



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

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACACGCGCCGCCGCCCTACCTGAGGCC **PvuII (239)** **Bsu36I (291)**

301 GCCATCCACGCGGTTGAGTGCAGTTCGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT **NgoMIV (441)**

NcoI (560)
BstXI (560)
BstEII (555)
KasI (535) 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCCTACCTGAGATCACCGGTACCCATGGCAATGGTATCAGAATTCCTCAAGCAGGCCGTTT **AgeI (552)** **EcoRI (577)**

601 TCTTAAAATCAAGAACAGGAATATGTTCAAGCTGAAAATCATAAAAAGGTGGTCTGGGTCAGCAGTGAGCCCTACCCTTCTTCAATGTATCCTCG **1 M A M V S E F L K Q A R F**
13▶ L E N Q E Q E Y V Q A V K S Y K G G P G S A V S P Y P S F N V S S
701 GATGTTGCTGCCTTGACAAAGCTATCATGTTAAAGTGTGGATGAAGCAACCATCATTGACATTCTTACCAAGAGGACCAATGCTCAGCGCCAGCAGA **47▶ D V A A L H K A I M V K G V D E A T I I D I L T K R T N A Q R Q Q**
801 TCAAGCCGCGTACTTACAGGAGAATGGAAGCCCTTGGAACTTGAAGTGTGAGAAAAGCCTTACAGGCCACCTGGAGGAGTTGTTTGGCTATGCTAAA **80▶ I K A A Y L Q E N G K P L D E V L R K A L T G H L E E V V L A M L K**

901 AACTCCAGCTCAGTTTGTGAGATGAACTCCGTGGTGCATGAAGGGACTTGGAAACAGATGAAGACACTCTCATTGAGATTTGACAACAAGATCTAAC **BglII (991)**
113▶ T P A Q F D A D E L R G A M K G L G T D E D T L I E I L T T R S N

MscI (1052)
AseI (1015) 1001 GAACAAATCAGAGAGATTAATAGAGTCTACAGAGAAGAGCTGAAAAGAGATCTGGCCAAAAGACATCACTTCAGATACATCTGGAGACTTTTCGAAAAGCCT **BglII (1047)**
147▶ E Q I R E I N R V Y R E E L K R D L A K D I T S D T S G D F R K A

PshAI (1120)
BstEII (1117) 1101 TGCTTGTCTTGCCAAAGGTGACCGTTGTGAGGACTTGAGTGTGAATCAAGATTTGGCTGATACAGATGCCAGGGCTTTGTATGAAGCTGGAGAAAGGAG **180▶ L L A L A K G D R C Q D L S V N Q D L A D T D A R A L Y E A G E R R**
1201 AAAGGGGACAGAGCTGAATGTCCTTACCACAATTCTGACCAGCAGGAGCTTTCCTCATCTTCGCAGAGTGTTCAGAATTACGGAAGTACAGTCAACAT **213▶ K G T D V N V F T T I L T S R S F P H L R R V F Q N Y G K Y S Q H**
1301 GACATGAACAAAGCTCTGGATCTGGAAGTGAAGGGTGAAGTGAAGTGCCTCACAACCATCGTGAAGTGTGCCACCAGCACTCCAGCTTTCTTTGCCG **247▶ D M N K A L D L E L K G D I E K C L T T I V K C A T S T P A F F A**
1401 AGAAGCTGTACGAAGCCATGAAGGGTGCAGCACTCGCCATAAGGCATTGATCAGGATTATGGTCTCCCGTTCGGAATTGACATGAATGAAATCAAAGT **280▶ E K L Y E A M K G A G T R H K A L I R I M V S R S E I D M N E I K V**

XcmI (1506) 1501 ATTTTACCAGAAGAAGTATGGAATCTCTCTTTGCAAGCCATCCTGGATGAAACCAAAGGAGACTATGAAAAATCCTGGTGGCTCTGTGTGGTGGAAAC **313▶ F Y Q K K Y G I S L C Q A I L D E T K G D Y E K I L V A L C G G N**

MscI (1630)
NheI (1624) 1601 TAGACATCCCACTATTCTGCAAGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTAAAAAATGCT **347▶ •**

HpaI (1762) **MfeI (1773)** 1701 TTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACCAATTGCATTCTTTATGTTTCAGGT

EcoRI (1858) 1801 TCAGGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAAATCTAAAATACAGCATAGCAAACTTTAACCTCCAAATC **191▶ •**
1901 AAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTCAT

SspI (2097) 2001 GGAGTTTAAAGATAGTGTATTTTCCCAAGGTTTGAAGTACTGCTTTCATTTCTTTATGTTTTAAATGCACTGACCTCCCACTTCCCTTTTGTAGTAAAT

SwaI (2111) **EcoO109I (2172)** 2101 ATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTAG **221▶ •**
2201 TAGTTGGACTTAGGGAACAAGGAACCTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTACTTGAGGGGGATGAGTTC **141▶ • N R T Y K L P I L E**

SacI (2372) 2301 CTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTG **130▶ 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 P S**
BstXI (2401) 2401 ACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGCTTGTCTACAGCAGACCCAATGG **96▶ 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 G I A**

StuI (2536)

2501 CAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCCTGATGGCCGCCCGACATG
63 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 V H

BspHI (2686)

2601 GTGCTTGTGTCCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTTCATGATGGCCCTC
30 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 (2744)

2701 CTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTATATCTGACGGTTCATAA
SacI (2801)

2800 ACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCCTTGATTT
SpeI (2899)

2900 ACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCAGGCCATTGATGTACTGCCAAAC
SnaBI (3027)

2999 CGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTATGTACTGGGCATAATGCCAGGCGGGCCATT
NdeI (3132)

3099 TACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGTACTGCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCA
3199 ATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCAATGGCGGGGGTCTGTTGGCGGTGACCCAGGCGGGCCATTTACCGTA
PstI (3311)
SdaI (3310) PacI (3318) BspLU11I (3328)

3299 AGTTATGTAACGCC 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 A A A A A G G C C G T T G C T G G C G T T T T T C C A T
3397 A G G C T C 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 G T G G C G A A C C C G A C A G G A C 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
3497 G C T C C C T C G T G C G C T C T 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 T C C T T C G G G A A G C G T G G C G T T T C T C A T A G C T C A C G C T G
ApaLI (3642)

3597 TAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGACGAAACCCCGTTACGCCCGACCGCTGCGCCTTATCCGGTAACTATCGT
3697 CTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCT
3797 TGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTG
3897 ATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTT
EagI (4078)
PacI (4058) SmaI (4067) NotI (4077)

3997 TCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGAATAAAATATC
4097 TTTATTTTCATTACATCTGTGTGGTTTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAG
4197 GCTGTCCCGAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA