



125

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

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTGCTGTACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) 201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCCGCCCTACCTGAGGCC **HindIII (245)** **Bsu36I (291)**

301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCTGACCTGCTTCTCAACTCTACGCTTTTGTTCGTTT **NgoMIV (441)**

501 TCTGTTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCCTACCTGAGATCACCGGTGAGCATGCCAGACCCCGCGGCACCTGCCCTTCTTACGG **KasI (535)** **AgeI (552)** **SphI (560)**
1 M P D P A A H L P F F Y G

601 CAGCATCTCGCTGCCGAGCGGAGGACCTGAAGCTGGCGGCATGGCGGACGGGCTCTTCTGCTGCGCAGTGCCTGCGCTCGCTGGCGGCTAT **NgoMIV (775)**
13 S I S R A E A E E H L K L A G M A D G L F L L R Q C L R S L G G Y

701 GTGCTGCTGCTGTGACGATGTGCGCTTCCACCACTTCCCATCGAGCGCCAGCTCAACGGCACCTACGCCATTGCCGGCGGCAAGCGCACTGTGGAC **FspI (854)** **XhoI (883)**
47 V L S L V H D V R F H H F P I E R Q L N G T Y A I A G G K A H C G

801 CGGCAGAGCTCTGCGAGTTCTACTCGCGCACCAGCGGCTGCCCTGCAACTGCGCAAGCCGTGCAACCCGCGCTCGAGCCGAGCCGGG **XhoI (883)**
80 P A E L C E F Y S R D P D G L P C N L R K P C N R P S G L E P Q P G

901 GGTCTTCCACTGCTGCGAGACCCATGGTGGCTGACTACGTGCGCCAGAGCTGGAAGCTGGAGGGCGAGGCCCTGGAGCAGGCCATCATCAGCCAGGCC **Acc65I (1049)** **MluI (1066)**
113 V F D C L R D A M V R D Y V R Q T W K L E G E A L E Q A I I S Q A

1001 CCGCAGGTGGAGAAGCTCATTGCTACGACGGCCACGAGCGGATGCCCTGGTACCACAGCAGCCTGACCGGTGAGGAGCCGAGCGCAAACCTTACTCTG **Acc65I (1049)** **MluI (1066)**
147 P Q V E K L I A T T A H E R M P W Y H S S L T R E E A E R K L Y S

1101 GGGCGCAGACCGACGCAAGTTCTGCTGAGGCCGCGGAAGGAGCAGGCCACATACGCCCTGTCCCTCATCTATGGGAAGACGGTGTACCACTACCTCAT **ScaI (1220)**
180 G A Q T D G K F L L R P R K E Q G T Y A L S L I Y G K T V Y H Y L I

1201 CAGCCAAGACAAGGCGGGCAAGTACTGCCGAGGGCACCAAGTTTACACGCTCTGGCAGTGGTGGATATCTGAAGCTGAAGCGGACGGGCTC **Bsu36I (1346)**
213 S Q D K A G K Y C I P E G T K F D T L W Q L V E Y L K L K A D G L

1301 ATCTACTGCTGAAGGAGCCTGCCCAACAGCAGTGGCAGCAACGCCACAGGGCTGCTGCTCCACACTCCAGCCACCCATCCAGTTGACTCATC **Bsu36I (1346)**
247 I Y C L K E A C P N S S A S N A S G A A A P T L P A H P S T L T H

1401 CTCAGAGACGAATCGACCCCTCAACTCAGATGCATACACCCCTGAGCCAGCAGCATAACCTCCAGACAAACCGGCCGATGCCATGGACACGAG **XmnI (1545)**
280 P Q R I D T L N S D G Y T P E P A R I T S P D K P R P M P M D T S

1501 CGTGTATGAGAGCCCTACAGCGACCCAGAGGAGCTCAAGGACAAGAAGCTCTTCTGAAAGCGGATAACCTCCTCATAGCTGACATTGAACCTGGCTGC **FspI (1637)**
313 V Y E S P Y S D P E E L K D K K L F L K R D N L L I A D I E L G C

1601 GGCAACTTTGGCTCAGTGCGCCAGGGCGTGTACCGCATGCGCAAGAAGCAGATCGACGTGGCCATCAAGGTGCTGAAGCAGGGCACGGAGAAGGCAGACA **SphI (1634)**
347 G N F G S V R Q G V Y R M R K K Q I D V A I K V L K Q G T E K A D

1701 CGAAGAGATGCGCGGAGCGCAGATCATGCACACGCTGGACAACCCCTACATGTCGCGGCTATTGGCGTCTGCCAGGCCGAGGCCCTCATGCTGGT **HpaI (1969)**
380 T E E M M R E A Q I M H Q L D N P Y I V R L I G V C Q A E A L M L V

1801 CATGGAGATGGCTGGGGGCGGGCGCTGCACAAGTTCTGGTGGCAAGAGGGAGGATCCCTGTGAGCAATGTGGCCGAGCTGCTGCACCAAGTGTCC **HpaI (1969)**
413 M E M A G G G P L H K F L V G K R E E I P V S N V A E L L H Q V S

1901 ATGGGGATGAAGTACCTGGAGGAGAAGAACTTTGTGCACCGTGACCTGGCGGCCGCAACGCTCTGTTAACCAGGCACTACGCCAAGATCAGCGACT **HpaI (1969)**
447 M G M K Y L E E K N F V H R D L A A R N V L L V N R H Y A K I S D

2001 TTGGCCTCTCAAAGCACTGGGTGCCGACGACGCTACTACACTGCCGCTCAGCAGGGAAGTGGCCGCTCAAGTGGTACGCCACCCGAATGCATCAACT **Ppu10I (2088)** **NsiI (2088)**
480 F G L S K A L G A D D S Y Y T A R S A G K W P L K W Y A P E C I N F

2101 CCGCAAGTTCTCCAGCCGAGCGATGTCTGGAGCTATGGGGTACCATGTGGGAGGCCTTGTCTACGGCCAGAAGCCCTACAAGAAGATGAAAGGGCCG **BstEII (2139)**
513 R K F S S R S D V W S Y G V T M W E A L S Y G Q K P Y K K M K G P

2201 GAGGTCATGGCTTCATCGAGCAGGGCAAGCGGATGGAGTGCCACCAGAGTGTCCACCCGAAGTGTACGCACTCATGAGTGACTGCTGGATCTACAAGT **BspHI (2273)**
547 E V M A F I E Q G K R M E C P P E C P P E L Y A L M S D C W I Y K

2301 GGGAGGATCGCCCGACTTCTGACCGTGGAGCAGCGCATGCGAGCCTGTTACTACAGCTGGCCAGCAAGGTGGAAGGGCCCCAGGCAGCACAGAA **SphI (2336)** **Bsp120I (2377)**
580 W E D R P D F L T V E Q R M R A C Y Y S L A S K V E G P P G S T Q K

2401 GGCTGAGGCTGCCTGTGCCTGAGCTCCCGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAAA **NheI (2428)**
613 A E A A C A •

2501 TGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAACAAACAATTGCATTCATTTATGTTTC **HpaI (2566)** **MfeI (2577)**

2601 AGGTTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTC **EcoRI (2662)** TAAAAATACAGCATAGCAAACTTTAACCTCCA

2701 AATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTT

2801 TCATGGAGTTAAGATATAGTGTATTTTCCAAGGTTTGAAGTCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTATGTA

2901 **SspI (2901)** AAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGT **SwaI (2915)**

3001 TTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTTAGTTCTGGTACTTGAGGGGGATGA

3101 GTTCTCAATGGTGGTTTTGACCAGCTTGCATTTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGG **141** **• N R T Y K L P I L**

3201 GCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTTCTGCCCGTTGCTCACAGCAGACCCA **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**

3301 ATGGCAATGGCTTTCAGCAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCGAGTCTTGGTCTGATGGCCGCCCGGA **98** **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**

3401 CATGGTGTGTTGTCCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGATGGC **64** **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 T K T R I A A G V** **BspHI (3490)**

3501 CCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAA **AseI (3548)** AACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCA **XmnI (3482)**

3600 CTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTACGACATTTTGGAAAGTCCCGTTG

3700 ATTTACTAGTCAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCA **SpeI (3703)**

3799 AAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAGGTCATGTACTGGGCATAATGCCAGGCGGGC **SnaBI (3831)**

3899 CATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGTACTGCTGCAAGTGGGCAGTTTACCGTAAATACTCCACCATTGAC **NdeI (3936)**

3999 GTCAATGGAAAGTCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGGCGGGTCTGTTGGGCGGTGAGCCAGGCGGGCCATTAC

4099 CGTAAGTTATGTAACGCCTGCAGGTTAA **PstI (4115)** **SdaI (4114)** **Pacl (4122)** **BspLU11I (4132)** TTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT

4197 CCATAGGCTCCGCCCCCTGACGAGCATCAGAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCGTTTCCCCT

4297 GGAAGCTCCCTCGTGGCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCATAGCTCAC

4397 GCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTGAGCCGACCGCTGCGCCTTATCCGGTAAC

4497 TCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAG

4597 TTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGATTGGTAGCT

4697 CTTGATCCGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGAT

4797 CTTTTCTACGGGCTCTGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCAATGGCTAGTTAATTAACATTTAAATC **Pacl (4862)** **SwaI (4871)** **NotI (4881)** AGCGCGCCGAATAAAA

4897 TATCTTTATTTTTCATTACATCTGTGTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAACGAAACAAACAACTAGCAAA

4997 ATAGGCTGTCCCCAGTGCAAGTGCAAGTGCCAGAACATTTCTCTATCGAA