



PvuI (7)
SgfI (6)
1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA

101 GAGAAGGTGGCGGGGTAACCTGGGAAAGTGTGCTGTACTGGCTCCGCCCTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

301 GCCATCCACGCCGGTTGAGTCGGCTTCTGCCCGCTCCCGCCTGTGGTGCCTCCTGAAGTCCGCTCCGCGCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGCTCAACTCTACGCTTTTGTTTCGTTT

NgoMI (441)
501 TCTGTTCTGGCGGTTACAGATCCAAGCTGTGACCGGCCCTACCTGAGATCACCGTAGGAGGGCCACCATGGTTCTCCGTGGAAGGACTCTGACCCCC

AgeI (552) **NotI (568)**
1► M V L R R R T L H P

Acc65I (648)
601 TTGTCCTCCTGGTACAGGCTGACGTGCTGGCTGAGACTCTGGCCCTGGGTACCTGCCTGCCTTCTACCTCTGTGAGCTGAAGCCTCATGGCCTGGTGG

11► L S L L V Q A A V L A E T L A L G T L P A F L P C E L K P H G L V

701 ACTGCAATTGGCTGTTCTGAAGTCTGTACCCCGTTCCTGCGGCAGCATCTGCTCCAACATCACCCGCTCTCCTTGATCTCCAACCGTATCCACCA

44► D C N W L F L K S V P R F S A A A S C S N I T R L S L I S N R I H H

Tth111I (813)
801 CCTGCACAACCTCCGACTTCGTCCACCTGTCCAACCTGCGGCAGCTGAACCTCAAGTGAAGTTCACCCACTGGCCTTAGCCCTGCACCTTCTCTTGC

77► L H N S D F V H L S N L R Q L N L K W N C P P T G L S P L H F S C

901 CACATGACCATTTGAGCCAGAACCTTCTGGCTATGCTACACTGGAGGAGCTGAACCTGAGCTATAATGGTATCACCACTGTGCCCGACTGCCAGCT

111► H M T I E P R T F L A M R T L E E L N L S Y N G I T T V P R L P S

XbaI (1040) **NgoMI (1059)**
1001 CCCTGGTGAATCTGAGCCTGAGCCACCAACATCTGGTCTAGATGCTAACAGCCTCGCCGGCCTATACAGCCTGCGCGTTCCTTTCATGGACGGGAA

144► S L V N L S L S H T N I L V L D A N S L A G L Y S L R V L F M D G N

BstEII (1136)
1101 CTGCTACTACAAGAACCCTGCACAGGAGCGGTGAAGGTGACCCAGCGCCCTCTGGGCTGAGCAATCTACCCATCTGTCTCTGAAGTATAACAAC

177► C Y Y K N P C T G A V K V T P G A L L G L S N L T H L S L K Y N N

1201 CTCACAAAGGTGCCCGCAACTGCCCGCAGCTGGAGTACCTCTGGTGTCTATAACCTCATTGTCAAGCTGGGCGCTGAAGACCTGGCCAACTCTGA

211► L T K V P R Q L P P S L E Y L L V S Y N L I V K L G P E D L A N L

ScaI (1310)
1301 CCTCCCTTCGAGTACTTGATGTGGGTGGGAATTGCCGTGCTGCGACCATGCCCAATCCCTGTATAGAATGTGGCCAAAAGTCCCTCCACCTGCACCC

244► T S L R V L D V G G N C R R C D H A P N P C I E C G Q K S L H L H P

1401 TGAGACCTTCATCACCTGAGCCATCTGGAAGGCTGGTGTGTAAGGACAGCTCTCCATACACTGAACTTCTCTGGTTCGAAGTCTGGTCAACCTC

277► E T F H H L S H L E G L V L K D S S L H T L N S S W F Q G L V N L

FspI (1576)
1501 TCGGTGCTGGACCTAAGCGAGAATTTCTCTATGAAGCATCAACCACCAATGCCTTTTCAAGCTAACCCTGCGCAAGCTCAACCTGTCCTTCA

311► S V L D A L S E N F L Y E S I N H T N A F Q N L T R L R K L N L S F

1601 ATTACCGCAAGAGTATCCTTTGCCCGCTCCACTGGCAAGTTCCTTCAAGAAGTGGTGTCACTGCAGGAGCTGAACATGAACGGCATCTTCTCCG

344► N Y R K K V S F A R L H L A S S F K N L V S L Q E L N M N G I F F R

1701 CTCGCTCAACAAGTACAGCTCAGATGGCTGGCCGATCTGCCAACTCCACACTCTGCATCTTCAAATGAAGTTCATCAACCAGGCACAGCTCAGCATC

377► S L N K Y T L R W L A D L P K L H T L H L Q M N F I N Q A Q L S I

Acc65I (1803)
1801 TTTGTACCTTCGAGCCCTTCGCTTTGTGGACTGTGACAGCAATCGATCAGTGGCCCTTCAACGCTGTGAGAAGCCACCCTGAAGAGGCAGATGATG

411► F G T F R A L R F V D L S D N R I S G P S T L S E A T P E E A D D

BamHI (1925) **NotI (1999)**
1901 CAGAGCAGGAGGCTGTTGTCTGCGGATCCTCACCGACTCCACTGAGCACCCCTGCTTCTAAGAAGTTCATGGACAGGTGAAGAAGTTCAGTTCAAGTTCAC

444► A E Q E E L S A D P H P A P L S T P A S K N F M D R C K N F K F T

2001 CATGGACCTGTCTCGAACAACCTGTGACTATCAAGCCAGAGATGTTTGTCAATCTCTCACGCCCTCAGTGTCTTAGCCTGAGCCCAACTGCAATTGCA

477► M D L S R N N L V T I K P E M F V N L S R L Q C L S L S H N S I A

2101 CAGGCTGTCAATGGCTCTCAGTTCCTGCCGCTGACTAATCTGAGGTGCTGGACCTGTCCATAACAACTGGACTGTACCCTGGAATCGTTGTCAGTG

511► Q A V N G S Q F L P L T N L Q V L D L S H N K L D L Y H W K S F S

2201 AGCTACCACAGTTGACGGCCTGGACCTGAGCTACAACAGCCAGCCCTTAGCATAAGGGTATAGGCCACAATTCAGTTTGTGGCCCTGTGTCAT

544► E L P Q L Q A L D L S Y N S Q P F S M K G I G H N F S F V A H L S M

2301 GCTACACAGCCTTAGCCTGGCACACAATGACATTATACCCGTGTGCTCCTCACATCTCAACAGCAACTCAGTGAAGTTTCTTGACTTCAGCGGCAACGGT

577► L H S L S L A H N D I H T R V S S H L N S N S V R F L D F S G N G

SfiI (2448)
2401 ATGGCCCGCATGTGGGATGAGGGGGCCTTTATCTCCATTTCTTCAAGCCTGAGTGGCCTGCTGAAGCTGGACCTGTCTCAAAAACCTGCATATCC

611► M G R M W D E G G L Y L H F F Q G L S G L L K L D L S Q N N L H I

2501 TCCGGCCCCAGAACCTTGACAACCTCCCAAGAGCCTGAAGTGTGAGCCTCCGAGACAACCTACCTATCTTTCTTAACTGGACAGTGTGCTCTTCT

644► L R P Q N L D N L P K S L K L L S L R D N Y L S F F N W T S L S F L

2601 GCCCAACCTGGAAGTCTAGACTGGCAGCAACAGCTAAAGCCCTGACCAATGGCACCTGCCTAATGGCACCTCCTCCAGAACTGGATGTCAGC

677► P N L E V L D L A G N K L A L T G L N G T L P N G T L L Q K L V S

2701 AGCAACAGTATCGTCTGTGGTCCAGCCTTCTTCTGCTGCGGGTGGAGTGAAGAGGTCAACCTCAGCCACAACATTCTCAAGACGGTGGATCGCT

711► S N S I V S V V P A F F A L A V E L K E V N L S H N I L K T V D R

Bsp120I (2808) **XbaI (2834)**
2801 CCTGGTTTGGGCCCATTTGATGAACCTGACAGTCTAGACGTGAGAAGCAACCTCTGCACTGTGCTGTGGGGCAGCCTTCTGAGACTTACTGTTGGA

744► S W F G P I V M N L T V L D V R S N P L H C A C G A A F V D L L L E

2901 GGTGACAGCAAGGTGCTGGCCTGGCTAATGGTGTGAAGTGTGGCAGCCCGCCAGCTGCAGGGCCGTAGCATCTTCCGACAGGACTGCGGCTGTGC

777► V Q T K V P G L A N G V K C G S P G Q L Q G R S I F A Q D L R L C

3001 CTGGATGAGTCTCTCTTGGGACTGCTTTGGCCTTCACTCTGGCTGTGGCCGTGGGCATGGTGGTGCCTATACTGCACCATCTCTGGGCTGGGAGC

811► L D E V L T S W D C F G L S L L L A V A G V G M V V P I L H H L C G W

3101 TCTGDACTGTTTTCATGCTGCTGCTACCTGCTTGTGCTGGCCGACGACGAGCCCAAGCTCTCCCTATGATGCTTCTGTGGTGTTCGA

844► V W Y C F H L C L A W L P L L A R S R R S A Q A L P Y D A F V V F D

3201 TAAGGCACAGAGCGCAGTTGCCGACTGGGTGTATAACGAGCTGCGGGTGGGCTGGAGGAGCGCGGTCGCCGAGCCCTACGCTTGTCTGGAGGAC
877▶ **K A Q S A V A D W V Y N E L R V R L E E R R G R R A L R L C L E D**
Tth111I (3390)
RsrII (3388)

3301 CGAGATTGGCTGCCTGCCAGACGCTCTTCGAGAACCTCTGGGCTTCATCTATGGGAGCCGCAAGACTCTATTTGTGCTGCCACACGGACCGCGTCA
911▶ **R D W L P G Q T L F E N L W A S I Y G S R K T L F V L A H T D R V**
FspI (3409)
BspEI (3485)

3401 GTGGCTCCTCGCACACGCTTCTGCTGGCTCAGCAGCGCCTGTGGAAGACCGCAAGGACGTGGTGGTGTGGTATCCTGCGTCCGGATGCCACCG
944▶ **S G L L R T S F L L A Q Q R L L E D R K D V V V L V I L R P D A H R**
Bsp120I (3586)

3501 CTCCCCTATGTGCGACTGCCAGCGTCTCTGCCAGAGTGTGCTCTTCTGCCAGCAGCCCAACGGGAGGGGGCTTCTGGCCAGCTGAGT
977▶ **S R Y V R L R Q R L C R Q S V L F W P Q Q P N G Q G G F W A Q L S**
3601 ACAGCCCTGACTAGGGACAACCGCACTTCTATAACCAGAACTTCTGCCGGGACCTACAGCAGAAAGATCCTACCCCTATGATGTGCCAGACTACGCCT
1011▶ **T A L T R D N R H F Y N Q N F C R G P T A E R S Y P Y D V P D Y A**
NheI (3703)

3701 AAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTAAATTTGTGATG
1044▶ •

HpaI (3841)

3801 **CTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAGTTAACAAACAACATTGCATTCAATTTATGTTTCAGGTTACAGGGGAGGTGGGAGGT**

EcoRI (3937)

3901 **TTTTAAAGCAAGTAAAACCTCTACAATGTGGTATGGAATTTCAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTT**
4001 **TCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTTGTCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTCATGGAGTTAAGATATAGTGTAT**

SspI (4176) **Swal (4190)**

4101 **TTTCCAAGTTTGAAGTAGCTCTTCAATTTCTTTATGTTTTAAATGCACTGACCTCCACATCCCTTTTAGTAAAAATATTCAGAAATAATTTAAATAAC**
4201 **ATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAA**
4301 **GGAACCTTTAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAG**
141▶ • **N R T Y K L P I L E E I T T K V L**
SacI (4451)
Ecl136II (4451)

4401 **CTTGCCATTCTCAATGAGCACAAAGCAGTCAAGGAGCATAGTCAAGATGAGCTCTGACATGCCACAGGGGCTGACCACCTGATGGATCTGTCC**
123▶ **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 I S R D**
4501 **ACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTGTCTCACAGCAGACCAATGGCAATGGCTTCAGCAGACAG**
89▶ **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 E A C V T**
4601 **TGACCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCAGTCTTGGTCTGATGGCCGCCGACATGGTCTTGTGCTCATAGAG**
56▶ **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 D E Y L**
BspHI (4765)

4701 **CATGGTGATCTTCTCAGTGGCAGCTCCACAGCTCCAGATCTGCTGAGAGATGTTGAAGTCTTCATGATGGCCCTCTATAGTGAGTCGATTATAAC**
23▶ **M T I K E T A V E V L E L D Q Q S I N F T K M**

AseI (4823) **SacI (4880)**
Ecl136II (4880)

4801 **TATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACC**

SpeI (4978)

4901 **TCCCACCGTACAGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAACTCCCAT**
5001 **TGACGTCAATGGGTGGAGACTTGGAAATCCCGTGAGTCAAACCGCTATCCAGCCCATGATGACTGCCAAAACCGCATCATCATGGTAATAGCGAT**

SnaBI (5106)

5101 **GACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAAGTCTGACTGGGCATAATGCCAGGCGGCCATTTACCGTCAATGACGTCAATAGGG**

NdeI (5211)

5201 **GGCGTACTTGGCATATGATACACTTGTACTGCAAGTGGGAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTA**

PacI (5397)
SdaI (5389)

5301 **CTATGGGAACATACGTCAATTTGACGTCAATGGGGGGGCTGTTGGGCGGTGAGCCAGGCGGCCATTTACCGTAAAGTTATGTAACGCTCGCAGGTTA**

BspLU11I (5407)

5401 **ATTAAGAACATGTGAGCAAAAGCCAGCAAAAGCCAGGAACCGTAAAAAGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATC**
5501 **ACAAAAATCGACGCTCAAGTCAAGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCGTGAAGCTCCCTGTCGGCTCTCTGTTC**
5601 **GACCTGCGCTTACCGGATACCTGTCCGCTTTCTCCCTCGGGAAGCGTGGCGTTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTGCGGTAGGTC**

ApaLI (5721)

5701 **GTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACG**
5801 **ACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTA**
5901 **CACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAACCCGCTGGT**
6001 **AGCGGTGGTTTTTTTGTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAA**

EagI (6157)
PacI (6137) **Swal (6146)** **NotI (6156)**

6101 **ACGAAAACCTCACGTTAAGGGATTTTGGTATGGCTAGTTAATTAACATTTAAATCAGCGCGCCCAATAAAATATCTTTATTTTATTACATCTGTGTGT**

6201 GGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCAGTGCAAGTGCAGGTG
6301 CCAGAACATTTCTATCGAA