



**PvuI (7)**  
**SgfI (6)**
**MfeI (82)** **EcoNI (96)**

1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
 101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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**Bsu36I (291)**  
**Psp1406I (203)** **HindIII (245)** **EcoNI (287)**

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCGCTACCTGAGGGCC  
 301 GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC  
 401 GGGCCTTTGTCCGGGCTCCCTTGAGGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGTTCTTTGTTTCGTTT

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**NcoI (560)**  
**BstEII (555)**  
**AgeI (552)**

501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGGCTACCTGAGATCACCGGTACCATTGGGACGGAGGCCACAGAGCAGGTTTCTGGGGCCA  
 1 M G T E A T E Q V S W G H

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**StuI (671)**

601 TTAAGTCTGGGATGAAGAGGACGCATACTCGGCTGAGCCACTGCGGAGCTTTGCTACAAGGCCGATGTCAGGCTTCAGCCGGCCTTCCAACCCAGT  
 13 Y S G D E E D A Y S A E P L P E L C Y K A D V Q A F S R A F Q P S

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**BssHII (778)**

701 GTCTCCCTGACCGTGGCTGCGCTGGGTCTGGCCGCAATGGCCTGGTCTGGCCACCCACCTGGCAGCCGACGCGCAGCGCGCTCGCCACCTCTGCC  
 47 V S L T V A A L G L A G N G L V L A T H L A A R R A A R R A A R S P T S A  
 801 ACCTGCTCCAGCTGGCCCTGGCCGACCTTTGCTGGCCCTGACTGCTCCGCTTCGCGGCAGCAGGGGCTTTGAGGCTGGAGTCTGGGAAGTCCACCTG  
 80 H L L Q L A L A D L L L A L T L P F A A A G A L Q G W S L G S A T C

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**Eco47III (964)** **Eco47III (993)**

901 CCGCACCATCTCTGGCCTCTACTCGGCCTCCTCCACGCGGCTTCTCTTCTGGCCTGTATCAGCGCTGACCCTACGTGGCCATCGCGGAGCGCTC  
 113 R T I S G L Y S A S F H A G F L F L A C I S A D R Y V A I A R A L

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**SacII (1009)** **EagI (1026)**

1001 CCAGCGGGCGCGGCCCTCCACTCCCGCGCGCACACTTGGTCTCCGTCATCGTGTGGCTGCTGCTACTGCTCCTGGCGCTGCTGCGCTGCTCTTCA  
 147 P A G P R P S T P G R A H L V S V I V W L L S L L L A L P A L L F

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**Tth111I (1127)**

1101 GCCAGGATGGGACGCGGGAAGGCCAACGACGCTGTGCCTCATTTCCCGAGGGCCTCACGCAGACGGTGAAGGGGGCAGCGCCGTGGCGCAGGTGGC  
 180 S Q D G Q R E G Q R R C R L I F P E G L T Q T V K G A S A V A Q V A

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**SgrAI (1285)**

**Bsp120I (1276)**

1201 CCTGGCTTCGCGCTGCCGCTGGGCGTCATGGTAGCCTGCTACGCGTCTTGGGCCGACGCTGCTGGCCGCCAGGGGGCCGAGCGCCGGCTGCGCTG  
 213 L G F A L P L G V M V A C Y A L L G R T L L A A R G P E R R R A L

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**BsrBI (1396)**

**PstI (1336)** **BssHII (1390)**

1301 CGCGTCTGGTGGCTCTGGTGGCGGCTTCTGGTGGTGCAGCTGCCCTACAGCCTCGCCCTGCTGCTGGATACTGCCGATCTACTGGCTGCGCGCAGC  
 247 R V V V A L V A A F V V L Q L P Y S L A L L L D T A D L L A A R E

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**BstEII (1440)**

1401 GGAGCTGCCCTGCCAGCAACGCAAGGATGTGCACTGCTGGTACCAGCGGCTTGGCCCTCGCCGCTGTGGCCTCAATCCCGTTCTCTACGCCCTTCT  
 280 R S C P A S K R K D V A L L V T S G L A L A R C G L N P V L Y A F L

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**Bsu36I (1553)** **SacII (1572)**

1501 GGGCTGCGCTTCCGCCAGGACTGCGGAGGCTGCTACGGGTGGGAGCTGCCCCTCAGGGCCTCAACCCCGCGCGGCTGCCCCCGCGGCCCGCCGCTT  
 313 G L R F R Q D L R R L L R G G S C P S G P Q P R R G C P R R P R L

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**XbaI (1660)**

1601 TCTTCTGCTCAGCTCCACGGAGACCCACAGTCTCTCTGGACAACCTAGGGCTGCGAATCTAGAGGAGGGGCGAGGCTGAGGGTCTGGGAAAGGGGA  
 347 S S C S A P T E T H S L S W D N •

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**NheI (1761)**

1701 GTAGTGGGGAACTGAGAAAGAGGCAGGGACCTAAAGGACTACCTCTGTGCTTGCCTGCTAGTGGCCAGACATGATAAGATACATTGATGAGTTT

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**HpaI (1899)**

1801 GGACAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAACAAG

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**EcoRI (1995)**

**MfeI (1910)**

1901 TTAACAACAACAATTGCATTCAATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATT  
 2001 CTAANAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTGAACTCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGCTGTTGCCA  
 2101 ATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCAAGGTTTGAAGTACTGCTCTTCAATTTCTTTATGTTT

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**SspI (2234)** **Swal (2248)**

2201 AATGACTGACCTCCACATTCCCTTTTGTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTTATTAGGCAGATCC  
 2301 AGATGCTCAAGGCCCTTCATAATATCCCCAGTTTGTAGTGGACTTAGGGAACAAAGGAACCTTAAATAGAAATTGGACAGCAAGAAAGCGAGCTTCT  
 2401 AGCTTTAGTTCCTGGTGTACTTGGGGGATGAGTTTCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAAGCAGTCAGGAGCATA  
 141 • 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

SacI (2509)  
 2501 GTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCA  
 109 D S 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

StuI (2673)  
 2601 AAGTCCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGA  
 75 F D 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

2701 TCTCCCCAGTCTTGGTCTGTATGGCCGCCCGACATGGTGCTTGTCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATC  
 42 E 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

BbsI (2819)  
 XmnI (2815) AseI (2881)  
 2801 CTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCCTATAGTGAGTCGATTATATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGG  
 9 Q Q S I N F T K M

SacI (2938)  
 2901 TGGATGGCGTCTCCAGCTTATCTGACGGTTCACATAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTGCGTCAATGGGGCGG

SpeI (3036)  
 3001 GAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAA

SnaBI (3164)  
 3101 ACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAA

NdeI (3269)  
 3201 GGTCATGTACTGGGCATAATGCCAGGGGCCATTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGG

3301 GCAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCAATGGCGGGGGT

PacI (3455)  
 PstI (3448) SdaI (3447) BspLU11I (3465)  
 3401 CGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATTAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC  
 3501 CGTAAAAGGCCGCGTGTGGCGTTTTCCATAGGCTCCGCCCTGACGAGCATCAGAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAG  
 3601 GACTATAAAGATACCAGGCGTTTCCCTGGAAGCTCCCTCGTGCGCTCTCTGTTCCGACCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTC

ApaLI (3779)  
 3701 GGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTTCAG  
 3801 CCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCA  
 3901 GAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGTGAAGCC  
 4001 AGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGA

PacI (4195)  
 4101 AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCAATGGCTAGTTAAT

EagI (4215)  
 SwaI (4204) NotI (4214)  
 4201 TAACATTTAAATC AGCGCCGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAA  
 4301 AACAAAACGAAACAAAACAAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA