



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAATGCGTCCCGCTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
 401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGTCTCAACTCTACGCTTTGTTTCGTTT

MscI (563)
BstEII (555)
AgeI (552) NcoI (560)
 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCATTGGCCAGTGATACCCAGGTTTCTACATGGACAACT

1 M A S D T P G F Y M D K L

SnaBI (633) 601 TAATAAATACCGCCAGATGCACGGAGTAGCATTACGTATAAAGAACCTTAGTACTCGGGACCTCCACATGACAGAAGGTTTACATTTCAAGTTTAAATA

13 N K Y R Q M H G V A I T Y K E L S T S G P P H D R R F T F Q V L I

701 GATGAGAAGGAATTTCCAGAAGCCAAAGGTAATCAAAGCAGGAGGCAAGAASCTGCGACCCAAATAGCTGTTGATATACTTGATAACGAAAACAAGG

47 D E K E F P E A K G K S K Q E A R N A A A K L A V D I L D N E N K

BstAPI (825) 801 TGGATTGTACACGAGTGCATCTGAGCAAGGCTTGCCCTATGGTAACTACATAGGCCCTTGTCATAGCTTTGCCAGAAGAAAAGCTGTCTGTAATTA

80 V D C H T S A S E Q G L P Y G N Y I G L V N S F A Q K K K L S V N Y

901 TGAACAGTGTGAGCCAACTCTGAGTTGCCTCAAAGATTTATTTGTAATGCAAAATGGGCAGACGATGTATGGTACTGGTTCAGGTGTACCAAACAG

113 E Q C E P N S E L P Q R F I C K K I G Q T M Y G T G S G V T K Q

1001 GAGGCAAAGCAGTTGGCTGCGAAAAGCCTATCAGAAGCTGTTAAAGAGCCCGCCGAAACTGCCGGAACATCCTCTAGCGTTGTCACTACATTCA

147 E A K Q L A A K E A Y Q K L L K S P P K T A G T S S S V V T S T F

XcmI (1143) 1101 GTGGCTTTTCCAGCAGCTCGTCTATGACAAGTAATGGTGTTCAGTCCAGTCCGAAAGTTTTCTCAGAGAACGTGTTTACGAACGGTCTCGGAGA

180 S G F S S S S M T S N G V S Q S A P G S F S S E N V F T N G L G E

1201 AAATAAAGGAAATCAGGAGTAAAAGTATCCCTGATGATGTGCAAAAGAAATAATATACCTTGACGCCAGGTTTAAACAGCGATTTGAAGCADIAGAA

213 N K R S G V K V S P D V Q R N K K I Y T L D A R F N S D F E I E

1301 GAAATTGCCTTAGGTGGATTTGGTCAAGTTTTCAAAGCGAAAACAGAAATGATGAAAGAGATACGCTATTAAGCGCGTTAAATATAACACGGAGAAAGG

247 E I G L G G F G Q V F K A K H R I D G K R Y A I K R V K Y N T E K

Eco47III (1416) 1401 CGGAGCACGAAGTACAAGCGCTGGCAGAACTCAATCACGTCAACATTGTCCAATACCATAGTTGTTGGGAGGGAGTTGACTATGATCCTGAGCACAGCAT

280 A E H E V Q A L A E L N H V N I V Q Y H S C W E G V D Y D P E H S M

EcoRI (1546) 1501 GAGTGATACAAGTCGATACAAAACCGGTGCCTCTTTATTCAAATGGAATCTGTGATAAAGGAATTTGGAGCAATGGATGAGAAAACAGAAATCAGAGT

313 S D T S R Y K T R C L F I Q M E F C D K G T L E Q W M R N R N Q S

HindIII (1610) 1601 AAAGTGGACAAAGCTTTGATTTTGGACTTATATGAACAAATCGTGACCGGAGTGGAGTATATACACTCGAAAGGGTTAATTCACAGAGATCTTAAGCCAG

347 K V D K A L I L D L Y E Q I V T G V E Y I H S K G L I H R D L K P

1701 GTAATATATTTTGTAGTAGATGAAAGACATTAAGATCGGAGACTTTGGCCTTGCAACAGCCCTGGAAAATGATGGAAAATCCCGAACAGGAGAACAGG

380 G N I F L V D E R H I K I G D F G L A T A L E N D G K S R T R R T G

BglII (1686) 1801 AACTCTTCAATATATGAGTCCAGAACAGTTATTTTTAAAGCACTATGGAAAAGAGTGGACATCTTTGCTTTGGGCCCTTATTCTAGCTGAACCTTCTTCCAC

413 T L Q Y M S P E Q L F L K H Y G K E V D I F A L G L I L A E L L H

BstBI (1933) 1901 ACGTGCTTACGGAGTCAGAGAAAATAAAGTTTTTCGAAAAGTCTAAGAAAAGGCGACTTCTCTAATGATATATTCGACAACAAAAGAAAAAGCCTTCTAA

447 T C F T E S E K I K F F E S L R K G D F S N D I F D N K E K S L L

2001 AAAAATACTCTCAGAGAAAACCAAGGACCGACTGAGACATCTGAAATCCTGAAGACCTTGGCTGAATGGAGGAACATCTCAGAGAAAAGAAAAGAAA

480 K K L L S E K P K D R P E T S E I L K T L A E W R N I S E K K K R N

MscI (2168)
NheI (2162)
BspLU11I (2101) 2101 CACATGTTAGGGCTTTCTGAGAAAACATTCCTCTGCCGTGGTTTTCTTTAACGATCTGCAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTT

513 T C •

2201 TGGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAA

HpaI (2300) 2301 GTTAAACAACAACATTGCATTCTTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAATGTGGTATGGAAT

MfeI (2311) EcoRI (2396)

2401 TCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCC

2501 AATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGTTTGAAGTCTTTCATTCTTTATGTTTT
SapI (2578)

2601 AAATGCACTGACCTCCACATTCCCTTTTTAGTAAAATATTCAGAAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATC
SspI (2635) **SwaI (2649)**

2701 CAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTAAATAGAAATTGGACAGCAAGAAAGCGAGCTTC

2801 TAGCTTTAGTTCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCAT
-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 F C D P A Y
SacI (2910) **BstXI (2939)**

2901 AGTCAGAGATGAGCTCTCTGCATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGC
109 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 V A V I T D
StuI (3074)

3001 AAAGTCCTTCTGCCGTTGCTCAGCAGACCCAATGGCAATGGCTCAGCACAGACAGTGCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATG
76 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 I H V A S I
3101 ATCTCCCAGTCTTGGTCTGATGGCCGCCGACATGGTGTCTTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGTCCAGAT
42 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 E V L E L D
AseI (3282)

3201 CCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGC
9 Q Q S I N F T K M
SacI (3339)

3301 GTGGATGGCGTCTCCAGCTTATCTGACGGTTACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGC

3401 GGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAACAACTCCCATGACGTCAATGGGGTGGAGACTTGAAATCCCGTGAGTCA
SpeI (3437)

3501 AACCGTATCCACGCCATTGATGTAAGTCCGATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATA
SnaBI (3565)

3601 AGGTCATGTAAGTGGCATAATGCCAGGCGGCCATTTACCGTCAATGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTAAGTCCCAAGT
NdeI (3670)

3701 GGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATATTGACGTCAATGGGCGGGG

3801 TCGTTGGCGGTGAGCCAGGCGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATAAGAACATGTGAGCAAAAGCCAGCAAAAGCCAGGAA
SdaI (3848) **Pacl (3856)** **BspLU11I (3866)**

3901 CCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACA
Pacl (3856)

4001 GGACTATAAAGATACCAGCGTTTTCCCTGGAAGCTCCCTCGTGGCTCTCTGTCCGACCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTT

4101 CGGAAGCGTGGCGCTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTCA
ApaLI (4180)

4201 GCCCGACCGTGCCTTATCCGGTAACTATCGTCTTGTAGTCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGC

4301 AGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGC

4401 CAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGTGGTAGCGGTGGTTTTTTGTTTGAAGCAGCAGATTACGCGCAG

4501 AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGCTGTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAA
Pacl (4596)

4601 TTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGGTTTTTTGTGTGAATCGTAACATACGCTCTCCATCA
EagI (4616) **SwaI (4605)** **NotI (4615)**

4701 AAACAAACGAAACAAACAAACTAGCAAAATAGGCTGTCCCAGTCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA