



125

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

Psp1406I (203) 201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCCGCCGCTACCTGAGGGCC **HindIII (245)** **Bsu36I (291)**
301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCGCTAGGTAAGTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT **NgoMIV (441)** **NaeI (441)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTCCACCATGGCTGGCAAGAAGTATCGGGCAAGCGGTATGGCC **NcoI (560)** **BstEII (555)** **AgeI (552)**
1 M A G K K S S G K R S W P

601 GCTTCTGGGGTGTGGTCACTGTAGCCACCATCCACCTGGTTATATGTCCTACACCAAGGTAGAAGAGAGCTTCAACCTTCAGGCCACACATGACCTC **XcmI (626)**
13 L L G L L V T V A T I H L V I C P Y T K V E E S F N L Q A T H D L

701 CTGTACCACCAGCTGGACATAGACAAGTACGACCACGAGTTTCTGGAGTTGTTCTTAGGACGTTTCTCGGGCCGCTGGTATCGCAGCGTTCTCCA **XcmI (735)** **AvrII (757)**
47 L Y H Q L D I D K Y D H H E F P G V V P R T F L G P L V I A A F S
801 GCCCGTGGTTTATGTGCTCTCGCTTTAGAAGTATCCAAATTTATTCTCAGCTGATAGTCAGAGGAGTCTTGGGCTTGGTGTGATTTCTGGACTCTG **EcoRV (960)**
80 S P V V Y V L S L L E V S K F Y S Q L I V R G V L G L G V I S G L W

901 GACATTACAAAAGGAAGTGAACAGCAGTTCGGAGCCACGGTGGCTGTATGTTCTGTGGATATCAGCCACACAGTTTCATCTCATGTTCTACTGTACG **Bsp120I (1070)**
113 T L Q K E V R Q Q F G A T V A V M F C W I S A T Q F H L M F Y C T

1001 AGGACACTCCCAACGTTGGCCCTGGCTGTGGTCTTACCAGCCCTCACAGCCTGGCTGCAGCGGAGGTGGGCCCTGTTGTCTGGCTCTCAGCCTTCG **BbsI (1169)**
147 R T L P N V L A L A V V L P A L T A W L Q R R W A L F V W L S A F

1101 TCATCATTGGCTTCAGGGCTGAGCTGGCCATGCTGCTGGGCATTGCGCTGCTGCTGACCTGTACCAAGAAGACTGACGGTGGCCAGAGTGTCCGACA **StuI (1374)**
180 V I I G F R A E L A M L L G I A L L L T L Y Q R R L T V A R V L R H
1201 CGCCATCCAGCAGGGCTTCTGTCTAGGGCTGACGGTTGCTGTGGACTCCTATTTCTGGCGATACCTGTATGGCCGAAGGAGTGGTGTCTTGGTAC **HindIII (1446)**
213 A I P A G L L C L G L T V A V D S Y F W R Y L V W P E G V V L W Y

1301 AACACTGTCTGAACAAAAGTTCACACTGGGGCACTTCCCACTCCTGTGGTATTTCTACTCAGCCCTGCCCCGAGGCTGGGCTGCAGCCTTCTCTTCA **HindIII (1446)**
247 N T V L N K S S N W G T S P L L W Y F Y S A L P R G L G C S L L F

1401 TACCCCTGGGTGACAGTGGACAGGAGACCTATGCACTGGCCCTGCCAAGCTTGGGATCTGGCTCTATACTACTCCTCCACACAAGGAGCTGCGGTT **Asp718I (1704)** **Acc65I (1704)** **PshAI (1716)**
280 I P L G A V D R R T Y A L A L P S L G F V A L Y S L L P H K E L R F
1501 CATCATCTATACCTTCCCTGTCCTCAACATCATGGCTGCCAGAGGCTGCACCTATATCTGAATAAAAAGTCTTGGCCATACAAGGTGAGAGCTATGCTG **BglII (2032)** **NheI (2055)**
313 I I Y T F P V L N I M A A R G C T Y I L N K K S W P Y K V R A M L
1601 GTGACAGGGCATATCTTGGTGAATGTGGCATATACAGCCACGTCCTCTATGTGCTCATTCAACTACCCTGGTGGGTTGCGATGCAGCAGCTACATG **BsrBI (1995)**
347 V T G H I L V N V A Y T A T S L Y V S H F N Y P G G V A M Q Q L H

1701 AGCTGGTACCACCTCAGACAGATGTCCTTCTCACATTGATGTGGCTGCTGCCAGACAGGAGTGTACGCTTCTACAGGTCAATGATGACTGGAGGTA **XbaI (1995)**
380 E L V P P Q T D V L L H I D V A A A Q T G V S R F L Q V N D D W R Y
1801 TGACAAGAGTGAAGATGTGGGAGCAGCGCCATGCTGAACTACCCACATCCTCATGGAGGAGTGCCTGGGACCCGGCCCTACAGGGACACACAT **HpaI (2193)**
413 D K S E D V G A A A M L N Y T H I L M E A V P G H P A L Y R D T H

1901 CGAGTCTGGCCAGTATTGAGGGCACTACAGGTATAAGCCTGAATTTGATGAACTGCCACCTTTGATGTCAACCTGCAGACAAAGCTGGTACTTCTAG **EcoRI (2289)**
447 R V L A S I E G T T G I S L N L M K L P P F D V N L Q T K L V L L

2001 AGCGGCTGCTTAGGCCAGCCTGAGAGGACAGGAGATCTCCAGGAACATCGAGTGTGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTGGACAA **MfeI (2204)** **EcoRI (2289)**
480 E R L L R P A •

2101 ACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAACAAGTTAACA **HpaI (2193)**

2201 ACAACAATTGCATTCATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTTCTAAAA **MfeI (2204)** **EcoRI (2289)**

2301 TACAGCATAGCAAACTTAACTCCAAATCAAGCCTCTACTGAACTCTTTCTGAGGGATGAATAAGCATAGGCATCAGGGGCTGTTGCCAATGTGC **EcoRI (2289)**

2401 ATTAGCTGTTTGCAGCCTCACCTCTTTTCATGGAGTTAAGATATAGTATTTTCCCAAGTTTGAAGTACTGCTTTCATTTCTTTATGTTTTAAATGCA

2501 CTGACCTCCACATTCCTTTTTAGTAAAAATTCAGAAAAATTTAAATACATCATTGCAATGAAAAAATGTTTTTTATTAGGCAGAATCCAGATGC **SspI (2528)** **SwaI (2542)**

2601 TCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTT
141 •

2701 AGTTCCTGGTGTACTTGAGGGGGATGAGTTCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGA
140 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 F C D P A Y D S

SacI (2803)

2801 GATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCC
107 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 V A V I T D F D

StuI (2967)

2901 TTCTGCCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCC
73 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 I H V A S I I E G

3001 CAGTCTTGGTCTGATGGCCGCCCGACATGGTCTTGTGTCCCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTG
40 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 E V L E L D Q Q

BspHI (3117)

BbsI (3113)

XmnI (3109)

AseI (3175)

3101 AGAGATGTTGAAGGTCTTCATGATGGCCCTCTATAGTGAGTCGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATG
7 S I N F T K M

SacI (3232)

3201 GCGTCTCCAGCTTATCTGACGGTTCACATAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTG

SpeI (3330)

3301 TTACGACATTTTGAAAGTCCCCTGATTACTAGTCAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGC

SnaBI (3458)

3400 TATCCACGCCCATTGATGTACTGCCAAAACCGCATCATCATGGAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCA

NdeI (3563)

3500 TGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGT

3600 TTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTG

SdaI (3741) PacI (3749) BspLU11I (3759)

3700 GCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCC T G 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 C A A A A G G C C A G G A A C C G T
A A A A A G G C C G G T T G C T G G C G T T T T C C A T A G G C T C 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 C A G A G T G G C G A A C C C G A C A G G A C

3798 A A A A A G G C C G G T T G C T G G C G T T T T C C A T A G G C T C 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 C A G A G T G G C G A A C C C G A C A G G A C

3898 T A T 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 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 A C T G T C C G C T T T C T C C T T C G G G

ApaLI (4073)

3998 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 T A G G T A T C T C A G T T C G G T G T A G G T C G T T C G T C C A A G C T G G G C T G T G C A C G A A C C C C C G T T C A G C C C

4098 G A C C G C T G C G C T T A T C C G G T A A C T A T C G T C T T G A G T C C A A C C C G T A A G A C A C A C T T A T C G C C A C T G G C A G C A G C C A C T G G T A A C A G G A T T A G C A G A G

4198 C G A G G T A T G T A G G C G G T G C T A C A G A G T T C T T G A A G T G G T G G C C T A A C T A C G G C T A C A C T A G A A G A A C A G T A T T T G G T A T C T G C G C T C T G C T G A A G C C A G T

4298 T A C C T T C G A A A A A G A G T T G G T A G C T C T T G A T C C G G C A A A C A A A C C A C C G C T G G T A G C G G T G G T T T T T T G T T G C A A G C A G C A G A T T A C G C G C A G A A A A

PacI (4489)

4398 A A A G G A T C T C A A G A A G A T C C T T T G A T C T T T T A C G G G G T C T G A C G C T C A G T G G A A C G A A A A C T A C G T T A A G G G A T T T T G G T C A T G G C T A G T T A A T T A A

EagI (4509)

Swal (4498) NotI (4508)

4498 C A T T T A A A T C A G C G G C C G C A A T A A A A T A T C T T T A T T T T C A T T A C A T C T G T G T T G G T T T T T T G T G T G A A T C G T A A C T A A C A T A C G C T C T C C A T C A A A A C

4598 A A A A C G A A A C A A A A C A A A C T A G C A A A A T A G G C T G T C C C C A G T G C A A G T G C A G G T G C C A G A A C A T T T C T C T A T C G A A