



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

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

301 GCCATCCACGCGGTTGAGTGCAGTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

NgoMIV (441)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGGCTACCTGAGATCACCGGTCATCATGAACTAGACATGACTGGGGACTGCATGCCAGTGC **KasI (535)** **AgeI (552)** **BspHI (560)** **SphI (587)**
1▶ M K L D M T G D C M P V L

601 GGTGCTGATGGCCGAGTGTGACCGTACTGGAGCAGTTCCTGTCGCCAGGCTCCGGGGCTCTCCGGATGCAAGGGGCTGCCACATAGCCAGTTC **SacII (654)**
13▶ V L M A A V L T V T G A V P V A R L R G A L P D A R G C H I A Q F

701 AAGTCCCTGTCTCCACAGGAGTGCAGGCCTTTAAGAGGGCCAAAGATGCCTTAGAAGAGTGCCTTCTGCTGAAGGACTGCAAGTGGCCCTCCCGCCTCT **BsrBI (786)**
47▶ K S L S P Q E L Q A F K R A K D A L E E S L L L K D C K C R S R L

PvuII (823)
801 TCCCAGGACCTGGGACCTGAGGAGCTGCAGGTGAGGGAGCGCCCGTGGCTTTGGAGGCTGAGTGGCCCTGACGCTGAAGTTCTGGAGGCCACCGC **Bsu36I (816)**
80▶ F P R T W D L R Q L Q V R E R P V A L E A E L A L T L K V L E A T A
901 TGACACTGACCCAGCCCTGGGGATGTCTTGACCAGCCCTCACACCTGCACCATATCTCTCCAGTCCGGGCTGTATCCAGCTCAGCCACG
113▶ D T D P A L G D V L D Q P L H T L H H I L S Q L R A C I Q P Q P T

XmaI (1013)
1001 GCAGGGCCAGGACCGGGCGCCCTCCACCATTGGCTGCACCGGCTCCAGGAGGCCAAAAAGGAGTCCCCTGGCTGCCTCGAGGCTCTGTACCT **Bsp120I (1003)** **XhoI (1081)**
147▶ A G P R T R G R L H H W L H R L Q E A P K K E S P G C L E A S V T
1101 TCAACCTCTCCGCTCTCACGCGAGACTGAATTGTGTGCCAGCGGGACCTGTGTGTGACCTTCCGCCAGACATGCAACCTGAGATTTTATGC
180▶ F N L F R L L T R D L N C V A S G D L C V •

NheI (1218)
1201 TAGTCAAAGGGCAATTCGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTT **EcoRI (1212)** **MscI (1224)**

1301 GTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAACAAGTTAACAACAACAAATTGCATTCATTTTATGTTTCAGGTTTCAGGG **HpaI (1356)** **MfeI (1367)**

1401 GGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCATAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCT **EcoRI (1452)**
1501 CTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCTCACCTTCTTTCATGGAGTT

1601 TAAGATATAGTGTATTTTCCAAGGTTTGAAGTACTCTTCTTCTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTATGAAAAATTCAG **SspI (1691)**

1701 AAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTG **SwaI (1705)**

1801 GACCTAGGGAACAAAGAACCTTTAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTACTTGAGGGGATGAGTTCCTCAAT **SacI (1966)** **BstXI (1995)**
141▶ • N R T Y K L P I L E I

1901 GGTGTTTTGACCAGCTTGCATTCTCAATGAGCACAAGAGCTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCAC **SacI (1966)** **BstXI (1995)**
128▶ 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 V V
2001 CTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGG **XmnI (2272)**
94▶ 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 I
2101 CTTCAGCAGACAGTACCCTGCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCCAAGTCTTGGTCTGATGGCCGCCCCGACATGGTGCTT
61▶ 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

BspHI (2280)
2201 GTTGCTCATAGAGCATGGTATCTTCTCAGTGGCGACTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTTCATGATGGCCCTCTATAG **BbsI (2276)**
28▶ 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

2301 TGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCT **AseI (2338)** **SacI (2395)**

2401 CTGCTTATATAGACCTCCACCCTACACGCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGT **SpeI (2493)**

2500 CAAAACAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCA
←

SnaBI (2621)

2600 TCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTC

NdeI (2726)

2700 ATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGTACTGCCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATGGAAA

2800 GTCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTACAGCCAGGCGGGCCATTTACCCTAAGTTATG

SdaI (2904) PacI (2912) BspLU11I (2922)

2900 TAACGCCTGCAGGTTAA TTAAGACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGCTGGCGTTTTTCCATAGGCTCC
←

2998 GCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCT

3098 CGTGCGCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTAT

ApaLI (3236)

3198 CTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGT

3298 CCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTG

3398 GTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTTTGATCCGGC

3498 AAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGG

EagI (3672)
NotI (3671)

3598 GGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGAATAAAAATATCTTTATTT
PacI (3652) SmaI (3661)

3698 TCATTACATCTGTGTGTTGGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCC

3798 CCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA