



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA MfeI (82) EcoNI (96)

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

**HindIII (245)** **Bsu36I (291)**  
**Psp1406I (203)** **PvuII (239)** **EcoNI (287)**  
201 GTGAACGTTCTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACCGCGCCCGCCCTACCTGAGGCC

301 GCCATCCACGCGGTTGAGTGCAGTTCGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

**BspLU11I (560)**  
**AgeI (552)**  
501 TCTGTTCTGCGCGGTTACAGATCCAAGCTGTGACCGCGCGCTACCTGAGATCACCGGTCAACATGTTGTCGCGTTTGGTCCCATTCTCGTCACGATCTC  
1▶ M L S R L L P F L V T I S

**EcoRI (613)**  
601 CAGCCTGAGCCTAGAATTCATGCATACGGGACAGAAGTCCAAAGCCCTTCTATGTGTGGTTTGAAGCCAGATTTTTCCAGCACATCTCCACTGGAAA  
13▶ S L S L E F I A Y G T E L P S P S Y V W F E A R F F Q H I L H W K

701 CCTATCCCAAACAGTCTGAGAGCACCTACTATGAAGTGGCCCTCAAACAGTACGAAACTCAACCTGGAATGACATCCATATCTGTAGAAAAGGCTCAGG  
47▶ P I P N Q S E S T Y Y E V A L K Q Y G N S T W N D I H I C R K A Q

**Psp1406I (819)** **BsaBI (832)** **PshAI (880)** **ScaI (890)**  
801 CATTGTCTGTGATCTCACACGTTTACCCTGGATCTGTATCACCGAAGCTATGGCTACCGGGCCAGAGTCCGGGCAGTCCGGGCAGTGGACACAGTCACTCCAA  
80▶ A L S C D L T T F T L D L Y H R S Y G Y R A R V R A V D N S Q Y S N

901 CTGGACCACCACTGAGACTCGTTCACAGTGGATGAAGTGATTCTGACAGTGGATAGCGTACTCTGAAAGCAATGGACGGCATCATCTATGGGACAATC  
113▶ W T T T E T R F T V D E V I L T V D S V T L K A M D G I I Y G T I

**BspEI (1082)**  
**BsaBI (1074)**  
1001 CATCCCCCAGGCCACGATAACCCTGCAGGGATGAGTACGAACAAGTCTTCAAGGATCTCCGAGTTTACAAGATTTCCATCCGGAAGTTCTCAGAAC  
147▶ H P P R P T I T P A G D E Y E Q V F K D L R V Y K I S I R K F S E

1101 TAAAGAATGCAACCAAGAGAGTGAACAGGAAACCTTACCCTCACGGTCCCCATAGGGGTGAGAAAGTTTGTGCAAGGTGCTGCCCGCTTGAATC  
180▶ L K N A T K R V K Q E T F T L T V P I G V R K F C V K V L P R L E S

1201 CCGAATTAACAAGGCAGAGTGGTCGGAGGAGCAGTGTTTACTTATCACGACGGAGCAGTATTTCACTGTGACCAACCTGAGCATCTTAGTCATATCTATG  
213▶ R I N K A E W S E E Q C L L I T T E Q Y F T V T N L S I L V I S M

**XmaI (1353)**  
1301 CTGCTATTCTGTGAATCCTGGTCTGTCTGGTTCTCCAGTGGTACATCCGGCACCCGGGAAGTTGCCTACAGTCTGGTCTTCAAGAAGCCTCAGGACT  
247▶ L L F C G I L V C L V L Q W Y I R H P G K L P T V L V F K K P H D

**DraIII (1444)**  
**XcmI (1439)** **Tth111I (1492)**  
1401 TCTTCCCAGCCAACCTCTCTGCCAGAAACTCCCAGTGCATTCACATCGTGGACCTGGAGGTTTTCCCAAAGGTGTCAGTACAGCTGAGAGACTCAGT  
280▶ F F P A N P L C P E T P D A I H I V D L E V F P K V S L E L R D S V

1501 CCTGCATGGCAGCACCGACAGTGGCTTTGGCAGTGGTAAACCATCACTTCAGACTGAAGAGTCCCAATCCTCCTCCCTGGCTCCCACCCAGATACAG  
313▶ L H G S T D S G F G S G K P S L Q T E E S Q F L L P G S H P Q I Q

1601 GGGACTCTGGGAAAAGAAGATCTCCAGGGCTACAGGCCACCTGTGGGACAACACGGACAGTGGGATCTGCCTGAGGAGCCCGGCTTACACTCCAGCA  
347▶ G T L G K E E S P G L Q A T C G D N T D S G I C L Q E P G L H S S

