



**PvuI (7)**  
**SgfI (6)**
**MfeI (82)**

1 GGATCTGCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA  
 101 GAGAAGGTGGCGCGGGTAAACTGGGAAAGTGTCTGTACTGGCTCCGCCCTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

**HindIII (245)**
**Psp1406I (203)**
**Bsu36I (291)**

201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCCGCCCTACCTGAGGCC  
 301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCGCCGCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

**NgoMI (441)**  
**NaeI (441)**

401 GGGCTTTGTCCGGCGCTCCCTTGAGGCTACCTAGACTCAGCCGGCTCCACGCTTTCCTGACCTGCTTGTCAACTCTACGCTTTGTTTCGTTT

**NcoI (560)**  
**BstEII (555)**  
**AgeI (552)**

501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCTACCTGAGATCACCGTCCACATGGAGATTGGAAACCGGAGCGGAAGCGGGCACCGCC  
1▶ M E D S E P E R K R A R A

**SacII (611)**
**SnaBI (658)**  
**NgoMI (686)**  
**NaeI (686)**

601 GGACGAGCGCACCGGGTGGGAGCCCTCCGAGGACGAGGATGAGGACGACGAGGACTACGTACCTATGTGCCGTTGCGGCAGCGCCGCGACTACTG  
 13▶ D E A T A G G S R S E D E D E D E D E D Y V P Y V P L R Q R R Q L L

**Bsp120I (798)**

701 CTCCAGAAGTGTCTGACGCAAGACGCAAGGGCGCTACGGAGGAAGAGCAGCAGGACAGTGGCAGTGGAGCCCGAGGAGATGAGGACGACATCCCGCTGG  
 47▶ L Q K L L Q R R R K G A T E E E Q Q D S G S E P R G D E D D I P L  
 801 GCCCTCAGTCCAATGTGAGCCTCTGGATCAGCACCAGCCTCAAAGAGAAGGCTGAAGCAGCAAGGAGTCCGCCAAGGAAAAGCAACTGAAGGAAGA  
 80▶ G P Q S N V S L L D Q H Q H L K E K A E A R K E S A K E K Q L K E E  
**XmnI (901)**
**SpeI (991)**

901 AGAAAAGATTCTGGAGAGTGTGGCTGAAGGCCGAGCCTTGATGTCTGAGTGAAGGAAATGGCCAAAGGCATCACCTATGACGATCCAATCAAACCTAGTTGG  
 113▶ E K I L E S V A E G R A L M S V K E M A K G I T Y D D P I K T S W  
 1001 ACACCCCGCGTTATGTCCTGAGCATGTCTGAGGAGCGGCATGAGCGAGTTCGGAAGAAGTATCACATCTGGTGGAGGGCGATGGTATCCCGCCACCCA  
 147▶ T P P R Y V L S M S E E R H E R V R K K Y H I L V E G D G I P P P  
 1101 TCAAGAGCTCAAGGAGATGAAGTTTCTGACGATATCCTTCGGGGCTGAAAAAAGGGCATCCTCCACCAACACCCATTGATCCAGGGCATCCC  
 180▶ I K S F K E M K F P A A I L R G L K K K G I L H P T P I Q I Q G I P  
 1201 TACCATTCTGTCGGTGGGACATGATCGGCATTGCCTTCACGGGGTCAAGCAAGCACTGGTATTCACCTCTGCCAGTTCATGTTCTGCTGGAACAG  
 213▶ T I L S G R D M I G I A F T G S G K T L V F T L P V I M F C L E Q

**NruI (1357)**

1301 GAGAAGCGGTTGCCCTTCTCAAGCGAGAGGGGCTTATGGACTCATCATCTGCCCTCGCGAGAGCTGGCTCGGCAGACCCAGGCATCCTGGAGTATT  
 247▶ E K R L P F S K R E G P Y G L I I C P S R E L A R Q T H G I L E Y  
 1401 ACTGCCGCTGCTGCAGGAGGACAGCTCACCCCTCTGCCGCTGTGCCCTGTGCATCGGGGGCATGTCGGTGAAGGAGCAGATGGAGACCTCCGACATGG  
 280▶ Y C R L L Q E D S S P L L R C A L C I G G M S V K E Q M E T I R H G  
 1501 TGTGCACATGATGGTAGCCACCTGGACGCTCATGGATTTGCTGCAGAAGAAATGGTCAAGCTAGACATCTGCCGCTACCTAGCCCTGGATGAAGCT  
 313▶ V H M M V A T P G R L M D L L Q K K M V S L D I C R Y L A L D E A  
 1601 GACCGCATGATTGACATGGGCTTTGAGGGTGCATTCGTACCATCTTCTCTACTTCAAGGGCAACCGCAGACTCTGCTCTTCAAGTCCACCATGCCGA  
 347▶ D R M I D M G F E G D I R T I F S Y F K G Q R Q T L L F S A T M P

**XcmI (1718)**

1701 AGAAGATTCAAACCTTGGCAAGAGTGCCTTGGTAAAGCCTGTACCATCAATGTGGGTGCTGCTGGAGCAGCCAGCCTTGATGTCATCCAGGAGGTGGA  
 380▶ K K I Q N F A K S A L V K P V T I N V G R A G A A S L D V I Q E V E  
 1801 GTATGTGAAGGAGGAAGCAAGATGGTGTACTTGTGAGTGCCTGCAGAAGACACCCACCTGTGCTCATCTTTGCAGAGAAGAAAGCAGATGTGGAT  
 413▶ Y V K E E A K M V Y L L E L C L K T P P P V L I F A E K K A D V D  
 1901 GCCATTACGAATACCTCCTGCTCAAGGGTGTGAGGCTGTAGCCATTCATGGGGCAAAGACCAGGAAGAGCGGACCAAGGCCATTGAGGCATTCCGGG  
 447▶ A I H E Y L L L K G V E A V A I H G G K D Q E E R T K A I E A F R  
 2001 AAGGAAGAAGGAGCTCTAGTGGCCACAGATGTGGCTCTAAAGGCCTGGACTTTCTGCCATCCAGCATGTCACTAATGACATGCCTGAAGAGAT  
 480▶ E G K K D V L V A T D V A S K G L D F P A I Q H V I N Y D M P E E I  
 2101 AGAAAATATGTGCACAGAATTGGACCTTCGGATCCTATCCGATGAGGCTTCAAGCAAGGCCTGCGATGAGTCAAGTCAAGTCAAGTCAAGTCAAGT  
 513▶ E N Y V H R I G R T G R S G N T G I A T T F I N K A C D E S V L M

**Asp718 (2235)**  
**Acc65I (2235)**

2201 GACCTCAAAGCCTTGTGCTGGAGGCCAAGCAGAAGTACCACCTGTTCTGCAAGTGTGCTGACTGTGGGACGAGTCCATGCTGGACATTGGAGGAGAAC  
 547▶ D L K A L L L E A K Q K V P P V L Q V L H C G D E S M L D I G G E  
 2301 GGGGCTGTGCCCTTGTGGAGGCTTGGCCATCGGATCACTGACTGCCCAAACTTGAAGCTATGCAGACCAAGCAGGTGAGCAACATTGGCCGAAGGA  
 580▶ R G C A F C G G L G H R I T D C P K L E A M Q T K Q V S N I G R K D

**NcoI (2417)** **BamHI (2428)** **NdeI (2468)**

2401 CTACCTGCCCCACAGCTCCATGGACCTTCGGATCCTATCCCTATGATGTGCCAGACTATGTGGCTATCCATATGATGTTCTGATTATGCTGATACCCCT  
 613▶ Y L A H S S M D F G S Y P Y D V P D Y A G Y P Y D V P D Y A G Y P

**NheI (2525)**

2501 TATGATGTGCCAGACTATGCCTAAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTGGACAAACCACAACTAGAATGCAGTGAAAAAATGC  
 647▶ Y D V P D Y A •

**HpaI (2663)** **MfeI (2674)**

2601 TTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACATTGCATTATTTTATGTTTCAGG

**EcoRI (2759)**

2701 TTCAGGGGAGGTGTGGAGGTTTTTTAAGCAAGTAAACCTCTACAAATGGTATGGAATTTAAAATACAGCATAGCAAACTTTAACCTCAAAT

2801 CAAGCTCTACTTGAATCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTGGCAATGTGCATTAGCTGTTGCAGCCTCACCTCTTTCA

2901 TGGAGTTTAAGATATAGTGTATTTTCCCAAGTTTGAACCTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTATAGTAAA

Swal (3012)

3001 TATTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTA

3101 GTAGTTGGACTTAGGGAACAAAGGAACCTTAAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGGATGAGTT

144 • N R T Y K L P I L E

SacI (3273)

Ec1136II (3273)

3201 CCTCAATGGTGGTTTTGACCAGCTTGCCATTCACTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCGCACATGCCACAGGGGCT

130 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 S

3301 GACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCACAGCAGACCCAATG

97 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

3401 GCAATGGCTTCAGCACAGACAGTGACCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTGGTCTGATGGCCGCCCGACAT

63 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 H

BspHI (3587)

XmnI (3579)

3501 GGTGCTTGTTCCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTATGATGGCCCT

30 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

AseI (3645)

3601 CCTATAGTGAGTCGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAA

SacI (3702)

Ec1136II (3702)

3701 ACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAGTCCCGTTGATTT

SpeI (3800)

3801 ACTAGTCAAACAAACTCCCATTGACGTCAATGGGGTGAGACTTGAAATCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAAC

SnaBI (3928)

3901 GCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGTCACTGACTGGGCATAATGCCAGGCGGCCATTT

NdeI (4033)

4001 ACCGTCATTGACGTCATAGGGGGCTACTTGGCATATGATACACTTGTACTGCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAA

4101 TGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGCGGGGGTCTGTTGGCGGTGAGCCAGGCGGGCCATTTACCGTAA

PacI (4219)

SdaI (4211)

SbfI (4211)

PciI (4229)

BspLU11I (4229)

4201 GTTATGTAACGCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG

4301 CTCGCCCCCTGACGAGCATCACAATAATCGACGCTCAAGTCAGAGGTGGCAAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCT

4401 CCTCGTGGCTCTCCTGTTCCGACCTGCGGCTTACCAGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGATG

4501 GTATCTCAGTTCGGTGTAGTTCGCTCAAGCTGGGCTGTGTGCAGAACCCCGTTCCAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTT

4601 GAGTCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGTACAGAGTCTTGA

4701 AGTGGTGGCCTAACTACGGCTACACTAGAAAGCAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATC

4801 CGGCAAAACAAACCCGCTGGTAGCGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT

EagI (4979)

PacI (4959) Swal (4968) NotI (4978)

4901 ACGGGTCTGACGCTCAGTGGAAACGAAACTCACGTTAAGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTT

5001 ATTTTCATTACATCTGTGTGTTGGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCT

5101 GTCCCCAGTGAAGTGCAAGTGCCAGAACATTTCTCTATCGAA