



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
**MfeI (82)**  
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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**HindIII (245)**  
**Psp1406I (203)** 201 GTGAACGTTCTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCCGCCGCTACCTGAGGCC  
**PvuII (239)**  
301 GCCATCCACGCGGTTGAGTGCAGTCTGCCGCTCCCGCCTGTGGTGCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC  
**Bsu36I (291)**

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**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGTTGCTCAACTCTACGCTTTGTTTCGTTT

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**NcoI (560)**  
501 TCTGTTCTGGCGGTTACAGATCCAAGCTGTGACCGCGGCTACCTGAGATCACCGGTACCATGGCTCCAGCAGCCCCGGCCGGCTGCCCGCACT  
**AgeI (552)** 1 M A P S S P R P A L P A L  
601 CCTGGTCTGCTCGGGGCTGTGCCAGGACCTGGCAATGCCAGACATCTGTGTCCCTCAAAGTCATCTGCCCGGGGAGGCTCCGTGCTGGTG  
13 L V L L G A L F P G P G N A Q T S V S P S K V I L P R G G S V L V  
701 ACATGCAGCACCTCTGTGACCAGCCCAAGTTGTTGGCATAGAGACCCGTTGCCTAAAAAGGAGTTGCTCCTGGGAACAACCGGAAGGTGTATG  
47 T C S T S C D Q P K L L G I E T P L P K K E L L L P G N N R K V Y  
801 AACTGAGCAATGTGCAAGAAGATAGCCAACCAATGTGCTATTCAAACTGCCCTGATGGGAGTCAACAGCTAAAACCTTCTCACCGTACTGGACTCC  
80 E L S N V Q E D S Q P M C Y S N C P D G Q S T A K T F L T V Y W T P  
**XcmI (966)** XcmI (992)  
901 AGAACGGGTGAACTGGCACCCCTCCCTCTTGGCAGCCAGTGGGCAAGAACCTTACCCTACGCTGCCAGGTGGAGGGTGGGGCACCCCGGCCAACCTC  
113 E R V E L A P L P S W Q P V G K N L T L R C Q V E G G A P R A N L

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**PvuII (1043)** **NcoI (1098)**  
1001 ACCGTGGTGTGCTCCGTGGGAGAAGGAGCTGAAACGGGAGCCAGCTGTGGGGAGCCCGCTGAGGTACGACCACGGTGTGGTGAGGAGAGATCAC  
147 T V V L L R G E K E L K R E P A V G E P A E V T T T V L V R R D H  
**PshAI (1191)**  
1101 ATGGAGCCAAATTTCTGTCGCCGACTGAACTGGACCTGCGGCCCAAGGGCTGGAGCTGTTTGAACACCTCGGCCCTACAGCTCCAGACCTTTGT  
180 H G A N F S C R T E L D L R P Q G L E L F E N T S A P Y Q L Q T F V  
**PshAI (1260)**  
1201 CCTGCCAGCGACTCCCCACAACCTGTGACCCCCGGGCTCTAGAGGTGGACACGAGGGGACCGTGGTCTGTTCCCTGGACGGGCTGTTCCAGTCTCG  
213 L P A T P P Q L V S P R V L E V D T Q G T V V C S L D G L F P V S  
1301 GAGGCCAGGTCCACTGGCACTGGGGACAGAGGTTGAACCCACAGTCACTATGGCAACGACTCCTTCTCGGCCAAGGCCCTCAGTCACTGTGACCG  
247 E A Q V H L A L G D Q R L N P T V T Y G N D S F S A K A S V S V T  
1401 CAGAGGACGAGGGCAGCCAGCGGCTGTCAGTAATACTGGGAAACAGAGGACACTGCAGACACTGCAGACACTACAGCTTCCGCGGCC  
280 A E D E G T Q R L T C A V I L G N Q S Q E T L Q T V T I Y S F P A P  
1501 CAACGTGATTCTGACGAAGCCAGAGGTCTCAGAAGGGACCGAGGTGACAGTGAAGTGTGAGGCCACCCCTAGAGCCAAGGTGACGCTGAATGGGGTTCCA  
313 N V I L T K P E V S E G T E V T V K C E A H P R A K V T L N G V P

