



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

**HindIII (245)** **Bsu36I (291)**  
**Psp1406I (203)** **PvuII (239)** **EcoNI (287)**  
201 GTGAACGTTCTTTTTCGCAACGGGTTTCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCCGCCGCCCTACCTGAGGCC  
301 GCCATCCACGCCGGTTGAGTGCCTTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

**NgoMIV (441)** **NaeI (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGTCTTTGTTTCGTTT

**KasI (535)** **AgeI (552)** **BspLU11I (560)** **NcoI (590)**  
501 TCTGTTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCCCTACCTGAGATCACCGGTCAACATGTCTGACAGTGGACCACAGCTTGATTCCATGGGTAG  
1 M S D S G P Q L D S M G S  
**Tth111I (674)**  
601 TCTGACCATGAAATCTCAACTTCAGATCACTGTCATCTCAGCCAAACTTAAAGAAAATAAAAAGAATTGGTTTGGACCAAGTCCTTATGTAGAAGTCACA  
13 L T M K S Q L Q I T V I S A K L K E N K K N W F G P S P Y V E V T  
701 GTAGATGGACAGTCAAAGAAGACAGAAAATGCAATAATACAAACAGTCCCAAGTGAAGCAGCCCTCACAGTTATTGTTACCCCTACGAGTAAATAT  
47 V D G Q S K K T E K C N N T N S P K W K Q P L T V I V T P T S K L  
801 GTTTTCGTGTGGAGTACCAGACCTGAAGTCTGATTTTTATTGGGAAGTCTGGATTAGATATTTATGAAACATTAAGTCAAACATATGAAACT  
80 C F R V W S H Q T L K S D V L L G T A G L D I Y E T L K S N N M K L  
901 TGAAGAAGTAGTTATGACTTTGACGCTTGTAGGTGACAAAGACCAACAGAGACGATGGGAGATTTGTCAGTTTGTCTTGTGGCTGCAAGTAGAAGCT  
113 E E V V M T L Q L V G D K E P T E T M G D L S V C L D G L Q V E A

**Scal (1036)**  
1001 GAGGTTGTTACTAACGGTAAACGTCATGCTCCGAGAGTACTACACAGAATGATGATGGCTGACAGAACAGAGATGATACAAGAGTGAACACAAATGGAT  
147 E V V T N G E T S C S E S T T Q N D D G C R T R D D T R V S T N G

**Bsu36I (1108)** **XbaI (1189)**  
1101 CAGAGGACCTGAGGTTGCAGCGTCAGGGGAAAACAAGAGGGCCAATGGGAACAATTCTCCGTCCTTTCAAATGGTGGTTTTAAGCCTTCTAGACCTCC  
180 S E D P E V A A S G E N K R A N G N N S P S L S N G G F K P S R P P  
1201 TAGACCTTCGAGACCACCTCCACCCACCCACGAGACGCTTCTGTCAATGGCTCACCATCCACGAATTCTGACAGTGTGGATCTAGTACAGGCTCC  
213 R P S R P P P P T P R R P A S V N G S P S T N S D S D G S S T G S

**StuI (1396)** **AvrII (1393)**  
**AseI (1356)** **Bsp120I (1389)**  
1301 TTGCCACCAACAATAACAATGTAATAACAAGTACATCTGAAGGAGCAACATCTGGATTAATAATTCCTTACTATATCTGGAGGCTCGGGCCCTAGGC  
247 L P P T N T N V N T S T S E G A T S G L I I P L T I S G G S G P R  
1401 CTCTGAATCTGTAAGCAAGCTCCCTACCACCTGGTGGGAGCAGAGAGTAGACCAGCATGGGCGTGTACTATGTAGACCATGTTGAAAAGCGAAC  
280 P L N A T V Q A P L P P G W E R R V D Q H G R V Y Y V D H V E K R Y T  
1501 AACATGGGATAGACCAGAACCTCTACCTCCTGGCTGGGAACGGCGTGTGGACAATATGGGACGTATTTATTATGTTGATCATTTACACAAGAACCACAACA  
313 T W D R P E P L P P G W E R R V D N M G R I Y Y V D H F T R T T T

**BspEI (1625)**  
1601 TGGCAGAGGCCAACCTTGAATCTGCCGAACATGAACAGTGGCAGCTACAGCGTAGTCAGCTTCAGGGAGCAATGCAGCAGTTTAAACAGAGATTCA  
347 W Q R P T L E S V R N Y E Q W Q L Q R S Q L Q G A M Q Q F N Q R F  
1701 TCTATGGGAATCAAGATTTGTTGCTACATCACAAAACAAGAATTTGATCCGCTTGGCCGTTGCCCTGGATGGGAGAAGAGAAGTATGATGCAATGG  
380 I Y G N Q D L F A T S Q N K E F D P L G P L P P G W E K R T D S N G  
1801 CAGAGTGTATTTGTCAACCACAACACTCGGATTAAGTACTCAGTGGGAAGACCCAGAAAGCAAGTCAAGTAAATGAAAAGCCCTTACCAGAAGGCTGGGAA  
413 R V Y F V N H N T R I T Q W E D P R S Q G Q L N E K P L P E G W E

**Bsp120I**  
1901 ATGAGATTCACAGTGGATGGAATTCATATTTTGTGGACCACAATAGAAGAGCAACTACTTATATAGATCCACGAACGGGAAAATCAGCCTTAGACAATG  
447 M R F T V D G I P Y F V D H N R R A T T Y I D P R T G K S A L D N

**MscI (2069)**  
2001 GGCCCCAGATAGCCTATGTGCGGGACTTCAAGGCAAAAGTTTCAAGTATTTCCGGTCTGGTGCCAGCAACTGGCCATGCCACAGCATATAAAGATCACAGT  
480 G P Q I A Y V R D F K A K V Q Y F R F W C Q Q L A M P Q H I K I T V  
2101 GACAAGAAAAACATTGTTGAGGATTCCTTTCAGCAGATCATGAGCTTCAGCCCGCAAGACCTGAGAAGACGTTTGTGGGTGATTTTCCAGGAGAAGAA  
513 T R K T L F E D S F Q Q I M S F S P Q D L R R R L W V I F P G E E  
2201 GGTTTAGATTATGGAGGTGTAGCAAGAGAATGTTTCTTTTGTGCATGAAGTGTGAACCAATGTATTGCCTGTTTGAATATGCAGGGAAGGATA  
547 G L D Y G G V A R E W F F L L S H E V L N P M Y C L F E Y A G K D

**NeoI (2381)**  
2301 ACTACTGCCTGCAGATAAACCCCGTCTTACATCAATCCAGACCACCTGAAATACTTTCGTTTTATTGGCAGATTTATTGCCATGGCTCTGTTTCATGG  
580 N Y C L Q I N P A S Y I N P D H L K Y F R F I G R F I A M A L F H G  
2401 GAAATTCATAGATACCGGATTTCTTTACCATTCTATAAACGTATCCTGAATAAACCAAGTGGACTTAAGGATTTAGAATCTATTGATCCAGAATTTTAT  
613 K F I D T G F S L P F Y K R I L N K P V G L K D L E S I D P E F F  
2501 AATTCGCTCATCTGGGTTAAAGAAAAACAACATCGAAGAATGTGGTTTGGAAATGTACTTCTCAGTTGATAAAGAAATTCAGGTGAAATTAAGAGTCATG  
647 N S L I W V K E N N I E E C G L E M Y F S V D K E I L G E I K S H

**XhoI (2684)**  
2601 ATTTGAAACCGAATGGTGGCAATATTTCTGTGACAGAAGAAAAACAAGGAGGAATACATCAGGATGGTAGCTGAGTGGAGTTGTCTCGAGGTGTTGAAGA  
680 D L K P N G G N I L V T E E N K E E Y I R M V A E W R L S R G V E E

HindIII (2708) XmnI (2731)

2701 ACAGACACAAGCTTTCTTTGAGGGCTTTAATGAAATTCCTCAGCAATATTTGCAATATTTTGATGCGAAGGAATTAGAGGTTCTTCTGTGTGGGATG  
713▶ Q T Q A F F E G F N E I L P Q Q Y L Q Y F D A K E L E V L L C G M

2801 CAGGAGATTGATTTGAATGACTGGCAGAGACATGCCATCTACCGCCACTACACCAGAACAAGCAAGCAGATCATGTGGTTTTGGCAGTTTGTAAAGAAA  
747▶ Q E I D L N D W Q R H A I Y R H Y T R T S K Q I M W F W Q F V K E

2901 TTGATAATGAGAAGAGGATGAGACTTCTGCAGTTTGTACTGGAACCTGCCGATTGCCAGTGGGAGGATTTGCTGACCTTATGGGGAGTAATGGACCACA  
780▶ I D N E K R M R L L Q F V T G T C R L P V G G F A D L M G S N G P Q

BstEII (3035)

3001 GAAGTTCTGCATCGAAAAAGTTGGCAAAGAAAATTTGGTTACCCAGAAGCCATACTTGTTTAAACCGCCTGGACCTCCCACCTTACAAGAGCTATGAGCAA  
813▶ K F C I E K V G K E N W L P R S H T C F N R L D L P P Y K S Y E Q

MscI (3191) NheI (3185)

3101 CTGAAGGAAAAGCTGTTATTTGCCATTGAAGAACTGAAGGATTGGACAAGAGTAATTTGTTAGACCTTAAGCCACCAGAGGCCCTAGCTGGCCAGAC  
847▶ L K E K L L F A I E E T E G F G Q E • L F R P •

3201 ATGATAAGATACATTGATGAGTTGGACAAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAA

HpaI (3323) MfeI (3334)

3301 CCATTATAAGCTGCAATAAACAAGTTAAACAACAACATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAAA

3401 CCTCTACAAATGTGGTATGGAATTCATAATACAGCATAGCAAACCTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGG

3501 CATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCAAGGTTTGA

SwaI (3672)

3601 AGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAAATTCAGAATAATTTAAATACATCATTGCAATGAAAAATA

3701 AATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAT

3801 TGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCTCAAT  
141▶ • N R T Y K L P I L E E I T T K V L K G N M E I

SacI (3933)

3901 GAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGG  
117▶ L V F C D P A Y D S I L E R C M G C P S V V R I S R D V E D S Y P

StuI (4097)

4001 TGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTGGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGG  
83▶ H R V A V I T D F D K Q G N S V A S G I A I A E A C V T V R G I Y A

4101 CCTCAATGTGGACAGCAGAGATGCTCCCAGCTTTGGTCTGTAGTGGCCGCCGACATGGTCTTGTGTCCTCATAGAGCATGGTATCTTCTCAGT  
50▶ E I H V A S I I E G T K T R I A A G V H H K N D E Y L M T I K E T

XmnI (4239)

4201 GGCAGCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGC  
17▶ A V E V L E L D Q Q S I N F T K M

AseI (4305) SacI (4362)

4301 CGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCTACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTA

SpeI (4460)

4401 CCGCCATTTGCGTCAATGGGGCGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATGACGTCATGGGGTGG

SnaBI (4588)

4500 AGACTTGAAATCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGTAATAGCGATGACTAATACGTAGATGT

NdeI (4693)

4600 ACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATG

4700 ATACACTTGATGTACTGCCAAGTGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTC

SdaI (4871) PacI (4879) BspLUII (4889)

4800 ATTATTGACGTCAATGGGCGGGGTCGTTGGGCGTCCAGCAGCGGGCCATTTACCGTAAGTTATGTAACGCC 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 C A A A G G C C A G G A A C C G T 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 T 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

4898 GCAAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCCGGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCT

4998 CAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCTGGAAGCTCCCTCGTGCGCTCTCTGTTCCGACCTGCCGCTTAC

5098 CGGATACCTGTCCGCCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTG

ApaLI (5203)

5198 GGCTGTGTGCACGAACCCCCGTTACGCCGACCCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGG

5298 CAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGT

5398 ATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACACCCTGGTAGCGGTGTTTTTTT

5498 GTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTACGGGGTCTGACGCTCAGTGAACGAAAACTCACGTT

EagI (5639) PacI (5619) SwaI (5628) NotI (5638)

5598 AAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTGAA

5698 TCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGAAGTGCAGGTGCCAGAACATTTCTCT

5798 ATCGAA