



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

Psp1406I (203) 201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACGCGCCCGCCCTACCTGAGGCC **HindIII (245)** **Bsu36I (291)**
301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCCTCCCGCTGTGGTGCCTCCTGAAGTCGCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGCTTTTGTTCGTTT **NgoMIV (441)**

501 TCTGTTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTCAGCATGCCGCGCTCATTTCTCGTCAAAGCAAGAAGGCTCA **SphI (560)** **AgeI (552)**
601 CAGCTACCACCAGCCGCGCTCCCGAGGACCAGACTATTCCTCCGTTTAGAGAATGTACCGGCGCTAGCCGAGCAGACAGCACTTCAAATGCAGGCGGG **1 M P R S F L V K S K K A H**
130 S Y H Q P R S P G P D Y S L R L E N V P A P S R A D S T S N A G G

701 GCGAAGGCGGAGCCCGGACCGTTTGTCCCGAATCGCAGCTGACCGAAGCCCGAGACAGCCTCCGCATCCCGAGACAGCTGCGAAGGCAGCGTCT **XmaI (713)**
470 A K A E P R D R L S P E S Q L T E A P D R A S A S P D S C E G S V
801 GCGAAGGAGCTCGGAGTTTGGAGACTTCTGGAGGCCCGGTCACCTCCGCGTCTCCAGCCTCGGAGAAGTCAATGTGCCCATCGCTGGACGAAGCCCA **BsrBI (933)** **DraIII (961)** **Bsp120I (989)**
800 C E R S S E F E D F W R P P S P S A S P A S E K S M C P S L D E A Q
901 GCCCTTCCCGCTGCTTTCAAACGTAATCATGGAGCGGCTGGCGGTTTCTGACCTGCGGCACCTGGTGCAGAGCTACCGACCGTGTGGGGCCCTGGAG **EagI (1052)** **NgoMIV (1081)**
1130 P F P L P F K P Y S W S G L A G S D L R H L V Q S Y R P C G A L E
1001 CGTGGCGCTGGCCTGGGCTCTTCTGTGAACCCGCCCCGGAGCCTGGCCACCCGGCGCGTGTACGGCCGAAGCGGGCTGCCGGCGCGGGGGGCCG **PstI (1113)** **AvrII (1149)**
1470 R G A G L G L F C E P A P E P G H P A A L Y G P K R A A G G A G A
1101 GGGCGCCAGGGAGCTGCAGCGCAGGGGCGGTGCCACCCTGGCCTAGGGCTCTACGGCGACTTCGGGTCTGCGGCAGCCGGGCTGTATGAGAG **BbrPI (1378)** **XhoI (1369)** **FspI (1382)** **Acc65I**
1800 G A P G S C S A G A G A T A G P G L G L Y G D F G S A A A G L Y E R
1201 GCCCAGGCGAGCGGGGCTTGTGTACCCGAGCGTGGCCACGGGCTGCACGCAGACAAGGGCGTGGCGTCAAGGTGGAGTCGGAGCTGCTGTGCAC **213 P T A A A G L L Y P E R G H G L H A D K G A G V K V E S E L L C T**
1301 CGCCTGCTGCTGGGCGGGGCTCCTACAAGTGCATCAAGTGCAGCAAGGTGTTCTCCACGCCGACGGGCTCGAGGTGCACGTGCCAGGTCCACAGCG **DraIII (1444)**
2470 R L L L G G G S Y K C I K C S K V F S T P H G L E V H V R R S H S
1401 GTACCAGACCCTTTCCTGCGAGATGTGCGGCAAGACCTTCGGGCACGCGGTGAGCCTGGAGCAGCACAAAGCCGTGCACTCGCAGGAACGGAGCTTTGA **BglIII (1505)** **ScaI (1589)**
2800 G T R P F A C E M C G K T F G H A V S L E Q H K A V H S Q E R S F D
1501 CTGTAAGATCTGTGGAAAGAGCTTCAAGAGGTCAATCCACTGTCCACACACCTGCTTATCCACTCAGACACTCGGCCCTACCCTGTCACTACTGTGGC **313 C K I C G K S F K R S S T L S T H L L I H S D T R P Y P C Q Y C G**
1601 AAGAGGTTCCACCAAGAGTCAAGATGAAGAAACACACTTTCATCCACTGGTGAGAAGCCTCACAAGTGCCAGGTGTGCGGCAAGGATTCAGCCAGA **347 K R F H Q K S D M K K H T F I H T G E K P H K C Q V C G K A F S Q**
1701 GCTCAACTCATCACCCAGCCGAAACACACAGGCTTCAAGCCCTTCGGCTGCACCTCTGTGGAAAGGTTCCAGAGGAAGGTGGACCTCCGAAG **380 S S N L I T H S R K H T F G F G C D L C G K G F Q R K V D L R R**
1801 GCACCGGGAGACGAGCATGGGCTCAAATGAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAAGTGAATGCAGTGAAAA **NheI (1831)**
4130 H R E T Q H G L K •

1901 AAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAATTGCATTATTTATGT **HpaI (1969)** **MfeI (1980)**

2001 TTCAGGTTACAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTCAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACTTTAACCT **EcoRI (2065)**
2101 CCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGCTGTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCT
2201 CTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGGTTTGAAGTACTCTTCAATTTCTTATGTTTTAAATGCAGTGCCTCCACATTCCCTTTTA

2301 GTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCC **SspI (2304)** **Swal (2318)**
2401 AGTTTAGTAGTTGGACTTAGGAAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGA **1414 • N R T Y K L P I**
2501 TGAGTTCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACA **1324 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 I L E R C M G C**
2601 GGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGTCTCACAGCAGAC **BstXI (2608)**
990 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 K Q G N S V A S

2701 CCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCCTGATGGCCGCC
65 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 T K T R I A A G
StuI (2743) BbsI (2889)

2801 CGACATGGTGCTTGTTCCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGT
32 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 S I N F T K M
AseI (2951)

2901 GGCCCTCCTATAGTGAGTCGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTT
3001 CACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCTACCGCCATTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGT

SpeI (3106)

3101 TGATTTACTAGTCAAAAACAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCC

SnaBI (3234)

3201 AAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGGGG

NdeI (3339)

3301 CCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGA
3401 CGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTGTTGGGCGGTGACCCAGGCGGGCCATTTA

PacI (3525)

PstI (3518)
SdaI (3517) BspLU11I (3535)

3501 CCGTAAGTTATGTAACGCTGCAGGTTAATAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTC
3601 CATAGGCTCCGCCCCCTGACGAGCATCAGAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTG
3701 GAAGTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACG
3801 CTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTCCAGCCGACCGCTGCGCTTATCCGGTAACTAT
3901 CGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGT
4001 TCTTGAAGTGGTGGCCTAACTACGGCTACTAGAGAAGCAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTC
4101 TTGATCCGGCAAAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACCGCGAGAAAAAAGGATCTCAAGAAGATCCTTTGATC

PacI (4265) SwaI (4274) EagI (4285)
NotI (4284)

4201 TTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGAATAAAAT

4301 ATCTTTATTTTATTACATCTGTGTGTTGGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAA
4401 TAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA