



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTCCGCAATTGAACGGGTGCCTA  
**MfeI (82)**  
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGCAGTAGTCGCC

**HindIII (245)**  
**Psp1406I (203)** 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACCGCGCCCGCCGCTACCTGAGGCC  
**PvuII (239)**  
301 GCCATCCACGCGGTTGAGTGCAGTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC  
**Bsu36I (291)**

**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

**NcoI (560)**  
**BstEII (555)**  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTCACCATGGTTCAATGGAAGAGACTCTGCCAGCTGCATTACTT  
**KasI (535)** **AgeI (552)** **PvuII (586)**  
601 GTGGGCTCTGGGCTGCTATATGCTGTGGCCACTGTGGCTCTGAAACTTTCTTTCAGGTTGAAGTGTGACTCTGACCACTGGGTCTGGAGTCCAGGGAA  
1 M V Q W K R L C Q L H Y L  
13 W A L G C Y M L L A T V A L K L S F R L K C D S D H L G L E S R E

**ScaI (710)** **BstEII (777)**  
701 TCTCAAAGCCAGTACTGTAGGAATATCTGTATAATTTCTGAAACTTCCAGCAAAAGAGGTCTATCAACTGTTCCAGGGTCCACCGAGGGGACCAAGAGG  
47 S Q S Q Y C R N I L Y N F L K L P A K R S I N C S G V T R G D Q E  
80 CAGTGCTTCAGGCTATTCTGAATAACCTGGAGGTCAAGAAGAAGCGAGAGCCTTTACAGACACCCACTACCTCTCCCTCACCAGAGAGTGTGAGCACTT  
80 A V L Q A I L N N L E V K K K R E P F T D T H Y L S L T R D C E H F  
90 CAAGGCTGAAAGGAAGTTCATACAGTCCCACTGAGCAAAAGAAGGTGGAGTCCCTATTGCATACTCTATGGTATTGATGAGAAGATTGAAAACCTT  
113 K A E R K F I Q F P L S K E E V E F P I A Y S M V I H E K I E N F  
100 GAAAGGCTACTGCGAGCTGTGTATGCCCTCAGAACATATACTGTGTCCATGTGGATGAGAAGTCCCAAGAACTTTCAAAGAGGGCGGTCAAAGCAATTA  
147 E R L L R A V Y A P Q N I Y C V H V D E K S P E T F K E A V K A I

**BstXI (1127)**  
1101 TTTCTTGCTTCCCAAATGTCTTCATAGCCAGTAAGCTGGTTCCGGTGGTTTATGCCTCCTGGTCCAGGGTGAAGCTGACCTCAACTGCATGGAAGACTT  
180 I S C F P N V F I A S K L V R V V Y A S W S R V Q A D L N C M E D L

**XmaI (1221)**  
1201 GCTCCAGAGCTCAGTGCCGTGGAATACCTTCTGAATACATGTGGGACGGACTTTCCTATAAAGAGCAATGCAGAGATGGTCCAGGCTCTCAAGATGTTG  
213 L Q S S V P W K Y F L N T C G T D F P I K S N A E M V Q A L K M L

**Acc65I (1326)**  
1301 AATGGGAGGAATAGCATGGAGTACCTCCTAAGCACAAGAAACCCGCTGGAATATCACTTTGAGGTAGTGAGAGACACATTACACCTAACCA  
247 N G R N S M E S E V P P K H K E T R W K Y H F E V V R D T L H L T

**BamHI (1410)**  
1401 ACAAGAAGAAGGATCCTCCCTTATAATTTAACTATGTTTACAGGGAATGCGTACATTTGGCTTCCCGAGATTTGTCCTCAACATGTTTTGAAGAACC  
280 N K K K D P P P Y N L T M F T G N A Y I V A S R D F V Q H V L K N P

**ApaLI (1574)**  
1501 TAAATCCCAACAAGTATTGAATGGGTAAGACACTTATAGCCAGATGAACACCTCTGGGCCACCTTCAGCGTGACGGTGGATGCCTGGCTCTGTT  
313 K S Q Q L I E W V K D T Y S P D E H L W A T L Q R A R W M P G S V

**ClaI (1678)**  
1601 CCCAACCCCAAGTACGACATCTCAGACATGACTTCTATTGCCAGGCTGGTCAAGTGGCAGGGTTCATGAGGGAGACATCGATAAGGGTGCCTTATG  
347 P N H P K Y D I S D M T S I A R L V K W Q G H E G D I D K G A P Y  
1701 CTCCTGCTCTGGAATCCACCAGCGGGCTATCTGCGTTTATGGGGCTGGGACTTGAATTGGATGCTTCAAAACCATCACCTGTTGGCCAACAAGTTGA  
380 A P C S G I H Q R A I C V Y G A G D L N W M L Q N H H L L A N K F D  
1801 CCCAAAGGTAGATGATAATGCTCTTCAAGTCTTGAAGAATACCTACGTTATAAGGCCATCTATGGGACTGAACCTTTGAGACACACTATGAGAGCGTTGC  
413 P K V D D N A L Q C L E E Y L R Y K A I Y G T E L •

**NheI (1907)**  
1901 TACCTGTGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGT

**HpaI (2045)** **MfeI (2056)**  
2001 GATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACCAAGTTAAACAACAACCAATTGCATTTATTTATGTTTCAGGTTACAGGGGAGGTGTGG

**EcoRI (2141)**  
2101 AGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATC  
2201 CTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTGCCAATGTGCATTAGCTGTTGCAGCCTCACCTTCTTTCATGGAGTTTAAAGATATAGT

**SspI (2380)** **SwaI (2394)**  
2301 GTATTTTCCCAAGGTTTGAAGTACTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAAATATTTAA

**EcoO109I (2455)**  
2401 ATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAA  
2501 CAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGA  
141 • N R T Y K L P I L E E I T T K V  
**BstXI (2684)**  
2601 CCAGCTTGCCATTCTCAATGAGCACAAGCAGTCCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCT  
124 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 V R I S R

2701 GTCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAG  
91 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 I A E A C

**StuI (2819)**

2801 ACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGCTTGTTCCTCAT  
57 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 H K N D E Y

**XmnI (2961)**

2901 AGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGATGGCCCTCTATAGTGAGTCGTATT  
24 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 (3027)**

3001 ATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATA

**SpeI (3182)**

3101 GACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTC

3201 CCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAG

**SnaBI (3310)**

3301 CGATGACTAATACGTAGATGTA CTGCCAAGTAGAAAGTCCCATAAGGTCATGTACTGGGCATAATGCCAGGGCGGCCATTTACCGTCATTGACGTCAAT

**NdeI (3415)**

3401 AGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGC

**PstI (3594)**  
**SdaI (3593)**

3501 GTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTACGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAG

**PacI (3601)**

3601 GTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAG

3701 CATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGGCTCTCCTG

3801 TTCCGACCCTGCCGTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTA

**ApaLI (3925)**

3901 GGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGTAGTCCAACCCGGTAAGA

4001 CACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACG

4101 GCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCCACCGC

4201 TGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAG

**EagI (4361)**  
**NotI (4360)**

4301 TGGAACGAAAACACGTTAAGGGATTTTGGTCAATGGCTAGTTAATTAACATTTAAATCAGCGGCCGAATAAAAATATCTTTATTTTTCATTACATCTGTG

**PacI (4341)** **SwaI (4350)**

4401 TGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAAACTAGCAAAATAGGCTGTCCCGAGTCAAGTGCA

4501 GGTGCCAGAACATTTCTCTATCGAA