



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

Psp1406I (203) 201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCAGAGGGCTCGCATCTCTCCTTACGCGCCCGCCGCTACCTGAGGGCC **PvuII (239)** **Bsu36I (291)**
301 GCCATCCAGCGCGGTTGAGTCGCGTTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT **NgoMIV (441)** **NaeI (441)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCCCTACCTGAGATCACCGGTCACCATGGGATGATTAAATCAAAAAGGAAAGACAATCTCAA **NcoI (560)** **BstEII (555)** **KasI (535)** **AgeI (552)**
1 M G C I K S K R K D N L N

601 TGACGATGAAGTAGATTCAAGACTCAACAGTACGTAATACTGACCGAACTATTTATGTGAGAGATCCAACGTCCAATAAACAGCAAAGGCCAGTTCCT **BstBI (615)** **SnaBI (632)**
13 D D E V D S K T Q P V R N T D R T I Y V R D P T S N K Q Q R P V P
701 GAATTTTCATCTTTTACCAGGACAGAGATTTCAAACAAAAGATCCAGAGGAACAAGGTGACATTGTGGTGGCCTTATACCTTATGATGGCATCCACCCAG
47 E F H L L P G Q R F Q T K D P E E Q G D I V V A L Y P Y D G I H P

801 ATGACTTGTCTTCAAGAAAGGAGAAAAGATGAAAGTTCTAGAAGAGCATGGGAATGGTGGAAAGCTAAGTCCCTTTTATCAAAAGAGAGAAGGCTTCAT **XbaI (837)**
80 D D L S F K K G E K M K V L E E H G E W W K A K S L S S K R E G F I

901 CCCAGCAACTACGTGGCCAAGTCAACACCTTAGAACTGAAGAGTGGTTCTCAAGGACATAACAAGGAAAGATGCAGAGCGACAGCTTCTGGCACCA **XemI (902)** **MscI (914)**
113 P S N Y V A K V N T L E T E E W F F K D I T R K D A E R Q L L A P

1001 GGGAACAGTGCAGGAGCTTCTTATCAGAGAAGCGAAACTTTAAAGGGAAGCTTCTCTCTTCTGTCAGAGATTATGACCCATGCGTGGTGTGCA **Ppu10I (1084)** **NsiI (1084)**
147 G N S A G A F L I R E S E T L K G S F S L S V R D Y D P M H G D V
1101 TTAAGCACTACAAAATTAGAAGTCTGGACAATGGTGGCTATTACATCTCTCCTCGCATCACTTTTCCCTGCATCAGTGACATGATTAAGCATTACAAAA
180 I K H Y K I R S L D N G G Y Y I S P R I T F P C I S D M I K H Y Q K

1201 GCAGTCTGATGGTCTATGCAGAAGACTGGAGAAGGCATGCATCAGTCCCAAACCTCAGAAGCCATGGGATAAAGATGCCTGGGAGATCCCCGGGAGTCC **Ppu10I (1236)** **NsiI (1236)** **SphI (1234)** **NcoI (1261)** **XmaI (1289)** **BstXI (1298)**
213 Q S D G L C R R L E K A C I S P K P Q K P W D K D A W E I P R E S
1301 ATTAAGTTGGTAAAAAGCTTGGCGCAGGGCAGTTTGGGAAGTCTGGATGGTACTATAACAACAGCACAAAGGTGGCTGTGAAGACCTCAAGCCCG
247 I K L V K K L G A G Q F G E V W M G Y Y N N S T K V A V K T L K P

1401 GCACCATGTCTGTGACGGCATTCTGGAAGAGGCCAACCTCATGAAGACCTTGAACATGACAAGCTAGTGCGGCTGTACGCTGTGGTACCAAGGAGGA **BstEII (1485)**
280 G T M S V Q A F L E E A N L M K T L Q H D K L V R L Y A V V T K E E
1501 GCCATCTACATCATCCAGGTTTCATGGCTAAGGGTAGTTTCTGGATTCTCCTCAAGAGTGTGAAGGTGGCAAGGTGCTGCTGCCAACGCTCATTGAC
313 P I Y I I T E F M A K G S L L D F L K S D E G G K V L L P K L I D

1601 TTCTCGGCCAGATTGCAGAAGGCATGGCGTACATCGAGCGGAAGAACTACATCCACCGTGATCTGCGAGCTGTAACGCTCTGGTCTCTGAGTCACTCA **BsrBI (1636)**
347 F S A Q I A E G M A Y I E R K N Y I H R D L R A A N V L V S E S L

1701 TGTGAAGATTGCAGACTTTGGCCTCGGAGAGTATCGAAGATAACGAGTACACAGCAAGGGAAGGTGCGAAGTTCCCTATCAAGTGGACAGCTCCAGA **NruI (1724)**
380 M C K I A D F G L A R V I E D N E Y T A R E G A K F P I K W T A P E

1801 GGCCATCAACTTGGCTGCTTCACTATCAAATCTGACGTGTGGTCTTCCGGAATCTCCTGTATGAGATTGTACCTATGGGAAGATTCCCTACCCAGGG **EcoRI (1850)**
413 A I N F G C F T I K S D V W S F G I L L Y E I V T Y G K I P Y P G

1901 AGAACCAACGCAGATGTGATGAGCGCACTGTACAGGGATATCGAATGCCACGCATGGAGAAGTCCAGATGAGCTCTATGACATCATGAAAAATGTGTT **EcoRV (1937)**
447 R T N A D V M S A L S Q G Y R M P R M E N C P D E L Y D I M K M C
2001 GGAAGAAAAGGCAGAGAGGAGGCAACTTTTACTACTTACAGAGTCTCCTGGATGACTTCTATACGCCACAGAAGGGCAGTATCAGCAGCAACCGTA
480 W K E K A E E R P T F D Y L Q S V L D D F Y T A T E G Q Y Q Q Q P •

2101 GTGGGCATGGAGACTAGCCTATTGTAGGTGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTGGACAAACCACAAGTGAATGCAGTGAATAAAA **MscI (2135)** **NheI (2129)**
513

2201 ATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATGCATTCAATTTATGTTT **HpaI (2267)** **MfeI (2278)**

2301 CAGGTTCCAGGGGAGGTGTGGGAGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACTCC **EcoRI (2363)**

2401 AAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCT

2501 TCCATGGAGTTAAAGATATAGTGTATTTTCCCAAGTTTGAAGTACTCTTCATTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTATG

2601 **SspI (2602)** SwaI (2616) **EcoO109I (2677)**
AAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCCAG

2701 TTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGGATG
141 • N R T Y K L P I

2801 AGTTCCTCAATGGTGGTTTTGACCAGTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGG
131 L E 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

2901 **BstXI (2906)**
GGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCACAGCAGACCC
98 S 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

3001 **StuI (3041)**
AATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCCG
65 I A 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

3101 **XmnI (3183)**
ACATGGTGTCTTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCAGCTCCACCAGTCCAGATCTGCTGAGAGATGTTGAAGGCTTTCATGATGG
31 V H 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

3201 **AseI (3249)**
CCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTATCTGACGGTTC

3300 ACTAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCCTT

3400 **SpeI (3404)**
GATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCC

3499 **SnaBI (3532)**
AAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTATGACTGGGCATAATGCCAGGGGG

3599 **NdeI (3637)**
CCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGACTGCCAAGTGGGAGTTTACCCTAAATACTCCACCATTGA

3699 CGTCAATGAAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATTATTGACGTCAATGGGGGGGGTCTGTTGGCGGTACAGCCAGGGGGCCATTTA

3799 **PstI (3816)** **SdaI (3815)** **PacI (3823)** **BspLU11I (3833)**
CCGTAAGTTATGTAACGCC TGCAG GTT AA TTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTCTGCGGTTTT

3897 TCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCC

3997 TGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCTGCCGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCA

4097 **ApaLI (4147)**
CGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCCTTATCCGGTAACT

4197 ATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGTACAGA

4297 GTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGC

4397 TCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGA

4497 **EagI (4583)** **PacI (4563)** **SwaI (4572)** **NotI (4582)**
TCTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAA

4597 ATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAA

4697 AATAGGCTGTCCCAGTGAAGTGCAAGTGCCAGGTGCCAGAACATTTCTATCGAA