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**Bsp120I (1619)** **NgoMIV (1693)**  
1601 GCCCAGCCACTGGGCCGAGGGCCAGCTCCTGCTGAAGGCCACCCAGAGGACAACGGGCGCAGCTTCTCCTGCTGCAACCTGGAGGTGGCCGGCC  
347 A Q P L G P R A Q L L L K A T P E D N G R S F S C S A T L E V A G  
**MscI (1786)**  
1701 AGCTTATACACAAGAACCAGACCCGGGAGCTTCTGTCCTGTATGCCCCGACTGGACGAGAGGGATTGTCGGGAAACTGGACGTGGCCAGAAAATTC  
380 Q L I H K N Q T R E L R V L Y G P R L D E R D C P G N W T W P E N S  
1801 CCAGCAGACTCCAATGTGCCAGGCTTGGGGAAACCCATTGCCGAGCTCAAGTGTCTAAAGGATGGCACTTCCCACTGCCCATCGGGGAATCAGTGACT  
413 Q Q T P M C Q A W G N P L P E L K C L K D G T F P L P I G E S V T

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**BglIII (1908)** **XhoI (1904)** **BstEII (1956)** **BstEII (1968)**  
1901 GTCACCTCGAGATCTTGGGGCACCTACCTCTGTCGGGCCAGGAGCACTCAAGGGGAGGTACCCGCGAGGTGACCGTGAATGTGCTCTCCCCGGTATG  
447 V T R D L E G T Y L C R A R S T Q G E V T R E V T V N V L S P R Y  
**BsaBI (2001)**  
2001 AGATTGTCATCACTGTGGTAGCAGCCGAGTCATAATGGGCACTGACGGCCTCAGCACGTACCTCTATAACGCCAGCGGAAGATCAAGAATACAG  
480 E I V I I T V V A A A V I M G T A G L S T Y L Y N R Q R K I K K Y R

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**SmaI (2119)**  
2101 ACTACAACAGGCCAAAAAGGGACCCCATGAAACCGAACACACAAGCCACGCCTCCCTGAACCTATCCCGGACAGGGCCTTCTCCTCGGCCTCCCAT  
513 L Q Q A Q K G T P M K P N T Q A T P P •  
**MscI (2209)**  
**NheI (2203)**  
2201 ATTGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATG

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**HpaI (2341)** **MfeI (2352)**  
2301 CTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTTGGGAGGT

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**EcoRI (2437)**  
2401 TTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTTAAAATACAGCATAGCAAACTTAACTCCAAATCAAGCCTCTACTGAAATCCTTT  
2501 TCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCTCACCTTCTTTCATGGAGTTAAGATATAGTGTAT

2601 **SapI (2619)** TTTCCAAGGTTTGAAGTCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTATGAAAAATTCAGAAAATAATTTAAATAC  
 2701 **SspI (2676)** ATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAA  
 2801 **SwaI (2690)** GGAACCTTTAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAG  
 2901 141 • N R T Y K L P I L E E I T T K V L  
 123 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 D  
 3001 CTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGCTGACCACCTGATGGATCTGTCC  
 89 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 T  
 3101 TGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAAGTCTTGGTCTGATGGCCGCCCCGACATGGTGCTTGTTCCTCATAGAG  
 56 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 L  
**BbsI (3261)**  
 3201 **XmnI (3257)** CATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTTCATGGTGCCCTCCTATAGTGAGTCGTATTATAC  
 23 M T I K E T A V E V L E L D Q Q S I N F T K M  
**AseI (3323)**  
 3301 TATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCATAAACGAGCTCTGCTTATATAGACC  
**SpeI (3478)**  
 3401 TCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCCAT  
 3501 TGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGAT  
**SnaBI (3606)**  
 3601 GACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGG  
**NdeI (3711)**  
 3701 GCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTTA  
**Pacl (3897)**  
 3801 **SdaI (3889)** CTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTA  
**BspLU11I (3907)**  
 3901 ATTAAAGACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATC  
 4001 ACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCGCTCTCTGTTC  
 4101 GACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTC  
**ApaLI (4221)**  
 4201 GTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACAGC  
 4301 ACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTA  
 4401 CACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGT  
 4501 AGCGGTGGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTACGGGGTCTGACGCTCAGTGGA  
**EagI (4657)**  
 4601 **Pacl (4637)** **SwaI (4646)** **NotI (4656)** ACGAAAACACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGAATAAAATATCTTTATTTTTCATTACATCTGTGTGT  
 4701 GGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTG  
 4801 CCAGAACATTTCTATCGAA