



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

MfeI (82) EcoNI (96)

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

**HindIII (245)**  
**Psp1406I (203)** 201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCAGAGGGCTCGCATCTCTCTTACACGCCGCCGCCCTACCTGAGGCC

PvuII (239) EcoNI (287) Bsu36I (291)

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGTCTTTGTTTCGTTT

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCAACATGTGTGACCGGAATGGTGGTCGGCGGCTTCGACAGTG

AgeI (552) BspLU11I (560) 1▶ M C D R N G R L R Q W

**XcmI (631)** 601 GCTGATCGAGCAGATTGACAGTAGCATGTATCCAGGACTGATTTGGGAGAATGAGGAGAAGAGCATGTTCCGGATCCCTTGGAAACACGCTGGCAAGCAA

13▶ L I E Q I D S S M Y P G L I W E N E E K S M F R I P W K H A G K Q

**BamHI (671)**  
BsaBI (700) 701 GATTATAATCAGGAAGTGGATGCCTCCATTTTTAAGGCTTGGGAGTTTTTAAAGGGAAGTTTAAAGAAGGGGACAAAGCTGAACCAGCCACTTGAAGA

47▶ D Y N Q E V D A S I F K A W A V F K G K F K E G D K A E P A T W K

AgeI (851) **RsrII (848)** 801 CGAGGTTACGCTGTGCTTTGAATAAGAGCCAGATTTTGGGAAAGTGACGGACCGTCCCAACTGGACATTTCCGAGCCATACAAAGTTTACCGAATTGT

80▶ T R L R C A L N K S P D F E E V T D R S Q L D I S E P Y K V Y R I V

Bsu36I (901) 901 TCCTGAGGAAGAGCAAAAATGCAAACTAGGCGTGGCAACTGCTGGCTGCGTGAATGAAGTTACAGAGATGGAGTGGGTGCGTCTGAAATCGACGAGCTG

113▶ P E E E Q K C K L G V A T A G C V N E V T E M E C G R S E I D E L

StuI (1061) 1001 ATCAAGGAGCCTTCTGTGGACGATTACATGGGGATGATCAAAAGGAGCCCTTCCCGCCGGAGGCTGTCGGAGTCAGCTCCTCCAGACTGGTGGGGCG

147▶ I K E P S V D D Y M G M I K R S P S P P E A C R S Q L L P D W W A

**BsaBI (1173)** 1101 AGCAGCCCAGCACAGCGTGCCTGCTGACGGGTACACCACCTACGACGCGCACCATTCAGCATTCTCCAGATGGTGCATCAGCTTCTACTATGGGGG

180▶ Q Q P S T G V P L V T G Y T T Y D A H H S A F S Q M V I S F Y Y G G

**Bsp120I (1288)** 1201 CAAGCTGGTGGGCCAGGCCACCACCTGCCCGAGGGCTGCCGCTGTCCCTGAGCCAGCCTGGGCTGCCCGCACCAAGCTGATGGGCCGAGGGC

213▶ K L V G Q A T T T C P E G C R L S L S Q P G L P G T K L Y G P E G

EagI (1322) 1301 CTGGAGCTGGTGCCTTCCCGCCGGCGACCCATCCCGAGGAGCGACAGAGGCGAGGTGACCGGAAGCTGTTCCGGCACCTGGAGCGCGGGTGTCTGC

247▶ L E L V R F P P A D A I P S E R Q R Q V T R K L F G H L E R G V L

1401 TGCACAGCAGCCGGCAGGGCGTGTTCGTCAGCGGCTGTGCCAGGGCCGCTGTTCGACGCGCAACGCCGTGGTGTCAAAGGCGAGCCCAACAGCT

280▶ L H S S R Q G V F V K R L C Q G R V F C S G N A V V C K G R P N K L

1501 GGAGCGTGTGAGGTGGTCCAGGCTTTCGACACCAGCCAGTTCCTCCGAGAGTGCAGCAGTTCTATAACAGCCAGGGCCGGCTTCTGACGGCAGGGTG

313▶ E R D E V V Q V F D T S Q F F R E L Q Q F Y N S Q G R L P D G R V

**PvuII (1672)** 1601 GTGCTGTGCTTTGGGGAAGAGTTTCCGGATATGGCCCCCTTGCCTCCAAACTATTCTCGTGCAGATTGAGCAGCTGTATGTCCGGCAACTGGCAGAAG

347▶ V L C F G E E F P D M A P L R S K L I L V Q I E Q L Y V R Q L A E

**Tth111I (1759)** 1701 AGGCTGGGAAGAGCTGTGGAGCCGGCTCTGTGATGCAGCCCCGAGGAGCCGCCAGACCAGGTCTTCCGGATGTTCCAGATATTTGTGCCTCACA

380▶ E A G K S C G A G S V M Q A P E E P P P D Q V F R M F P D I C A S H

1801 CCAGAGATCATTTCAGAGAAAACCAAGATCACCGTCTAAGTGCCTGGTGGGGCCCCACCCCGTCTGCTCCTGCATCCATCCTCCTGTTACAG

413▶ Q R S F F R E N Q Q I T V •

**MscI (1907)**  
**NheI (1901)** 1901 TGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCT

**HpaI (2039)** MfeI (2050) 2001 ATTGCTTTATTTGTAACCATTATAAGCTGCAATAACAAGTTAAACAACAATTCATTCTTTATGTTTCAGGTTACGGGGAGGTGTTGGAGGTTT

**EcoRI (2135)** 2101 TTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTGAATCCTTTTC

2201 TGAGGGATGAATAAGGCATAGGCATCAGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTCTTTTCATGGAGTTTAAAGATATAGTATTT

**SspI (2374)** SwaI (2388) 2301 TCCCAAGTGTGAACTAGCTCTTCAATTTCTTTATGTTTAAATGCACTGACCTCCACATTCCCTTTTATGATAAATTCAGAAATAATTTAAATACAT

2401 CATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGG

2501 AACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTTCTCAATGGTGGTTTTGACCAGCT

141 • N R T Y K L P I L E E I T T K V L K

SacI (2649)

2601 TGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCAC  
122 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 V R I S R D V  
2701 CTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTG  
89 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 A E A C V T

StuI (2813)

2801 ACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTCTTGTGTCTCATAGAGCA  
55 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 K N D E Y L M  
2901 TGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCCTATAGTGAGTCGTATTATACTA  
22 T I K E T A V E V L E L D Q Q S I N F T K M

AseI (3021) SacI (3078)

3001 TGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACATAACGAGCTCTGCTTATATAGACCTC

SpeI (3176)

3101 CCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCCTTGATTACTAGTCAAAACAAACTCCCATTG  
3201 ACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGA

SnaBI (3304)

3301 CTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAAGTCAATGACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGG

NdeI (3409)

3401 CGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCCTAAATACTCCACCATTGACGTCAATGAAAAGTCCCTATTGGCGTACT

PacI (3595)

SdaI (3587)

3501 ATGGGAACATACGTCATTATTGACGTCAATGGCGGGGGTCTGTTGGCGGTGACGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAAT

BspLU11I (3605)

3601 TAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAC  
3701 AAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCTGTTCCGA  
3801 CCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGT

ApaLI (3919)

3901 TCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC  
4001 TTATCGCCACTGGCAGCAGCCACTGTTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACA  
4101 CTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAG  
4201 CGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTCTACGGGGTCTGACGCTCAGTGAAC

EagI (4355)

PacI (4335) SwaI (4344) NotI (4354)

4301 GAAAACCTACGTTAAGGGATTTTGGTATGCGTAGTTAATTAACATTTAAATCAGCGGCCAATAAAAATATCTTTATTTTCATTACATCTGTGTGTTGG  
4401 TTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAAACTAGCAAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCC  
4501 AGAACATTTCTCTATCGAA