



PvuI (7)
SgfI (6) 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
MfeI (82)
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACAGCGCCCGCCGCCCTACCTGAGGGCC
PvuII (239)
301 GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCCTCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC
Bsu36I (291)

NgoMIV (441)
NaeI (441) 401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGTCTTTGTTTCGTTT

KasI (535) 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTTCATCATGAGGCTTCGGGAGCCGCTCCTGAGCGGCAGCGCCGC
AgeI (552) 1► M R L R E P L L S G S A A
BspHI (560) 601 GATGCCAGGCGCGTCCCTACAGCGGGCTGCGCGTCTGCTGGCCGCTGCGCTCTGCACCTGGCGTCACCCTCGTTTACTACCTGGTCGGCCGCGAC
13► M P G A S L Q R A C R L L V A V C A L H L G V T L V Y Y L A G R D
BsrBI (577) 701 CTGAGCCGCTGCCCAACTGGTCGGAGTCTCCACACCGCTGCAGGGCGGCTCGAACAGTCCGCGCCCATCGGGCAGTCTCCGGGGAGCTCCGGACC
BsrBI (585) 47► L S R L P Q L V G V S T P L Q G G S N S A A A I G Q S S G E L R T
RsrII (793)
BspEI (791) 801 GAGGGGCCCGCCGCGCCTCCTAGCGCCTCCTCCAGCGCGCCGGGTGGCGACTCCAGCCAGTCTGGATTCTGGCCCTGGCCCGCTAGCAA
80► G G A R P P P P L G A S S Q P R P G G D S S P V V D S G P G P A S N
Bsp120I (803) 901 CTTGACCTCGGTCCAGTCCCCACACCACCGACTGTCGCTGCCGCTGCCCTGAGGAGTCCCGCTGCTTGTGGGCCCATGCTGATTGAGTTTAA
KasI (826) 113► L T S V P V P H T T A L S L P A C P E E S P L L V G P M L I E F N
XmaI (846)
XcmI (860)
Bsu36I (952)
Bsp120I (975)
MscI (1094) 1001 ATGCCTGTGGACCTGGAGCTCGTGGCAAAGCAGAACCCAAATGTGAAGATGGGCGGCCGCTATGCCCCAGGACTGCGTCTCTCCTACAAGGTGGCCA
147► M P V D L E L V A K Q N P N V K M G G R Y A P R D C V S P H K V A
ScaI (1136) 1101 TCATCATTCCATTCCGCAACCGGCAGGAGCACCTCAAGTACTGGCTATATTATTTGCACCAGTCTGCAGCGCCAGCTGGACTATGGCATCTATGT
180► I I I P F R N R Q E H L K Y W L Y Y L H P V L Q R Q Q L D Y G I Y V
PvuII (1177) 1201 TATCAACCAGGCGGGAGACACTATATTCATCGTCTAAGCTCCTCAATGTTGGCTTTCAAGAAGCCTGAAGGACTATGACTACACCTGCTTTGTGTTT
213► I N Q A G D T I F N R A K L L N V G F Q E A L K D Y D Y T C F V F
1301 AGTGACGTGGACCTCATTCCAATGAATGACCATAATGCGTACAGGTGTTTTTACAGCCACGGCACATTTCCGTTGCAATGGATAAGTTTGGATTACGCC
247► S D V D L I P M N D H N A Y R C F S Q P R H I S V A M D K F G F S
1401 TACCTTATGTTTCAGTATTTTGGAGGTGCTCTGCTCTAAGTAAACAACAGTTTCTAACCATCAATGGATTTTCCATAAATTATTGGGCTGGGGAGGAGA
280► L P Y V Q Y F G G V S A L S K Q Q F L T I N G F P N N Y W G W G G E
1501 AGATGATGACATTTTAAACAGATTAGTTTTAGAGGCATGCTATATCTGCCCAAATGCTGTGGTCCGGAGGTGTCGATGATCCGCCACTCAAGAGAC
313► D D D I F N R L V F R G M S I S R P N A V V G R C R M I R H S R D
1601 AAGAAAAATGAACCAATCCTCAGAGTTTGGACGAATGCACACACAAGGAGACAATGCTCTCTGATGGTTTGAATCACTCACCTACCAGGTGCTGG
347► K K N E P N P Q R F D R I A H T K E T M L S D G L N S L T Y Q V L
BsrGI (1701) 1701 ATGTACAGAGATACCCATTGTATACCCAAATCACAGTGGACATCGGGACCCGAGCTAGCGTTTTGGTACACGGATAAGAGACCTGAATTGCTAGCTCG
380► D V Q R Y P L Y T Q I T V D I G T P S •
Bst1107I (1719) 1801 ACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGT
EcoRI (1785)

HpaI (1954) 1901 GAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTCATTCTTTATGTTTCAGGTTTCAGGGGG
MfeI (1965)

EcoRI (2050) 2001 AGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTTCTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCT
2101 ACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTCTTTTCATGGAGTTTA

SspI (2289) 2201 AGATATAGTATTTTTCCAAGGTTTGAAGTACTCTTCAATTTCTTTATGTTTAAATGCACTGACCTCCACATTCCCTTTTGTAGTAAATATTAGAA

Swal (2303) 2301 ATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTATAATATCCCCAGTTTAGTAGTTGGA
2401 CTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTACTTTGAGGGGATGAGTTCTCTCAATGG
141► • N R T Y K L P I L E E I T
BstXI (2593) 2501 TGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCT
127► 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 S V V R
2601 GATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCT
94► 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 I A I A

2701 **StuI (2728)**
TCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCCTGATGGCCGCCCGACATGGTGCTTGT
60 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 H H K N
BspHI (2878)

2801 **XmnI (2870)**
TGTCCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGATGGCCCTCCTATAGTG
27 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

2901 **AseI (2936)**
AGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACGCGTGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTC

3000 **SpeI (3091)**
TGCTTATATAGACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTC
3099 AAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCAT

3199 **SnaBI (3219)**
CATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGCGGGCCATTTACCGTCA

3299 **NdeI (3324)**
TTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATGAAAG
3399 TCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGCGGGGGTCTTGGCGGTCAGCCAGCGGGCCATTTACCGTAAGTTATGT

3499 **SdaI (3502)** **PaeI (3510)** **BspLU11I (3520)**
AACGCCTGCAGGTTAA TTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCTTGTGGCGTTTTTCCATAGGCTCCG
3597 CCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTC
3697 GTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCCTTCGGAAGCGTGGCGCTTTCATAGCTCACGCTGTAGGTATC

3797 **ApaLI (3834)**
TCAGTTCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTC
3897 CAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGG
3997 TGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCA
4097 AACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGG

4197 **PacI (4250)** **Swal (4259)** **NotI (4269)**
GTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGCCGCAATAAAAATATCTTTATTTT
4297 CATTACATCTGTGTGTTGGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAAACAAAACGAAAACAAAACAACTAGCAAAATAGGCTGTCCC
4397 CAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA