



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

---

**HindIII (245)**  
**Psp1406I (203)** 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCCGCCCTACCTGAGGCC  
**PvuII (239)**  
**Bsu36I (291)**  
301 GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

---

**NaeI (441)**  
**NgoMIV (441)** 401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCAACTCTACGTCTTTGTTTCGTTT

---

**NcoI (560)**  
**BstEII (555)**  
**AgeI (552)** 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCCTACCTGAGATCACCGGTACCATTGGCTGTGAGCGAGCTCTGCTCCCGTCTTCTCCAC  
1▶ M A V S D A L L P S F S T  
601 GTTCGCGTCCGGCCCGGGGAAAGGAGAAGACTGCGTCCAGCAGGTGCCCGACTAACCGTTGGCGTGGGAACTCTCACATGAAGCGACTTCCC  
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

---

**BstXI (740)**  
**MscI (737)** 701 CCCTTCCCGCCCGCCCTACGACCTGGCGGCGACGGTGGCCACAGACCTGGAGAGTGGCGGAGCTGGTGCAGCTTGCAGCAGTAACAACCCGGCCCTCC  
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 A C S S N N P A L  
801 TAGCCCGGAGGGAGACCGAGGAGTTCAACGACCTCCTGGACCTAGACTTTATCCTTTCCAACCTCGTAACCCACCAGGAATCGGTGGCCGCCACCGTGAC  
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

---

**BssHII (953)** **PstI (966)** **BstEII (997)**  
901 CACCTCGGCGTCAGTTCATCCTCGTCTTCCCCAGCGAGCAGCGGCCCTGCCAGCGGCCCTCCACCTGCAGCTTCAGCTATCCGATCCGGGCCGGGGT  
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  
**XmaI (1002)**  
1001 GACCCGGCGTGGCTGCCAGCAACACAGGTGGAGGGCTCCTCTACAGCCGAGAATCTGCCACCTCCCACGGCCCCCTCAACCTGGCGGACATCAATG  
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

---

**Bst1107I (1156)**  
1101 ACGTGAGCCCTCGGGCGCTTCTGGCTGAGCTCCTGCGGCCGAGTTGGACCCAGTATACATTCCGCCACAGCAGCCTCAGCCGCCAGGTGGCGGGCT  
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 GATGGGCAAGTTTGTGCTGAAGCGTCTCTGACCACCCCTGGCAGCGAGTACGACAGCCCTCCGTCATCAGTGTAGCAAAGGAAGCCAGACGGCAGC  
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

---

**DraIII (1300)**  
1301 CACCCCGTGGTAGTGGCGCCCTACAGCGGTGGCCCGCCGCGCATGTGCCCAAGATTAAGCAAGAGGGTCCCGTCTGCACGGTACGCGGTCCTTAG  
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

---

**Eco47III (1411)**  
**AfeI (1411)**  
**XcmI (1404)** 1401 AGGCCATTTGAGCGTGGACCCAGCTCAGCAACGGCCACCGCCCAACACACAGACTTCCCCTGGGGCGGAGCTCCCCACCAGGACTACCCCTAC  
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

---

**Bsp120I (1579)**  
1501 ACTGAGTCCCGAGGAACTGCTGAACAGCAGGACTGTACCCTGGCCTGCTTCTCCCGAGGATTCCATCCCATCCGGGCCCAACTACCCTCCTTTCC  
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 CTGCCAGACAGATGCAGTCACAAGTCCCCTCTCTCCATTATCAAGAGCTCATGCCACCGGGTTCCTGCCTGCCAGAGGACCCAAAGCAAAGAGGGGAA  
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 GAAGTGTGGCCCGGAAAAGAACAGCCACCCACTGTGACTATGCAGGCTGTGGCAAACCTATACCAAGAGTTCTCATCTCAAGGCACACCTGCG  
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

---

**BsrBI (1860)**  
1801 AACTCACACAGGCGAGAAACCTTACCCTGTGACTGGGACGGCTGTGGGTGAAAATTCGCCCGCTCGGATGAAGTACCAGGCACTACCACAAACACACA  
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

---

**BspEI (1987)**  
1901 GGGACCGGCCCTTTAGTGCCAGAAGTGCACAGGGCCCTTTCCAGGTCGGACCACCTTGCTTACACATGAAGAGGCACTTTGAGTCCGGAGGGGGTG  
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 E S G G G

---

**BamHI (2044)** **MscI (2059)**  
2001 GCTCTCTGGCAGACGTCGTGCGCCGAGACGCAGGCGCCCGCGGATCCTGAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGACAAAC  
480▶ G S P G R R R R R R R R R R R R G S •

---

**Tth111I (2012)** **SacII (2040)** **NheI (2053)**  
2101 CACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAAC

---

**MfeI (2202)** **EcoRI (2287)**  
2201 AACCAATTGCATTCATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTTACAAAATGGTATGGAAATCTAAAATA  
2301 CAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGCTGTTGCCAATGTGCAT  
2401 TAGCTGTTTGACGCTCACCTTCTTTATGAGGTTAAGATATAGTGTATTTCCCAAGGTTGAACTAGCTCTTCAATTTCTTTATGTTTAAATGCACT

2501 **SspI (2526)** **SwaI (2540)**  
GACCTCCACATTCCCTTTTGTAGTAAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTC

2601 AAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAG  
141 •

2701 TTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTTCATCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGA  
139 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 I

2801 **BstXI (2830)**  
TGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCCTT  
106 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 K

2901 **StuI (2965)**  
**Eco147I (2965)**  
CTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGCAGCAGAGATGATCTCCCA  
73 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 G

3001 GTCTTGGTCTGATGGCCGCCGACATGGTGTCTGTGCTCATAGAGCATGGTGTCTTCTCAGTGGCGACTCCACCAGCTCCAGATCCTGCTGAG  
39 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 S

3101 **BspHI (3115)** **VspI (3173)**  
**XmnI (3107)** **AseI (3173)**  
AGATGTTGAAGGTCTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGC  
6 I N F T K M

3201 GTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGT

3300 **SpeI (3328)**  
TACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCT

3399 **SnaBI (3456)**  
**Eco105I (3456)**  
ATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCAT

3499 **NdeI (3561)**  
GTACTGGGCATAATGCCAGGCGGGCATTACCCTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCCAAGTGGGCAGTT

3599 TACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGGGGGGTCTGGG

3699 **PstI (3740)** **SdaI (3739)** **PacI (3747)** **BspLU11I (3757)**  
GCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTG CAG 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 A A G G C C A G G A A C C G T A  
AAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT

3797 ATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGA

3897

3997 **ApaLI (4071)**  
AGCGTGGCGCTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCC

4097 ACCGCTGCGCCTTATCCGGTAATATCGTCTTGTAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGC

4197 GAGGTATGTAGGCGGTGCTACAGAGTTCTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTT

4297 ACCTTCGAAAAAGAGTTGGTAGCTCTTGTATCCGCAAAACACCACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAA

4397 **PacI (4487)**  
AAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAAC

4497 **SwaI (4496)** **NotI (4506)**  
ATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGGTTTTTTTGTGTAATCGTAACTAACATACGCTCTCCATCAAAACA

4597 AAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA