



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA **MfeI (82)**

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

**HindIII (245)**  
**Psp1406I (203)** 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCAGAGGGCTCGCATCTCTCTTACAGCGCCCGCCGCCCTACCTGAGGCC **PvuII (239)** **Bsu36I (291)**

301 GCCATCCACGCGGTTGAGTGCAGTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT **NgoMIV (441)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTACCATTGGCTGTCAGCGAGCTCTGCTCCCGTCCCTTCCAC **NcoI (560)**  
**BstEII (555)**  
**KasI (535)** **AgeI (552)** 1▶ M A V S D A L L P S F S T

601 GTTCGCTCCGGCCGGCGGAAGGAGAGACACTGCGTCCAGCAGGTGCCCGACTAACCGTTGGCGTGAGGAACCTCTCACATGAAGCGACTTCCC **BstEII (997)**  
13▶ F A S G P A G R E K T L R P A G A P T N R W R E E L S H M K R L P

701 CCACTTCCCGCCGCCCTACGACCTGGCGGCGACGGTGGCCACAGACCTGGAGAGTGGCGGAGCTGGTGCAGCTTGCAGCAGTAACAACCCGGCCCTCC **MscI (737)**  
47▶ P L P G R P Y D L A A T V A T D L E S G G A G A C S S N N P A C L

801 TAGCCCGAGGAGACCGAGGAGTTCAACGACCTCTGACCTAGACTTTATCCTTTTCAACTCGCTAACCCACAGGAATCGGTGNGCCGCCAGTGC **BssHIII (953)** **PstI (966)** **BstEII (997)**  
80▶ L A R R E T E E F N D L L D L D F I L S N S L T H Q E S V A A T V T

901 CACCTCGGCGTCACTTATCCTCGTCTTCCCAAGCGAGCAGCGCCCTGCCAGCGCCCTCCACTGCACTTCACTATCCGATCCGGGCCGGGGT **XmaI (1002)**  
113▶ T S A S A S S S S S P A S S G P A S A P S T C S F S Y P I R A G G

1001 GACCCGGCGTGGCTGCCAGCAACAGGTGGAGGGCTCTCTACAGCCGAGAATCTGCCACCTCCACGGCCCTTCAACTGGCGGACATCAATG **Bst1107I (1156)**  
147▶ D P G V A A S N T G G G L L Y S R E S A P P P T A P F N L A D I N

1101 ACGTGAGCCCTCGGGCGCTTCTGGCTGAGCTCTGCGCCGAGTTGGACCAAGTATACATTCCGCCACAGCAGCTCAGCCGCCAGGTGGCGGGCT **Bsp120I (1579)**  
180▶ D V S P S G G F V A E L L R P E L D P V Y I P P Q Q P Q P P G G G L

1201 GATGGCAAGTTTGTGCTGAAGGCTCTCTGACCACCCCTGGCAGCGAGTACAGCAGCCCTTCCGTCATCAGTGTAGCAAAGGAAGCCAGACGGCAGC **Bsp120I (1579)**  
213▶ M G K F V L K A S L T T P G S E Y S S P S V I S V S K G S P D G S

1301 CACCCGGTGGTAGTGGCGCCCTACAGCGGTGGCCCGCCGCGCATGTGCCCAAGATTAAGCAAGAGGGGTCCCGTCTGCACGGTCAAGCGGTCCCTAG **DraIII (1300)** **KasI (1314)**  
247▶ H P V V V A P Y S G G P P R M C P K I K Q E A V P S C T V S R S L

1401 AGGCCATTGTAGCGCTGGACCCAGCTCAGCAACGGCCACCGCCCAACACACAGACTTCCCCTGGGGCGGAGCTCCACCAGGACTACCCCTAC **XcmI (1404)**  
280▶ E A H L S A G P Q L S N G H R P N T H D F P L G R Q L P T R T T P T

1501 ACTGAGTCCCGAGGAAGTGTGAACAGCAGGACTGTCACCTGGCTGCTCTTCCCCAGGATCCATCCCATCCGGGCGCACTACCTCCTTTCC **Bsp120I (1579)**  
313▶ L S P E E L L N S R D C H P G L P L P P G F H P H P G P N Y P P F

1601 CTGCCAGACCAGATGCAATCACAAGTCCCTCTCTCATTATCAAGAGCTCATGCCACCGGGTCTGCTGCGCAGAGGACCCAAAGCAAAGAGGGAA **Bsp120I (1579)**  
347▶ L P D Q M Q S Q V P S L H Y Q E L M P P G S C L P E E P K P K R G

1701 GAAGGTGTCGGCCCGGAAAAGAACAGCCACCCACACTTGTGACTATGCAAGGTGTGGCAAACTTATACCAAGAGTTCTCATCTCAAGGCACACCTGCG **BsrBI (1860)**  
380▶ R R S W P R K R T A T H T C D Y A G C G K T Y T K S S H L K A H L R

1801 AACTCACACAGGCGAGAAACCTTACCACTGTGACTGGGACGGCTGTGGGTGAAATTCGCCCGCTCGGATGAAGTACAGGCACTACCGCAACACACA **DraIII (1991)**  
413▶ T H T G E K P Y H C D W D G C G W K F A R S D E L T R H Y R K H T

1901 GGGACCGGCCCTTTTCAAGTCCAGAGTGGCAGGGCCCTTTTCCAGGTCCGACCTTGCCTTACACATGAAGAGGCACTTTTAAATCCCAAGTGTG **DraIII (1991)**  
447▶ G H R P F Q C Q K C D R A F S R S D H L A L H M K R H F •

2001 GATGTGACCCACACTGCCAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATT **MscI (2025)** **NheI (2019)**

2101 TGTGAAATTTGTGATGCTATTGCTTTATTTGTAACATTATAAGTGCATAAACAAGTTAAACAACAATTGCATTATTTATGTTTCAGGTTCCAGG **HpaI (2157)** **MfeI (2168)**

2201 GGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACTTTAACCTCCAAATCAAGCC **EcoRI (2253)**

2301 TCTACTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGT

2401 TTAAGATATAGTGTATTTTCCCAAGTTTGAAGTAGCTCTTCACTTTTATGTTTTAAATGCACTGACCTCCACATCCCTTTTGTAGTAAATATTTCA **SspI (2492)**

SwaI (2506)  
 2501 GAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTT  
 2601 GGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGATGAGTTCCTCAA  
 2701 TGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCAC  
 128 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 G C P S V V  
 2801 CCTGATGGATCTGTCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATG  
 95 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 S G I A I  
 StuI (2931)  
 2901 GCTTCAGCACAGACAGTGAACCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGTCT  
 61 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 A G V H H K  
 BspHI (3081)  
 3001 TGTTGTCCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGTCCAGATCCTGCTGAGAGATGTTGAAGTCTTTCATGATGGCCCTCTATA  
 28 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 M  
 XmnI (3073)  
 3101 GTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACGCTGGATGGCGTCTCCAGCTATCTGACGGTTCACTAAACGAGC  
 AseI (3139)  
 3201 TCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGT  
 SpeI (3294)  
 3301 CAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGTATCCACGCCATTGATGACTGCCAAAACCGCATCA  
 SnaBI (3422)  
 3401 TCATGGTAATAGCGATGACTAATACGTAGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTC  
 NdeI (3527)  
 3501 ATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTAAGTCCAAAGTGGGCGAGTTTACCCTAAATACTCCACCCATTGACGTCAATGAAAA  
 3601 GTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGGGGGGTCTTGGGCGGTGAGCCAGGCGGGCCATTTACCCTAAGTTATG  
 PacI (3713)  
 PstI (3706)  
 SdaI (3705) BspLU11I (3723)  
 3701 TAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAAGGCCAGCAAAAAGGCCAGAAACCGTAAAAAGGCCGTTGCTGGCGTTTTTCCATAGGCTCCGC  
 3801 CCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCG  
 3901 TGGCTCTCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCT  
 ApaLI (4037)  
 4001 CAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTTCCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCC  
 4101 AACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGT  
 4201 GGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAA  
 4301 ACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGG  
 PacI (4453) SwaI (4462) NotI (4472)  
 4401 TCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTTCATGGCTAGTAAATTAACATTTAAATCAGCGGCCGAATAAAATATCTTTATTTTC  
 4501 ATTACATCTGTGTGGTTTTTTTGTGTGAATCGTAACATAACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCC  
 4601 AGTGCAAGTGCAGGTGCCAGAACATTTCTATCGAA