



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGTGCCTA  
**MfeI (82)**  
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGCTGTACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

---

**Psp1406I (203)** 201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACGCGCCCGCCCTACCTGAGGCC  
**HindIII (245)**  
301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCCCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

---

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGTCTTTGTTTCGTTT

---

**NgoMIV (441)**  
**NgoMI (441)**  
**NaeI (441)**

---

501 TCTGTTCTGCGCGCTTACAGATCCAAGCTGTGACCGCGCGCTACCTGAGATCACCGGTAGGAGGGCCACCATGGAAGGGAGAGGACCGTACCGGATCTAC  
**KasI (535)** **AgeI (552)** **NcoI (568)**  
601 GACCCTGGGGCAGCGTGCCCTCAGGAGAGGCATCCGCAGCTTTTGGCGCCTAGTGAAGGAGAATTCGGCTGAAGGAAAAATGCAAGGGATAAAGA  
11▶ D P G G S V P S G E A S A F E R L V K E N S R L K E K G Q G I K  
701 TGTTAGGGGAGCTTTTGAAGAGTCCAGATGGAAGCGACCGCTCCGGCAGAAGGCAGAGGAGCTAGTGAAGGACAACGAGCTGCTCCACACCTTC  
44▶ M L G E L L E E S Q M E A T R L R Q K A E E L V K D N E L L P P P S

---

801 TCCCTCTTGGGCTCCTTCGACCCCTGGCTGAGCTCACAGGAAAGGACTCAATGTCACAGCATCTCCACAGCCCTGCATGCCCCAGTGACAAGCCA  
**SphI (879)**  
77▶ P S L G S F D P L A E L T G K D S N V T A S P T A P A C P S D K P  
901 GCACCAGTCCAGAAGCCTCCATCCAGTGGCACCTCCTGTAATTTGAAGTGGTCACTCCTGAGGAGCAGAATTCACCAGAGAGCAGCAGCCATGCCAATG  
111▶ A P V Q K P P S S G T S S E F E V V T P E E Q N S P E S S S H A N

---

1001 CGATGGCGCTGGGCCCCCTGCCCGTGAGGACGGCAACCTGATGCTGCACCTGCAGCGCTGGAGACCACGCTGAGTGTGTGCGGAGGAGCCGGACCA  
**Bsp120I (1010)**  
144▶ A M A L G P L P R E D G N L M L H L Q R L E T T L S V C A E E P D H

---

1101 CGCCAGCTCTTACCCACCTGGCCGATGGCCCTGGAGTTCACCCGACTGGCATCCAAGGTGCACAAGAATGAGCAGCGCACCTCCATTCTGCAGACC  
**ApaLI (1161)**  
177▶ G Q L F T H L G R M A L E F N R L A S K V H K N E Q R T S I L Q T  
1201 CTGTGTGAGCAGTTCGGAAGGAGAACGAGGCTCTGAAGCCAAAGTTGGATAAGGGCTGGAACAGCGGGATCAGGCTGCCGAGAGGCTGCGGGAGAAA  
211▶ L C E Q L R K E N E A L K A K L D K G L E Q R D Q A E R L R E E  
1301 ATTTGGAGCTCAAGAAGTTGTTGATGAGCAATGGCAACAAAGAGGGTGCCTGGCGGCCAGGCTCACCGAAGTGAAGGGACAGGCAAGAAGGCAGT  
244▶ N L E L K K L L M S N G N K E G A S G R P G S P K M E G T G K K A V  
1401 GGCTGGACAGCAGCAGGCTAGTGTGACGGCAGGTAAGTCCCAGAGGTGGTGGCCTGGTGCAGCCGAGAAGAAGGTGAAGATGCTGGAGCAGCAGCGC  
277▶ A G Q Q A S V T A G K V P E V V A L G A A E K K V K M L E Q Q R  
1501 AGTGAAGCTGGAAGTGAACAAGCAGTGGGACCACTTTCCGGTCCATGVAAGCAGCATATGAGCAGAAGTCACTGAGCTGCTCAGAAGCTGGCTG  
311▶ S E L L E V N K Q W D Q H F R S M K Q Q Y E Q K I T E L R Q K L A

---

1601 ATTTGAGAAGCAGGTGACTGACCTGGAGGCCGAGCGGGAGCAGAAGCAGCGTACTTTGACCGCAAGCTCCTCCTGGCCAAGTCCAAGATTGAAATGGA  
**BsrBI (1632)** **XcmI (1684)**  
344▶ D L Q K Q V T D L E A E R E Q K Q R D F D R K L L L A K S K I E M E

---

1701 GGAGACCGACAAGGAGCAGCTGACAGCAGAGGCCAAGGAGCTGCGCCAAAAGGTCAAGTACCTGCAGGATCAGCTGAGCCACTACCCGACAGCGTGAG  
**SdaI (1760)**  
377▶ E T D K E Q L T A E A K E L R Q K V K Y L Q D Q L S P L T R Q R E  
1801 TACCAGAAAAGGAGATCCAGCGGCTCAACAAGGCCCTGGAGGAAGCACTGAGCATCCAAACCCCGCCATCATCTCCACCAACAGCATTGGGAGCCAG  
411▶ Y Q E K E I Q R L N K A L E E A L S I Q T P P P S S P P T A F G S P

---

1901 AAGGAGCAGGGGCCCTCCTAAGGAAACAGGAGCTGGTCAAGCAGAATGAGTTGCTGAAACAGCAGGTGAAGATCTTCGAGGAGGACTTCAGAGGGAGCG  
**Bsp120I (1909)** **XmnI (1967)**  
444▶ E G A G A L L R K Q E L V T Q N E L L K Q Q V K I F E E D F Q R E R

---

2001 CAGTGATCGTGAGCGCATGAATGAGGAGAAGGAAGAGCTGAAGAAGCAAGTGGAGAAGCTGCAGGCCAGGTACCCTGTCAAATGCCAGCTAAAAGCA  
**BglII (1969)** **XmnI (1967)**  
477▶ S D R E R M N E E K E E L K K Q V E K L Q A Q V T L S N A Q L K A  
2101 TTCAAAGATGAGGAGAAGGCAAGAGAAGCCCTCAGACAGCAGAAGAGGAAAGCAAAGGCTCAGGAGAGCGTTACCATGTGGAGCCCCACCAAGACATC  
511▶ F K D E E K A R E A L R Q Q K R K A K A S G E R Y H V E P H P E H

---

2201 TCTGCGGGCCTACCCCTACGCCTACCCGCCATGCCAGCCATGGTGCACACCATGGCTTCGAGGACTGGTCCAGATCCGCTACCCCTCCCCCAT  
**XcmI (2230)** **NcoI (2239)** **NcoI (2252)** **NcoI (2296)**  
544▶ L C G A Y P Y A Y P P M P A M V P H H G F E D W S Q I R Y P P P P M

---

2301 GGCCATGGAGCACCCGCCCTCCCAACTCGCGCTCTTCCATCTGCGGAATACCTGGCGTCTACCTGTGGAGGGGTTTCGAAATCCAAATCAG  
**BstBI (2383)** **Bsp119I (2383)** **AsuII (2383)**  
577▶ A M E H P P P L P N S R L F H L P E Y T W R L P C G G V R N P N Q  
2401 AGCTCCAAAGTATGAGCCCTCCACAGCCAGGCTACAGAACCAGAGTCTCCAAAAATGACCGTGAAGGGCCCTCAGTGAGACAGATTGTGTCAATTTG  
611▶ S S Q V M D P P T A R P T E P E S P K N D R E G P Q •

---

2501 GCTCCACCTTCATCTTGACAGAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTA

---

2601 TTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAACAAACAATTGCATTCATTTATGTTTCAGTTCA  
**HpaI (2659)** **MfeI (2670)**

2701 GGGGGAGGTGTGGGAGGTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAG  
2801 CCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGA  
2901 GTTTAAGATATAGTGTATTTTCCAAGTTTGAAGTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTGTAGAAAATATT  
SspI (2994)  
3001 CAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAG  
SwaI (3008)  
3101 TTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCT  
141 • N R T Y K L P I L E E  
3201 AATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCGCACATGCCACAGGGGCTGACC  
129 I 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 A G C P S V  
3301 ACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAA  
95 V 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  
3401 TGGCTTACGACAGAGTACCTGCCAATGTAGGCCTAATGTGGACAGCAGAGATGATCTCCCGAGTCTTGGTCTGATGGCCGCCCGACATGGTG  
62 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  
BspHI (3583)  
3501 CTTGTTGCCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGATGGCCCTCCTA  
29 K 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 (3575)  
3601 TAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGA  
VspI (3641)  
AseI (3641)  
3701 GCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGCGGAGTTGTTACGACATTTTGAAAGTCCCCTTGATTTA C T  
SpeI (3796)  
3800 A G T C A A A A C A A A C T C C C A T T G A C G T C A A T G G G G T G G A G A C T T G G A A A T C C C C G T G A G T C A A A C C G T A T C C A C G C C A T T G A T G T A C T G C A A A A C C G C A  
SnaBI (3924)  
Eco105I (3924)  
3900 T C A T C A T G G T A A T A G C G A T G A C T A A T A C G T A G A T G T A C T G C C A A G T A G G A A G T C C C A T A A G G T C A T G T A C T G G G C A T A A T G C C A G G C G G C C A T T T A C C  
NdeI (4029)  
4000 G T C A T T G A C G T C A A T A G G G G C G T A C T T G G C A T A T G A T A C A C T T G A T G T A C T G C C A A G T G G G C A G T T T A C C G T A A A T A C T C C A C C A T T G A C G T C A A T G G  
4100 A A A G T C C C T A T T G G C G T T A C T A T G G G A A C A T A C G T C A T T A T T G A C G T C A A T G G G C G G G G T C G T T G G G C G G T C A G C C A G G C G G G C C A T T T A C C G T A A G T T  
SdaI (4207) PacI (4215) BspLU11I (4225)  
4200 A T G T A A C G C C T G C A G G T T A A T T A A G A A C A T G T G A G C A A A A G G C C A G A A C C G T A A A A A G G C C G G T T G C T G G C G T T T T C C A T A G G C  
4298 T C C G C C C C C T G A C G A G C A T C A C A A A A T C G A C G C T C A A G T C A G A G G T G G C G A A A C C C G A C A G G A C T A T A A G A T A C C A G G C G T T T C C C C T G G A A G C T C  
4398 C C T C G T G C G C T C C T G T T C C G A C C T G C C G T T A C C G G A T A C C T G T C C G C T T T C T C C T T C G G A A G C G T G G C G T T T C T C A T A G C T C A C G C T G T A G G  
ApaLI (4539)  
4498 T A T C T C A G T T C G G T G T A G G T C G T T C G C T C C A A G C T G G G C T G T G T G C A C G A A C C C C G T T C A G C C G A C C G C T G C G C T T A T C C G G T A A C T A T C G T C T T G  
4598 A G T C C A A C C C G T A A G A C A C G A C T T A T C G C C A C T G G C A G C A G C C A C T G G T A A C A G G A T T A G C A G A G C G A G G T A T G T A G G C G G T G C T A C A G A G T T C T T G A A  
4698 G T G G T G G C C T A A C T A C G G C T A C T A G A A G A A C A G T A T T T G G T A T C T G C G C T C T G C T G A A G C C A G T T A C C T T C G G A A A A A G A G T T G G T A G C T C T T G A T C C  
4798 G G C A A A C A A A C C A C C G C T G G T A G C G G T G G T T T T T T G T T T G C A A G C A G A G A T T A C G C G C A G A A A A A A G G A T C T C A A G A A G A T C C T T T G A T C T T T T C T A  
EagI (4975)  
PacI (4955) SwaI (4964) NotI (4974)  
4898 C G G G T C T G A C G C T C A G T G G A A C G A A A A C T C A C G T T A A G G G A T T T T G G T C A T G G C T A G T T A A T T A A C A T T T A A A T C A G C G C C G C A A T A A A A T A T C T T T A  
4998 T T T T C A T T A C A T C T G T G T G T T T T T T G T G T G A A T C G T A A C T A A C A T A C G C T C C A T C A A A A C A A A A C G A A A C A A A A C A A A C T A G C A A A A T A G G C T G  
5098 T C C C A G T G C A A G T G C A G G T G C C A G A A C A T T T C T A T C G A A