



PvuI (7)
SgfI (6) 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA **MfeI (82)**

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTGTCTGTACTGGCTCCGCCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGCTTTTGTTCGTTT **NgoMIV (441)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGGTTCGACCAGCATGCTACGAACCGCAGGCAGGGACGGCCTCTG **SalI (558)** **SphI (566)**
1 M L R T A G R D G L C

XhoI (625) 601 TCGCCTGTCCACCTACTTGAAGAAGCTCAGAGCTGTGAACTGAAGAAGTTCAAGTTATACCTGGGACCGGCACAGAGCTGGGAGAAGCAAGATCCCC **BsrBI**
11 R L S T Y L E E L E A V E L K K F K L Y L G T A T E L G E G K I P

701 TGGGAAGCATGGAGAAGGCCGGTCCCTGGAAATGGCCAGCTGCTCATCACCCTTCGGGCCAGAGGGCTGGAGTTGGCTCTCAGCACCTTTG **StuI (770)**

45 W G S M E K A G P L E M A Q L L I T H F G P E E A W R L A L S T F **BsrBI**

801 AGCGGATAAACAGGAAGGACCTGTGGGAGAGAGACAGAGAGAGGACCTGGTGAAGGATACCCACCTGGTGGCCGCTCCTCACTTGGGAACAGTCAAC **BsrBI**
78 E R I N R K D L W E R G Q R E D L V R D T T P P G G P S S L G N Q S T

901 ATGCCTTCTGGAAGTCTCTCTTGTCACTCCAAGAAAAGATCCCCAGGAAACCTACAGGACTATGTCCGAGGAAATCCGGCTCATGGAAGACCGCAAT **Tth111I (958)**
111 C L L E V S L V T P R K D P Q E T Y R D Y V R R K F R L M E D R N

AvrII (1005) 1001 GCGCGCTAGGGGAATGTGTCAACCTCAGCCACCGGTACACCCGGCTCCTGCTGGTGAAGGAGCACTCAAACCCATGCAGGTCCAGCAGCAGCTTCTGG **BssHII (1000)** **AgeI (1031)**
145 A R L G E C V N L S H R Y T R L L L V K E H S N P M Q V Q Q Q L L

1101 ACACAGGCCGGGACACGCGAGGACCTGGGACACCAGCTAGCCCACTCAAGATAGAGACCCTCTTTGAGCCAGACGAGGAGCGCCCCGAGCCACCGCG **NheI (1138)**
178 D T G R G H A R T V G H Q A S P I K I E T L F E P D E E R P E P P R

1201 CACCGTGGTCATGCAAGGCGCGGAGGATAGGCAAGTCCATGCTGGCACACAAGGTGATGCTGGACTGGGCGGACGGGAAGCTCTTCCAAGGAGATTT **NheI (1138)**
211 T V V M Q G A A G I G K S M L A H K V M L D W A D G K L F Q G R F

1301 GATTATCTTCTACATCAACTGCAGGGAGATGAACCAGAGTGCCACGGAATGCAGCATGCAAGACCTCATCTTCAAGCTGCTGGCCTGAGCCACGCGCC **SphI (1355)** **BssHII (1394)**
245 D Y L F Y I N C R E M N Q S A T E C S M Q D L I F S C W P E P S A

1401 CTCTCCAGGAGCTCATCCGAGTCCCGAGCGCCTCTTTTCATCATCGACGGCTTCGATGAGCTCAAGCCTTCTTTCCAGGATCCTCAGGACCTGGTG **SandI (1488)**
278 P L Q E L I R V P E R L L F I I D G F D E L K P S F H D P Q G P W C

1501 CCTCTGCTGGGAGGAGAACCAGCCAGGAGCTGCTTAAACAGCTTAATTCGGAAGAGCTGCTCCCTGAGCTATCTTTGCTCATCACCACAGGCC **SandI (1488)**
311 L C W E E K R P T E L L N S L I R K K L L P E L S L L I T T R P

1601 ACGGCTTTGGAGAAGCTCCACCGTCTGCTGGAGACCCAGGCATGTGGAGATCCTGGGCTTCTGAGGAGAAAGGAATACTTCTACAAGTATT **SandI (1488)**
345 T A L E K L H R L L L E H P R H V E I L G F S E A E R K E Y F Y K Y

1701 TCCACAATGCAGAGCAGGCGGGCAAGTCTTCAATTACGTGAGGACAACGAGCCTCTTCCACATGTGCTTCCCTGGTGTGCTGGTGGTGTG **SandI (1488)**
378 F H N A E Q A G Q V F N Y V R D N E P L F T M C F V P L V C W V V C

1801 TACCTGCCTCCAGCAGCAGCTGGAGGGTGGGGGCTGTTGAGACAGAGCTCCAGGACCACCACTGCAGTGATACCTGCTGAGTCTGATGCAA **PshAI (1841)** **BsrGI (1868)**
411 T C L Q Q Q L E G G G L L R Q T S R T T T A V Y M L Y L L S L M Q

1901 CCCAAGCCGGGGCCCGCCTCCAGCCCCACCAACCAGAGAGGGTGTGCTCCTTGGCGCAGATGGGCTCTGGAATCAGAAAATCCTATTTGAGG **Bsp120I (1910)**
445 P K P G A P R L Q P P P N Q R G L C S L A A D G L W N Q K I L F E

2001 AGCAGGACCTCCGGAAGCAGCGCTAGACGGGAAGACGTCTCTGCCTTCTCAACATGAACATCTTCCAGAAGGACATCAACTGTGAGAGGTACTACAG **BspEI (2009)**
478 E Q D L R K H G L D G E D V S A F L N M N I F Q K D I N C E R Y Y S

2101 CTTATCCACTTGAGTTTCCAGGAATCTTTGAGCTATGTACTATATCTGGACGAGGGGGAGGGCGGGCAGGCCAGACCAGGACGTGACCAGGCTG **EcoRI (2122)**
511 F I H L S F Q E F F A A M Y Y I L D E G E G G A G P D Q D V T R L

2201 TTGACCGATACCGGTTTTCTGAAAGGAGCTTCTGGCACTCACCAGCCGCTTCTGTTTGGACTCCTGAACGAGGAGACCAGGACCTGGAGAAGA **MluI (2210)**
545 L T E Y A F S E R S F L A L T S R F L F G L L N E E T R S H L E K

2301 GTCTCTGCTGGAAGGTCTCGCCGCACATCAAGATGGACCTGTTGAGTGGATCAAAGCAAAGCTCAGAGCGACGGCTCCACCCTGCAGCAGGGCTCCTT **BamHI (2348)**
578 S L C W K V S P H I K M D L L Q W I Q S K A Q S D G S T L Q Q G S L

2401 GGAGTTCTTCAAGTCTGTTACGAGATCCAGGAGGAGGTTTATCCAGCAGGCCCTGAGCCACTTCCAGGTGATCGTGGTCAAGCATTGCCTCCAAG **BamHI (2348)**
611 E F F S C L Y E I Q E E E F I Q Q A L S H F Q V I V V S N I A S K

2501 ATGGAGCACATGGTCTCCTGTTCTGTGAAGCGCTGCAGGAGCGCCAGGTGCTGCACTTGTATGGCGCCACTACAGCGCGGACGGGAAGACCGCG **Eco4VII (2531)**
645 M E H M V S S F C L K R C R S A Q V L H L Y G A T Y S A D G E D R

2601 CGAGGTGCTCCGAGGAGCGCACAGCTGTTGGTGCAGCTACCAGAGAGGACCGTTCTGCTGGACGCCTACAGTGAACATCTGGCAGCGCCCTGTGCAC **ApaLI (2694)**
678 A R C S A G A H T L L V Q L P E R T V L L D A Y S E H L A A A L C T

2701 CAATCCAAACCTGATAGAGCTGTCTCTGTACCGAAATGCCTGGGAGCCGGGGGTGAAGCTGCTCTGTCAAGGACTCAGACACCCCAACTGCAAACCT
711▶ N P N L I E L S L Y R N A L G S R G V K L L C Q G L R H P N C K L
2801 CAGAACCTGAGGCTGAAGAGGTGCCGATCTCCAGCTCAGCCTGCGAGGACCTCTCTGCAGCTCATAGCCAATAAGAATTTGACAAGGATGGATCTCA
745▶ Q N L R L K R C R I S S S A C E D L S A A L I A N K N L T R M D L
2901 GTGGCAACGGCGTTGATTCCCAGGCATGATGCTGCTTTGCGAGGGCCTGCGGCATCCCCAGTGCAGGCTGCAGATGATTGAGTTGAGGAAGTGCAGCT
778▶ S G N G V G F P G M M L L C E G L R H P Q C R L Q M I Q L R K C Q L
3001 GGAGTCCGGGGCTTGTGAGGAGATGGCTTCTGTGCTCGGCACCAACCCACATCTGTTGAGTTGGACCTGACAGGAAATGCAGTGGAGGATTTGGGCCTG
811▶ E S G A C Q E M A S V L G T N P H L V E L D L T G N A L E D L G L

BglII (3158)

3101 AGGTTACTATGCCAGGGACTGAGGCACCCAGTCTGCAGACTACGGACTTTGTGGCTGAAGATCTGCCGCTCACTGCTGCTGCTGTGACGAGCTGGCCT
845▶ R L L C Q G L R H P V C R L R T L W L K I C R L T A A A C D E L A
3201 CAACTCTCAGTGTGAACAGAGCCTGAGAGAGCTGGACCTGAGCTGAATGAGCTGGGGGACCTCGGGGTGCTGCTGTGTGAGGGCCTCAGGCATCC
878▶ S T L S V N Q S L R E L D L S L N E L G D L G V L L L C E G L R H P

BbrPI (3300) **NgoMIV (3335)**

3301 CACGTGCAAGCTCCAGACCTGCGGTTGGGCATCTGCCGGTGGGCTCTGCCGCTGTGAGGGTCTTTCTGTGGTCTCAGGCCAACCAACCTCCGG
911▶ T C K L Q T L R L G I C R L G S A A C E G L S V V L Q A N H N L R
3401 GAGCTGGACTTGTGTTCAACGACCTGGGAGACTGGGGCTGTGGTGTGGCTGAGGGGCTGCAACATCCCGCTGCAGACTCCAGAACTGTGGCTGG
945▶ E L D L S F N D L G D W G L W L L A E G L Q H P A C R L Q K L W L

AvrII (3594)

3501 ATAGCTGTGGCTCACAGCCAAGGCTTGTGAGAATCTTTACTTACCCTGGGATCAACCAGACCTTGACCGACCTTTACCTGACCAACAACGCCCTAGG
978▶ D S C G L T A K A C E N L Y F T L G I N Q T L T D L Y L T N N A L G
3601 GGACACAGGTGTCGACTGCTTTGCAAGCGGCTGAGCCATCCTGGCTGCAAACTCCGAGTCTCTGGTATTTGGGATGGACCTGAATAAAATGACCCAC
1011▶ D T G V R L L C K R L S H P G C K L R V L W L F G M D L N K M T H

Eco47III (3711) **XbaI (3775)** **MscI (3786)**

3701 AGTAGTTGGCAGCGCTTCGAGTAACAAAACCTTATTTGGACATTGGCTGCTGAATGGTCTATCTGCTGGCTCTTAGACTAGCTGGCCAGACATGAT
1045▶ S R L A A L R V T K P Y L D I G C •

3801 AAGATACATTGATGAGTTTGACAAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATT

HpaI (3918) **MfeI (3929)**

3901 ATAAGCTGCAATAAAACAAGTTAAACAACAACAATTGCATTCATTTTATGTTTCAGTTCAGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAACCTCT

EcoRI (4014)

4001 ACAAATGGGTATGGAATTTCAAATACAGCATAGCAAACTTAACTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAG
4101 GCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTCTTTTCATGGAGTTTAAGATATAGTGTATTTCCCAAGTGTGAACTAGCTC

SspI (4253) **SwaI (4267)**

4201 TTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAATGT
4301 TTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTAAATAGAAATTGGAC
4401 AGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCA
141▶ • N R T Y K L P I L E E I T T K V L K G N M E I L V
4501 CAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGTCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCCT
115▶ 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 H R

StuI (4692)

4601 GACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCCAGCACAGACAGTACCCTGCCAATGTAGGCCATCA
82▶ 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 E
4701 ATGTGGACAGCAGAGATGATCTCCCAAGTCTGGTCTGATGGCCGCCGACATGGTGTGTTGTCCTCATAGAGCATGGTATCTTCTCAGTGGCGA
48▶ 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 A V

BspHI (4842)

4801 CCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTTCATGATGGCCCTCTATAGTGAATGCTATTATACTATGCCGATATACTATGCCGATG
15▶ E V L E L D Q Q S I N F T K M

AseI (4900)

4901 ATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCC

SpeI (5055)

5001 CATTTGCGTCAATGGGGCGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCCATGACGTCATGGGGTGGAGACT

SnaBI (5183)

5100 TGGAAATCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGC

NdeI (5288)

5200 CAAGTAGGAAAGTCCATAAGGTCATGTACTGGCATAATGCCAGGCGGGCATTACCCTGATTGACGTCAATAGGGGGCTACTTGGCATATGATACA
5300 CTTGATGTACTGCCAAGTGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTAT

SdaI (5466) **PacI (5474)** **BspLU11I (5484)**

5400 TGACGTCAATGGGCGGGGTCTGTTGGCGGTGACCCAGCGGGCCATTTACCCTAAGTTATGTAACGCC T G C A G G T T A A T T A A G A A C A T G T G A C A A A
5498 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 T T G 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 C A A G T
5598 C A G A G G T G G C G A A C C C G A C A G G A C T A T A A A G A T A C C A G G C G T T T C C C C T G G A A G C T C C C T C G T G C G C T C T C T G T T C C G A C C C T G C C G T T A C C G G A T
5698 A C C T G T C C G C T T T C C C C T T C G G G A A G C G T G G C G T T T C T C A T A G C T C A G C T G A G G T A T C T C A G T T C G G T G A G G T C G T T C G C T C C A A G C T G G G C T G

ApaI (5798)

5798 TGTGACGAACCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCA
5898 GCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTG
5998 GTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTGTTTG
6098 CAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTCTACGGGTCTGACGCTCAGTGAACGAAAACACGTTAAGGG

EagI (6234)

PacI (6214) SmaI (6223) NotI (6233)

6198 ATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTA
6298 ACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAGGTGCAGGTGCCAGAACATTTCTCTATCGA
6398 A