**Bsp120I (1702)** **HpaI (1759)**  
**EcoO109I (1701)**  
1701 TGGGGCCCGCCTGGAAGCAGCAGCTTGGATATACCCATCAGGACCAGGATGACAGTACGCTTAACTAGTCCAGAAGTCTCCAGGGCAGCCTAAGTACAC  
380▶ M G P A W K Q Q L G Y T H Q D Q D D S D V N L V Q N S P G Q P K Y T

**NsiI (1805)** **Bsu36I (1849)** **Tth111I (1861)**  
1801 ACAGGATGCATCTGCCTTGGCCATGTCTGTCTCCTAGAACCTAAAGCCCTGAGGAGAAAGACCAAGTCATGGTGACATTCCAGGGCTACCAGAAAACAG  
413▶ Q D A S A L G H V C L L E P K A P E E K D Q V M V T F Q G Y Q K Q

1901 ACCAGATGGAAGGCAGAGGCAGCAGGCCAGCAGAATGCTTGGACGAAGAGATTCCTTGGACAGATGCCTTTGATCCTGAAGTGGGGTACACCTGCAGG  
447▶ T R W K A E A A G P A E C L D E E I P L T D A F D P E L G V H L Q

**XcmI (2086)**  
2001 ATGATTTGGCTTGGCCCTCACCAGCTCTGGCCGAGGTTATTTGAAACAGGAGTCTCAAGGGATGGCTTCTGCTCCACCAGGGACACCAAGTAGACAGTG  
480▶ D D L A W P P P A L A A G Y L K Q E S Q G M A S A P P G T P S R Q W

**BglIII (2148)**  
2101 GAATCAACTGACCGAAGAGTGGTCACTCCTGGGTGTGGTTAGCTGTGAAGATCTAAGCATAGAAAGTTGGAGGTTTGGCCATAAACTTGACCCTCTGGAC  
513▶ N Q L T E E W S L L G V V S C E D L S I E S W R F A H K L D P L D

**BstEII (2247)**  
2201 TGTGGGGCAGCCCTGGTGGCCTCCTGGATAGCCTTGGCTTAACCTGGTCACCTGGCGTTGATCTCCAGCCTGAGGTAGAAGAATGACAGCGGCTAA  
547▶ C G A A P G G L L D S L G S N L V T L P L I S S L Q V E E •

**NheI (2323)** **NcoI (2318)** **MscI (2329)**  
2301 GAGTATTGTATTCCAGCCATGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAAGTGAATGCAGTAAAAAATGCTT

**HpaI (2461)** **MfeI (2472)**  
2401 TATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAACAAACAATTGCATTTTATGTTTCAGGTT

2501 CAGGGGGAGGTGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAAATCTAAAATACAGCATAGCAAACTTTAACCTCCAATCA  
2601 AGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATG

EcoRI (2557)

2701 GAGTTTAAGATATAGTGATTTTTCCAAGGTTTGAAGTCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCCACATTCCTTTTTAGTAAAATA  
2801 TTCAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTGT  
2901 AGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCC  
141 • N R T Y K L P I L E

SapI (2739) SspI (2796)

3001 TCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGA  
129 E 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 G C P S V  
BstXI (3100)

3101 CCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCACAGCAGACCAATGGC  
96 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

StuI (3235)

3201 AATGGCTTCCAGCACAGCAGTGACCTGCCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCCGACATGG  
63 I 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  
3301 TGCTTGTGCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGTCTTATGGTGGCCCTCC  
29 H 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

AseI (3443)

3401 TATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACCTAAC

SacI (3500) SpeI (3598)

3501 GAGCTCTGCTTATATAGACCTCCCACCGTACACGCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTACGACATTTTGAAAGTCCCCTGTTGATTTAC  
3601 TAGTCAAACAAACTCCCATTGACGTCAATGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGC

SnaBI (3726)

3701 ATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCCATAAGGTCATGACTGGGCATAATGCCAGGGGGCCATTTAC

NdeI (3831)

3801 CGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGACTGCCAAGTGGGCGAGTTTACCGTAAATACTCCACCCATTGACGTCAATG  
3901 GAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGCTGTTGGGCGGTGAGCCAGGGGGCCATTTACCGTAAGT

Pacl (4017) BspLU11I (4027)

4001 TATGTAACGCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCT  
4101 CCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCC  
4201 CTCGTGCGCTCTCTGTTCCGACCTGCCGCTTACCGGATACCTGTCCGCTTCTCCCTTCCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGT

ApaLI (4341)

4301 ATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCAGAACCCCCGTTCCAGCCGACCGTGCCTTATCCGGTAACTATCGTCTTGA  
4401 GTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGTACAGAGTCTTGAAG  
4501 TGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCG  
4601 GCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGATCTCAAGAAGATCCTTTGATCTTTTCTAC

EagI (4777)

4701 GGGGCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGCCGCAATAAAATATCTTTAT  
4801 TTTCATTACATCTGTGTGTTGGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAACGAAACAAACAACTAGCAAATAGGCTGT  
4901 CCCAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA