L E L D Q Q S I N F T K M

**AseI (2113)** **SacI (2170)**

2101 TACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCCACCGTA

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**SpeI (2268)**

2201 CACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAACTCCCATTGACGTCAAT

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**SnaBI (2396)**

2301 GGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTGGCAAAACCGCATCATCATGGTAATAGCGATGACTAATACG

2401 TAGATGTACTGCCAAGTAGGAAAGTCCCATAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTG

**NdeI (2501)**

2501 GCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAAC

PacI (2687)

**PstI (2680)**

**SdaI (2679)**

**BspLU11I (2697)**

2601 ATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTACGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAAITAGGAACA

2701 TGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTTCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCG

2801 ACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCG

2901 CTTACCGGATACCTGTCCGCTTCTCCCTTCGGAAGCGTGGCGTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCA

**ApaLI (3011)**

3001 AGCTGGGCTGTGTGCACGAACCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCC

3101 ACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGA

3201 ACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGGTT

3301 TTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAACTC

**EagI (3447)**

PacI (3427) SmaI (3436) **NotI (3446)**

3401 ACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTGT

3501 GTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATT

3601 TCTCTATCGAA