



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

**Psp1406I (203)** **HindIII (245)** **Bsu36I (291)**  
201 GTGAACGTTCTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCCGCCGCCCTACCTGAGGGCC  
**EcoNI (287)**  
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

**KasI (535)** **AgeI (552)** **BspHI (560)**  
501 TCTGTTCTGGCGGTTACAGATCCAAGCTGTGACCGCGGCTACCTGAGATCACCGGTCATCATGAACCGGCTCCGGTTGCACGCCTCACGCCGTTGGA  
1 M N R L R V A R L T P L E  
601 GCTTCTGCTGCTGATGTCGCTGCTGCTCGGGACGCGGCCACGGCAGTCCAGGCCACTGCAGTGTACAGCGTCCGTCCTCCGGGAATCCTGAAC  
13 L L L S L M S L L L G T R P H G S P G P L Q C Y S V G P L G I L N  
701 TGCTCCTGGGAACCTTTGGGCGACTGGAGACTCCACCTGTGCTGTATCACCAGAGTCAAGAAATACCATCCCAATAGAGTCTGGGAGGTGAAGGTCCTT  
47 C S W E P L G D L E T P P V L Y H Q S Q K Y H P N R V W E V K V P  
801 CCAAACAGAGTTGGGTGACCATTCCCGGGAACAGTTCACCATGGCTGACAAACTCCTCATCTGGGGACACAAAAGGACGGCCTCTGTGGTCTCTGT  
80 S K Q S W V T I P R E Q F T M A D K L L I W G T Q K G R P L W S S V  
**BstEII (813)** **XmaI (824)** **NcoI (839)**  
901 CTCTGTGAACCTGGAGACCCAAATGAAGCCAGACACACCTCAGATCTTCTCTCAAGTGGATATTTCTGAGGAAGCAACCTGGAGGCCACTGTGCAGTGG  
113 S V N L E T Q M K P D T P Q I F S Q V D I S E E A T L E A T V Q W  
**BglII (941)** **KasI (999)**  
1001 GCGCCGCCGTGTGGCCACCGCAGAAAGCTCTCACCTGTGAGTCCGGTACAAGGAATGCCAGGTGAAGCATGGACCCGGCTGGAGCCCGAGTGAAGA  
147 A P P V W P P Q K A L T C Q F R Y K E C Q A E A W T R L E P Q L K  
**BbsI (1095)**  
1101 CAGATGGGCTGACTCCTGTTGAGATGCAGAACCTGGAACCTGGCACCTGCTACCAGGTGTCTGGCCGCTGCCAGTGGAGAACGGATATCCATGGGGCGCA  
180 T D G L T P V E M Q N L E P G T C Y Q V S G R C Q V E N G Y P W G E  
1201 GTGGAGTTCGCCCTGTCTCCAGACGCCATTCTTAGATCCTGAAGATGTGTGGGTATCGGGGACCGTCTGTGAAACTCTGGCAAACGGGACGCCCTG  
213 W S S P L S F Q T P F L D P E D V W V S G T V C E T S G K R A A L  
1301 CTTGTCTGGAAGACCCAAAGACCTTGTGTGACGTTACACAGTCTGGTTGGGGCTGGAGATATTACTACAACCAAGAAGAGGTCCTGCTGCA  
247 L V W K D P R P C V Q V T Y T V W F G A G D I T T T Q E E V P C C  
1401 AGTCCCCTGTCCCTGCATGGATGGAGTGGGCTGTGGTCTCTCTGGCAACAGCACCAGCTGGGTGCCTCCACCAACCTGTCTCTGGTGTGCTGGCTCC  
280 K S P V P A W M E W A V V S P G N S T S W V P P T N L S L V C L A P  
**BstEII (1557)**  
1501 AGAATCTGCCCCCTGTGACGTGGGAGTGGAGTGTGATGGGAGCCAGGGATAAAGGTGACCTGGAACAAGGACCAGGAACCAATTGGAGTATGTG  
313 E S A P C D V G V S S A D G S P G I K V T W K Q G T R K P L E Y V  
1601 GTGGACTGGGCTCAAGATGGTGACAGCTGGACAAGCTCAACTGGACCCGCTCCCCCTGGAACCTCAGCACATTGTTACCAGGGGAGTTCAAAGGAG  
347 V D W A Q D G D S L D K L N W T R L P P G N L S T L L P G E F K G

**SmaI (1700)** **Bst1107I (1729)**  
1701 GGGTCCCCTATCGAATTACAGTACTGACGTATCTGAGGATTAGCTGCTGCACCCTCAGTTTGGGATTACAGAGGAGTTAGTACCCCTTGTGCG  
380 G V P Y R I T V T A V Y S G G L A A A P S V W G F R E E L V P L A G  
1801 GCCAGCAGTTTGGCGACTTCCAGATGACCCCCAGGGACACCTGTTGTAGCCTGGGAGAAGTACCAAGACACAGCTCAGAGGCCAGGCTACTCACTAC  
413 P A V W R L P D D P P G T P V V A W G E V P R H Q L R G Q A T H Y

**StuI (1920)**  
1901 ACCTTCTGCATACAGAGCAGAGGCTTCCACTGTCTGCAGGAACGTGAGCAGTCAAACCCAGACTGCCACTCTGCCAACCTTCACTCGGGTTCCTTCA  
447 T F C I Q S R G L S T V C R N V S S Q T Q T A T L P N L H S G S F

**Tth111I (2010)** **Bsp120I (2034)**  
2001 AGCTGTGGGTGACGGTGTCCACCGTTGCAGGACAGGGCCACCTGGTCCCGACCTTCACTTCCACTACCAGATAATAGGATCAGGTGGAAAGCTCTGCC  
480 K L W V T V S T V A G Q G P P D L S L H L P D N R I R W K A L P  
2101 CTGGTTTCTGTCCCTGTGGGTTGCTTCTGATGGGCTGTGGCCTGAGCCTGGCCAGTACCAGGTGCCTACAGGCCAGGTGCTTACACTGGCGACACAAG  
513 W F L S L W G L L L M G C G L S L A S T R C L Q A R C L H W R H K  
2201 TTGCTTCCCAGTGGATCTGGGAGAGGTTCTGATCCTGCCAACAGCAATTCTGGGCAACCTTACATCAAGGAGGTGAGCCTGCCCAACCGCCCAAG  
547 L L P Q W I W E R V P D P A N S N S G Q P Y I K E V S L P Q P P K  
**XmnI (2388)**  
2301 ACGGACCCATCCTGGAGTGGAGGAAGTGGAGTACAGCCTGTTGTGGAGTCCCTAAAGCCTCTGCCCGATTACTCTGGGTATGAGAAACACTCTCT  
580 D G P I L E V E E V E L Q P V V E S P K A S A P I Y S G Y E K H F L  
**NheI (2453)**  
2401 GCCACACCAGAGGAGCTGGGCCTTCTAGTCTGATCTGCTTACGGCTAGGGGCGTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAC  
613 P T P E E L G L L V •

**HpaI (2591)**  
2501 CACAACCTAGAATGCAGTGAACCAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACCAAGTTAACAA  
**MfeI (2602)** **EcoRI (2687)**  
2601 AACAAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCATAAATA

2701 CAGCATAGCAAACCTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCAT  
2801 TAGCTGTTTGAGCCTCACCTTCTTTTCATGGAGTTAAGATATAGTGATTTTTCCAAGGTTTGAAGTCTCTTCATTTCTTTATGTTTTAAATGCACT

2901 **SspI (2926)** **SwaI (2940)**  
GACCTCCACATTCCCTTTTGTAGTAAATATTCAGAAAATATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTC

3001 AAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAG  
141 •

3101 TTCCTGGTACTTGAGGGGATGAGTTCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGA  
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  
**SacI (3201)**

3201 TGAGCTCTGCACATGCCACAGGGGTGACCACCTGATGGATCTGCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCCTT  
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

3301 CTGCCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGAGGCCTCAATGTGGACAGCAGAGATGATCTCCCA  
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  
**StuI (3365)**

3401 GTCTTGGTCTGATGGCCGCCGACATGGTGTCTTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACAGCTCCAGATCCTGCTGAG  
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  
**BspHI (3515)**  
**BbsI (3511)**

3501 **XmnI (3507)** **AseI (3573)**  
AGATGTTGAAGGTCCTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGC  
6 I N F T K M

3601 GTCTCCAGCTTATCTGACGGTTCATAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTT  
**SacI (3630)**

3701 ACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTAT  
**SpeI (3728)**

3801 CCACGCCATTGATGACTGCCAAAACGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTCATGT  
**SnaBI (3856)**

3901 ACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGTACTGCCAAGTGGGCAGTTTA  
**NdeI (3961)**

4001 CCGTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCAATGGGGCGGGGTCGTTGGGC

4101 GGTAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATTAAAGAACATGTGAGCAAAAAGCCAGCAAAAAGCCAGGAACCGTAAAAA  
**PacI (4147)** **SdaI (4139)** **BspLU11I (4157)**

4201 GGCCGCTTGTGCGGTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAA  
**BspLU11I (4157)**

4301 AGATACCAGGCGTTTCCCTGGAAGCTCCCTCGTGGCTCTCTGTTCGACCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCG

4401 TGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACAGCCGACCG  
**ApaLI (4471)**

4501 CTGCGCTTATCCGGTAACTATCGTCTTGTAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGG

4601 TATGTAGGCGGTGTACAGAGTCTTGAAGTGGTGGCCTAACTACGGTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCT

4701 TCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGCAAGCAGCAGATTACGCGCAGAAAAAAGG

4801 ATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGATTTTGGTCATGGCTAGTTAATTAACATTT  
**PacI (4887)** **SwaI (4896)**

4901 **EagI (4907)**  
AAATC AGCGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAAC  
**NotI (4906)**

5001 GAAACAAAACAACTAGCAAAATAGGCTGTCCCAAGTCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA