



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
**MfeI (82)**  
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTATGTCGTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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**HindIII (245)**  
**Psp1406I (203)** 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCGCCCTACCTGAGGCC  
**PvuII (239)**  
**Bsu36I (291)** 301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCTGACCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

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**AgeI (552)** **SphI (560)** **BssHII (577)**  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGTCAGCATGCCTGGGAAGAAGCGCGCAAGAACGCTCAACCGAG  
1▶ M P G K K A R K N A Q P S  
**EcoRV (696)**  
601 CCCCAGCGGGCTCCAGCAGAGCTGGAAGTCGAGTGTGCTACTCAACTCAGGAGATTTGGAGACAACTGAAGTTCGGCAGAACTTCTGAATCTGATA  
13▶ P A R A P A E L E V E C A T Q L R R F G D K L N F R Q K L L N L I

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**MscI (762)**  
701 TCCAAACTCTTCTGCTCAGGAACCTGACTGCATCAAAAATTGCATGAGGGACTCGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACA  
47▶ S K L F C S G T •

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**NheI (756)**  
801 AACCAACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAAC  
**HpaI (894)**

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**MfeI (905)** 901 AACAAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTTGATGGAATCTGAAATCTAA  
**EcoRI (990)**  
1001 ATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTG

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**SapI (1172)**  
1101 CATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCAAGGTTTGAAGTCTCTTCTTCTTTATGTTTTAAATGC

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**SspI (1229)** **Swal (1243)**  
1201 ACTGACCTCCACATTCCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATG

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**EcoO109I (1304)**  
1301 CTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTT  
141▶  
1401 TAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAG  
140▶ • 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 D S

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**SacI (1504)** **BstXI (1533)**  
1501 AGATGAGCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGTGCTGACAGCCACAATGGTGTCAAAGTC  
107▶ 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 F D

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**StuI (1668)**  
1601 CTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCC  
74▶ 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 I E  
1701 CCAGTCTTGGTCTGATGGCCGCCCGACATGGTGCTTGTGCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCT  
40▶ 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 Q Q

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**BbsI (1814)** **XmnI (1810)** **AseI (1876)**  
1801 GAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGAT  
7▶ S I N F T K M

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**SacI (1933)**  
1901 GCGTCTCCAGCTTATCTGACGGTTCATAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCTACCGCCATTTGCGTCAATGGGGCGGAGTT

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**SpeI (2031)**  
2001 GTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGC

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**SnaBI (2159)**  
2101 TATCCACGCCATTGATGTAAGTCCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTCCCAAGTAGGAAAGTCCCATAAAGTCA

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**NdeI (2264)**  
2201 TGTAAGTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCAAGTGGGCAGT

2301 TTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTG

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PacI (2450)

PstII (2443)  
SdaI (2442)                      BspLU11I (2460)

2401 GGCGGTCAGCCAGGCGGGCCATTTACC GTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAA

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2501 AAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTA

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2601 TAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCCTCTCTGTCCGACCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAA

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ApaLI (2774)

2701 GCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCCAGCCGA

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2801 CCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCG

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2901 AGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTA

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3001 CCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAA

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PacI (3190) SwaI (3199)

3101 AGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACA

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EagI (3210)  
NotI (3209)

3201 TTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGGTTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAA

3301 AACGAAACAAACAAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA