



125

**PvuI (7)**  
**SgfI (6)**  
1 GGATCTGGCATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA  
101 GAGAAGGTGGCGCGGGGTAACCTGGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

**HindIII (245)**  
**Psp1406I (203)** **PvuII (239)** **Bsu36I (291)**  
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTACGCGCCCGCCGCCCTACCTGAGGCC  
301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCGCCGCTAGGTAAGTTAAAGCTCAGGTCGAGACC

**NgoMIV (441)**  
**NaeI (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

**AgeI (552)** **BspHI (560)**  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCCCTACCTGAGATCACCGGTATCATGAGCCTCTCCATGAGAGATCCGGTATTCTGGGAC  
1 M S L S M R D P V I P G T

**BstEII (664)**  
601 AAGCATGGCCTACCATCCGTTCTTACCTCACCGGGCGCCGACTTCGCCATGAGCGCGGTGCTGGGTACCAGCCGCCGTTTCTCCCGCGCTGACGCTG  
13 S M A Y H P F L P H R A P D F A M S A V L G H Q P P F F P A L T L

**XcmI (743)**  
701 CCTCCCAACGGCGCGGGCGCTCTCGTGCCGGGCGCCCTGGCCAAGCCGATCATGGATCAATTGGTGGGGCGGCCGAGACCAGGATCCCGTTCTCCT  
47 P P N G A A A L S L P G A L A K P I M D Q L V G A A E T G I P F S

**BbsI (831)** **XcmI (869)**  
801 CCCTGGGGCCCCAGGCGCATCTGAGGCTTTGAAGACCATGGAGCCCCGAAGAAGAGTGGAGGACGACCCCAAGGTGCACCTGGAGGCTAAAGAAGTTG  
80 S L G P Q A H L R P L K T M E P E E E V E D D P K V H L E A K E L W  
901 GGATCAGTTTCAACAGCGGGGACCCGAGATGGTATTACCAAGTCGGGAAGCGAATGTTTCTCCATTTAAAGTGAAGTGTCTGGGCTGGATAAAAA  
113 D Q F H K R G T E M V I T K S G R R M F P P F K V R C S G L D K K  
1001 GCCAAATACATTTTATTGATGGACATTATAGCTGCTGATGACTGCTGTATAAATTTCAAAATCTCGGTGGATGGTGGCTGGTAAGGCCGACCCCGAAA  
147 A K Y I L L M D I I A A D D C R Y K F H N S R W M V A G K A D P E

**BsrGI (1112)**  
1101 TGCCAAAGAGGATGTACATTCACCCGGACAGCCCCGCTACTGGGGAACAGTGGATGTCCAAAGTCGTCACCTTTCCACAAACTGAAACTACCAACAACAT  
180 M P K R M Y I H P D S P A T G E Q W M S K V V T F H K L K L T N N I  
1201 TTCAGACAAACATGGATTTACTTTGGCCTTCCCAAGTATCAGCTACGTTGGCAGGGGAATTATAGTTTTGGTACTCAGACTATATTGAATCCATGCAC  
213 S D K H G F T L A F P S D H A T W Q G N Y S F G T Q T I L N S M H

**EcoRI (1390)**  
1301 AAATACCAGCCCCGTTCCACATTGTAAGAGCCAATGACATCTTGAAGTCCCTTATAGTACATTTCCGACATACTTGTTCGCCGAAACTGAATTCATCG  
247 K Y Q P R F H I V R A N D I L K L P Y S T F R T Y L F P E T E F I  
1401 CTGTGACTGCATACCAGAATAAGATAACCCAGTTAAAAATAGACAACAACCCCTTTGCAAAAGTTTCCGGGACTGGAATGGCCGAAGAGAAAA  
280 A V T A Y Q N D K I T Q L K I D N N P F A K G F R D T G N G R R E K  
1501 AAGAAAACAGTCCACCTGCAGTCCATGAGGGTGTGATGAAAGACAAAAAGGAGAATGGGACCTCTGATGAGTCTCCAGTGAACAAGCAGCTTTC  
313 R K Q L T L Q S M R V F D E R H K K E N G T S D E S S S E Q A A F  
1601 AACTGCTTCGCCAGGCTTCTTCCAGCCGCTCCACTGTAGGGACATCGAACCTCAAAGATTTATGTCACGCGAGGGTGAAGAGCGACGCCGAGGGCCG  
347 N C F A Q A S S P A A S T V G T S N L K D L C P S E G E S D A E A

**BglII (1742)**  
1701 AGAGCAAAGAGGAGCATGGCCCCGAGGCTGCGACGCGGCCAAGATCTCCACCACCAGTGGAGGAGCCTGCCGTGACAAGGGCAGCCCCGCGGTCAA  
380 E S K E E H G P E A C D A A K I S T T T S E E P C R D K G S P A V K  
1801 GGCTACCTTTTCTGCTGTGAGCGGCCCGGGACAGCGGGCGGCTGGACAAAGCGTGGCCGACTCACGCCATAGCCCCGCCACCATCTCGTCCAGCACT  
413 A H L F A A E R P R D S G R L D K A S P D S R H S P A T I S S S T

**NgoMIV (1950)**  
**NruI (1935)** **NaeI (1950)**  
1901 CGCGGCTGGGCGCGGAGGAGCGCAGGAGCCCGGTTCCGCGAGGGCACAGCGCCGCGCAAGGTGGAAGAGGCGCGCGCTCCCGGCAAGGAGGCTTCG  
447 R G L G A E E R R S P V R E G T A P A K V E E A R A L P G K E A F

**SfiI (2077)**  
2001 CGCCGCTCACGGTGCAGACGGACGCGGCCCGCGGCACCTGGCCAGGGCCCCCTGCCTGGCCTCGGCTTCGCCCGGGCCTGGCGGGCAACAGTCTT  
480 A P L T V Q T D A A A H L A Q G P L P G L G F A P G L A G Q Q F F

**SandI (2178)**  
2101 CAACGGGACCCGCTCTTCTGCACCCAGCCAGTTTGCATGGGGGGCGCTTCTCCAGCATGGCGCCGCTGGCATGGTCCCCTCTGGCCAGGTT  
513 N G H P L F L H P S Q F A M G G A F S S M A A A G M G P L L A T V

**AgeI (2212)**  
**SgrAI (2211)** **BstXI (2234)**  
2201 TCTGGGGCTCCACCGTGTCTCGGCGCTGGATTCCACGGCCATGGCCTCTGCCGCTGGCGCAGGACTGTCCGGGGCTCCGCGGCCACCTGCCCT  
547 S G A S T G V S G L D S T A M A S A A A A Q G L S G A S A A T L P  
2301 TCCACCTCAGCAGCAGTCTCGGCTCTCAGGGCTGGCCATGTCCCTTTTCGGAAGCTGTCCCTTACCCTACAGTACATGGCCGAGCGGGGC  
580 F H L Q Q H V L A S Q G L A M S P F G S L F P Y P Y T Y M A A A A A  
2401 CGCCTCTCGGCGAGCTCCAGCTCGGTGCACCCCTTCTCAATCTGAACACCATGCGCCCGCGGCTGCGCTACAGCCCTACTCCATCCCG  
613 A S S A A A S S V H R H P F L N L N T M R P R L R Y S P Y S I P  
2501 GTGCCGGTCCCGGACGGCAGCAGTCTGCTCACCACCGCCTGCCTCCATGGCGCGCCGCGGGGCCCTGGACGGCAAGTGCAGCGCCCTGGCCGCA  
647 V P V P D G S S L L T T A L P S M A A A A G P L D G K V A A L A A  
2601 GCCCGCCTCGGTGGCAGTGGACTCGGGCTCTGAAGTCAACAGCGCTCCTCCAGCTCTCCTCAGCTCCATGCTTGTGCGCCAACTCTGCGCGGA  
680 S P A S V A V D S G S E L N S R S S T L S S S S M S L S P K L C A E  
2701 GAAAGAGGCGCCACAGCGAAGTGCAGAGCATCCAGCGGTTGGTTAGCGGCTTGAAGCAAGCGGACAGGTCGCCGAGCGCTCCCGTAGACCCGT  
713 K E A A T S E L Q S I Q R L V S G L E A K P D R S R S A S P •

2801 CCCAGACACGCTTTTCATTCCAGTC**NheI (2827)**CGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAAT

2901 **HpaI (2965)**  
GCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAACAAACAACAAATGCATTCAATTTTATGTTTCA

3001 **EcoRI (3061)**  
GGTTCAGGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACTTTAACCTCCAA

3101 ATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTT

3201 CATGGAGTTTAAGATATAGTGTATTTTCCCAAGTTTGAAGTACTGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTATGTA

3301 **SspI (3300)** **SwaI (3314)**  
AATATTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTTATTAGCGAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTT

3401 TAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGGATGAG  
141 • N R T Y K L P I L

3501 **SacI (3575)**  
TTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCACTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGG  
131 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 L E R C M G C P

3601 **BstXI (3604)**  
CTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCACAGCAGACCCAA  
97 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 Q G N S V A S G I

3701 TGGCAATGGCTTCAGCACAGACAGTACCTGCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGAC  
64 A 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

3801 **BspHI (3889)** **BbsI (3885)** **XmnI (3881)**  
ATGGTGCTTGTTCCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGATGGCC  
31 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 I N F T K M

3901 **AseI (3947)**  
CTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCAC

4000 **SacI (4004)**  
TAAACGAGCTCTGTTATATAGACCTCCCACCGTACACGCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCCTTGA

4100 **SpeI (4102)**  
TTTACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGACTGCCAA

4199 **SnaBI (4230)**  
AACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCC

4299 **NdeI (4335)**  
ATTACCCTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACG

4399 TCAATGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTGTTGGCGGTGAGCCAGGCGGGCCATTTACC

4499 **SdaI (4513)** **PacI (4521)** **BspLU11I (4531)**  
GTAAGTTATGTAACGCTG 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 A A A A G G C C A G A A C C G T A A A A A G G C C G T T G C T G G C G T T T T T C

4597 CATAGGCTCCGCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAAGTCAAGGTTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTG

4697 GAAGTCCCTCGTGCCTCTCTGTTCCGACCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTCGGGAAGCGTGGCGCTTTCTCATAGCTCAG

4797 CTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTCCAGCCGACCGCTGCGCTTATCCGGTAACTAT

4897 CGTCTTGAAGTCCAAACCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGT

4997 TCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTC

5097 TTGATCCGCAAAACAAACCCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATC

5197 **PacI (5261)** **SwaI (5270)**  
TTTTCTACGGGTCTGACGCTCAGTGGAAACGAAAACTCACGTTAAGGGATTTGGTCAATGGCTAGTTAATTAACATTTAAATCAGCGGCCGAATAAAAT

5297 ATCTTTATTTTACATCTGTGTGTTGGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAA

5397 TAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA