



PvuI (7)
SgfI (6) 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA **MfeI (82)**
101 GAGAAGTGGCGCGGGTAAACTGGAAAGTGATGCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) 201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACGCGCCCGCCGCTACCTGAGGCC **HindIII (245)** **Bsu36I (291)**
301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGTCAACTCTACGCTTTTGTTCGTTT **NgoMIV (441)**

501 TCTGTTCTGCGCGGTTACAGATCCAAGCTGTGACCGCGCGCTACCTGAGATCACCGGTACCATTGGCGGGGCCGAGCGCTGGGGCCCTGCTCCTGTG **NcoI (560)** **BstEII (555)** **Eco47III (575)**
1 M A G P E R W G P L L L C

601 CCTGCTGACGGCCGCTCCAGGGAGGCCCGTCTGGCCCTCCCGAGAATGTGACGCTGCTCTCCAGAACTTACGCGTGTACCTGACATGGTCCCAGGG **PstI (604)** **BsrBI (611)**
13 L L Q A A P G R P R L A P P Q N V T L L S Q N F S V Y L T W L P G
701 CTTGGCAACCCCGAGGATGTGACCTATTTGTGCCTATCAGAGCTCTCCACCCGTAGACGGTGGCGGAAGTGAAGAGTGTGCGGAACCAAGGAGC
47 L G N P Q D V T Y F V A Y Q S S P T R R R W R E V E E C A G T K E

801 TGCTATGTTCTATGATGTGCTGAAGAAACAGGACCTGTACAACAAGTTCAAGGGACGCGTGGCAGCGTTTCTCCAGCTCCAAGTCCCCTGGGTGGA **BsrGI (836)** **MluI (855)**
80 L L C S M M C L K K Q D L Y N K F K G R V R T V S P S S K S P W V E
901 GTCCGAATACCTGGATTACCTTTTTGAAGTGGAGCCGCCCCACCTGTCTGGTGTCTACCCAGACGGAGGAGATCCTGAGTGCCAATGCCACGTACCAG **NgoMIV (933)**
113 S E Y L D Y L F E V E P A P P V L V L T Q T E E I L S A N A T Y Q

1001 CTGCCCCCTGCATGCCCCACTGGATCTGAAGTATGAGGTGGCATTCTGGAAGGAGGGGGCCGAAACAAGACCTATTTCCAGTCACTCCCATGGCC **SphI (1010)** **NeoI (1092)**
147 L P P C M P P L D L K Y E V A F W K E G A G N K T L F P V T P H G
1101 AGCCAGTCCAGATCACTCTCCAGCCAGCTGCCAGCGAACCACTGCCTCAGTSCCAGAACCCTACACGTTTCACTGTCGCGAAATACAGCAAGTTCTC
180 Q P V Q I T L Q P A A S E H H C L S A R T I Y T F S V P K Y S F S
1201 TAAGCCCACTGTTCTTGTGGAGGTCCAGAAAGCAACTGGGCTTTCTGGTGTCTGCCATCGCTTCTGATACTGCTGTTAGTAATTGCCGAGGGGT
213 K P T C F L L E V P E A N W A F L V L P S L L I L L L V I A A G G

1301 GTGATCTGGAAGACCTCATGGGAACCCCTGGTTTCAGCGGGCAAAGATGCCACGGCCCTGGACTTTTCTGGACACACACCTGTGGCAACCTTTT **BbsI (1308)** **DraIII (1381)**
247 V I W K T L M G N P W F Q R A K M P R A L D F S G H T H P V A T F

1401 AGCCAGCAGACCAGAGTCCGTGAATGACTTGTCTCTGTCCCAAAAAGAACTGACCAGAGGGGTGACGGCCGACGCTCGAGTCAGGGCCCCAGCCAC **PshAI (1409)** **XhoI (1478)**
280 Q P S R P E S V N D L F L C P Q K E L T R G V R P T P R V R A P A T
1501 CCAACAGACAAGATGGAAGAAGGACCTTGACAGAGCAAGAGGAGGATGAGGAGGACACAGAAGATGGCGTCAGCTTCCAGCCCTACATTGAACCA
313 Q Q T R W K K D L A E D E E E D E D T E D G V S F P Y I E P
1601 CCTTCTTCTGGGGCAAGAGCACCAGGCTCCAGGGCACTCGGAGGCTGGTGGGTGGACTCAGGGAGGCCAGGGCTCCTCTGGTCCCAAGCGAAGGCT
347 P S F L G Q E H Q A P G H S E A G G V D S G R P R A P L V P S E G

1701 CCTCTGTTGGGATTCTTTCAGACAGAAGCTGGCCAGCACTGTGACTCCTCCTGGGACAGGGCTGGTCTCTGGCTATTTGGCTGAGAAGGGGCCAGG **BstXI (1733)**
380 S S A W D S S D R S W A S T V D S S W D R A G S S G Y L A E K G P G

1801 CCAAGGGCCGGTGGGATGGGCACCAAGAATCTCTCCACCACCTGAATTTCTCAAGGACTCGGGTTTCTGGAAGAGCTCCAGAAGATAACCTCTCC **EcoRI (1846)**
413 Q G P G G D G H Q E S L P P P E F S K D S G F L E E L P E D N L S

1901 TCCTGGGCCACTGGGGCACCTTACCACCGGAGCCGAATCTGGTCCCTGGGGACCCCAAGTTTCTCTTCCAGACTGACCTTCTGCTGGGAAAGCAGCC **SandI (1950)** **Bsu36I (1999)**
447 S W A T W G T L P P E P N L V P G G P P V S L Q T L T F C W E S S
2001 CTGAGGAGGAAGAGGAGGCGAGGGAATCAGAAATTGAGGACAGCGATCGGGCAGCTGGGGGGCTGAGAGCACCCAGAGGACCAGGACAGGGGCCGGAC
480 P E E E E A R E S E I E D S D A G S W G A E S T Q R T E D R G R T

2101 ATTGGGGCATTACATGGCCAGGTGAGCTGTCCCCGACATCCCACCGAATCTGATGCTAGCTGGCCAGACATGATAAGATAATTGATGAGTTTGACAA **NheI (2155)**
513 L G H Y M A R •

2201 ACCACAACCTAGAATCGAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACA **HpaI (2293)**

2301 ACAACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAAATCTAAAA **MfeI (2304)** **EcoRI (2389)**

2401 TACAGCATAGCAAACTTAACTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGC **SspI (2628)** **SwaI (2642)**

2501 ATTAGCTGTTTGCAGCCTCACCTCTTTTCTGAGGTTTAAAGATATAGTATTTTCCCAAGGTTTGAAGTACTGCTTCTTCTTTTATGTTTTAAATGCA

2601 CTGACCTCCACATTCCCTTTTTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGC

2701 TCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTT
141 •

2801 AGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGA
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

BstXI (2932)

2901 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 (3067)

3001 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

3101 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 (3217)

BbsI (3213)

XmnI (3209) AseI (3275)

3201 AGAGATGTTGAAGGTCTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATG
7 S I N F T K M

3301 CGCTCTCCAGCTTATCTGACGGTTCATAAACGAGCTCTGCTTATATAGACCTCCCACCCTACACGCCTACCGCCATTGCGTCAATGGGGCGGAGTTG

SpeI (3430)

3401 TTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGC

SnaBI (3558)

3500 TATCCAGCCCATTTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTCA

NdeI (3663)

3600 TGTACTGGCATAATGCCAGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGT

3700 TTACCGTAAATACTCCACCATTGACGTCAATGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATTATTGACGTCAATGGCGGGGGTCTGTTG

PstI (3842)

SdaI (3841) PacI (3849) BspLU11I (3859)

3800 GCGGTGACGCAGCGGGCCATTTACCGTAAGTTATGTAACGCC 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
3898 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 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
3998 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 G T G C G C T C T C C T G T T C C G A 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 C C T T C G G G

ApaLI (4173)

4098 AAGCGTGGCGCTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCCGGTGTAGGTGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCC

4198 GACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAG

4298 CGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGT

4398 TACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAA

PacI (4589)

4498 AAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAAACACGTTAAGGGATTTTGGTCATGGCTAGTTAATTTAA

EagI (4609)

Swal (4598) NotI (4608)

4598 CATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAC

4698 AAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAAGTCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA