



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA **MfeI (82)**
101 GAGAAGTGGCGCGGGTAAACTGGAAAGTGTGTCGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTCGCAACGGGTTTGGCCGACAGTGAAGCTTCAGAGGGCTCGCATCTCTCTTACAGCGCCCGCCGCTACCTGAGGCC **PvuII (239)**
301 GCCATCCACGCGGTTGAGTGCAGTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441) 401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTGTTTCGTTT

SphI (560)
AgeI (552) 501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCAGCATGCAGCCTTGGCACGGAAAGCCATGCAGAGAGCTTC **1 M Q P W H G K A M Q R A S**
601 CGAGGCCGAGCCACTGCCCCAAAGGCTTCCGCACGGAATGCCAGGGGCGCCCGATGGATCCACCCAGTCTCCGGCTGCCCGGAGGCCGCTCGCT **BstAPI (631)** **BamHI (657)**
13 E A G A T A P K A S A R N A R G A P M D P T E S P A A P E A A L P

BamHI (733) 701 AAGCGGGAAAGTTCGGCCCGCCAGGAAGTCCGGATCCCGGCAGAAAAAGAGCGCCCGGACACCCAGGAGAGGCCGCGCTCCGCGCAACTGGGGCCC **Bsp120I (794)**
47 K A G K F G P A R K S G S R Q K K S A P D T Q E R P P V R A T G A

NgoMIV (897) 801 GCGCAAAAAGGCCCTCAGCGCGCCAGGACACGAGCCGTCTGACGCCACAGCGCCCTGGGGCAGAGGGGCTGGAGCCTCTGCGGCTCGGGAGCC **80 R A K K A P Q R A Q D T Q P S D A T S A P G A E G L E P P A A R E P**

Bsp120I (970)
XmaI (967)
SrfI (966) 901 GGCTCTTTCCAGGCTGGTTCTTCCCGCCAGAGGGCGCGCTGCTCCACGAAGCAAGACCTCCGCGGGCCCTGGGACGTGCCAGCCCGGCCTG **113 A L S R A G S C R Q R G A R C S T K P R P P P G P W D V P S P G L**

BsiWI (1020) 1001 CCGGTCTCGGCCCCATTCTCGTACGGAGGGATGCGGCGCTGGGGCCTCGAAGCTCCGGGCGGTTTTGGAGAAGTTGAAGCTCAGCCGCGATGATATCT **EcoRV (1093)**
147 P V S A P I L V R R D A A P G A S K L R A V L E K L K L S R D D I

BbrPI (1210) 1101 CCACGGCGCGGGGATGGTGAAGGGGTTGTGGACCACCTGCTGCTCAGACTGAAGTGCAGCTCCGCGTTCAGAGGCGTCCGGCTGCTGAACCCGGGAG **180 S T A A G M V K G V V D H L L L R L K C D S A F R G V G L L N T G S**

PmeI (1248) 1201 CTAATATGAGCACGTGAAGATTTCTGCACCTAATGAATTTGATGTCATGTTTAACTGGAAGTCCCGAGAATCAACTAGAAGAATATCCAACACTCGT **213 Y Y E H V K I S A P N E F D V M F K L E V P R I Q L E E Y S N T R**
1301 GCATATTACTTTGTGAAATTTAAAGAAATCCGAAAGAAATCCTCTGAGTCAAGTGTGAAAGTGAATATATCAGCTTCTAAGATGCTGTCAAAGT **247 A Y Y F V K F K R N P K E N P L S Q F L E G E I L S A S K M L S K**

BspHI (1451) 1401 TTAGGAAATCATTAAGGAAGAAATTAACGACATTAAGATACAGATGTCATCATGAAGAGGAAAGAGGAGGAGCCCTGCTGTAACACTTCTTATTAG **280 F R K I I K E E I N D I K D T D V I M K R K R G G S P A V T L L I S**

NheI (1555) **StuI (1569)**
FspI (1574) 1501 TGAAAAATATCTGTGGATATAACCTGGCTTTGGAATCAAAAAGTAGCTGGCCTGCTAGCACCAAGAAGGCTGCGCATTCAAAAAGGCTTTTCAGCA **313 E K I S V D I T L A L E S K S S W P A S T Q E G L R I Q N W L S A**

SphI (1647) 1601 AAAGTTAGGAAGCAACTACGACTAAAGCCATTTACCTTGACCAAGCATGCAAGGAAGAAATGGTTTCCAAGAAGAAACATGGCGGTATCCTTCT **347 K V R K Q L R L K P F Y L V P K H A K E G N G F Q E E T W R L S F**
1701 CTCACATCGAAAAGGAAATTTGAAACAATCATGAAAAATCTAAAACGTGCTGTGAAAAAAGAGAAATGTTGCAGGAAAGATTGTTAAAACTAAT **380 S H I E K E I L N N H G K S K T C C E N K E E K C C R K D C L K L M**

PvuII (1816) 1801 GAAATACCTTTTAGAACAGCTGAAAGAAAGTTTAAAGACAAAAACATCTGGATAAATCTCTTCTTATCATGTGAAAAGTGCCTTCTTTCAGTATGT **413 K Y L L E Q L K E R F K D K K H L D K F S S Y H V K T A F F H V C**
1901 ACCAGAACCTCAAGACAGTCAAGTGGGACCGAAAGACCTGGGCTCTGCTTTGATAACTGCGTGACATACTTCTTTCAGTGCCTCAGGACAGAAAAAC **447 T Q N P Q D S Q W D R K D L G L C F D N C V T Y F L Q C L R T E K**
2001 TTGAGAATATTTTATTCTGAATTTCAATCTATTCTAGCAACTAATTGACAAAAGAGTAAAGAAATTTCTGACAAAGCAATTTGAATATGAAAGAAA **480 L E N Y F I P E F N L F S S N L I D K R S K E F L T K Q I E Y E R N**

AvrII (2131)
PshAI (2129) **MscI (2143)** 2101 CAATGAGTTTCCAGTTTTTGTGAATTTTGACCTAGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAG **513 N E F P V F D E F •**

HpaI (2275) **MfeI (2286)** 2201 TGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACATTGCATTCAAT
2301 TTATGTTTCAGGTTACGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAATGTGGTATGGAATTTAAAATACAGCATAGCAAACTT
2401 TAACCTCAAATCAAGCCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTGCAGCCT

2501 **SapI (2553)**
CACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGGTTTGAAGTCTCTTCATTCTTTATGTTTTAAATGCACTGACCTCCCACATTCCC

2601 SwaI (2624)
TTTTTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATA

2701 TCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGA
141 • N R T Y K L

2801 GGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACAT
134 P I 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
SacI (2885)

2901 GCCACAGGGGCTGACCACCTGATGGATCTGCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCACA
101 G C P 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
BstXI (2914)

3001 GCAGACCCAATGGCAATGGCTTCAAGCAGACAGTACCTGCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGG
67 A S G 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
StuI (3049)

3101 CCGCCCCGACATGGTGTGTTGTCTCATAGAGCATGGTGTCTTCTAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTT
34 A G 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
BspHI (3199)
BbsI (3195)
XmnI (3191)

3201 CATGATGGCCCTCTATAGTGTGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACGCGTGGATGGCGTCTCCAGCTTATCTG
1 M
AseI (3257)

3301 ACGGTTCACTAAACGAGCTCTGTTATATAGACCTCCACCCTACACGCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAG
SacI (3314)

3401 TCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGCTATCCACGCCATTGATGT
SpeI (3412)

3501 ACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTCCCAAGTAGGAAAAGTCCCATAAAGTCATGTACTGGGCATAATGCCA
SnaBI (3540)

3601 GCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACC
NdeI (3645)

3701 CATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGAAACATACGTCAATTATTGACGTCAATGGGCGGGGGTCTTGGGCGGTGAGCCAGGCGGGC
PacI (3831)

3801 CATTACCCTAAGTTATGTAACGCTGCGAGGTTAATTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCG
PstI (3824)
SdaI (3823)
BspLU11I (3841)

3901 TTTTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTC
NdeI (3645)

4001 CCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAG
ApaLI (4155)

4101 CTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTACGCCGACCGCTGCGCTTATCCGGT
EagI (4591)

4201 AACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTA
PacI (4571) SwaI (4580) **NotI (4590)**

4301 CAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGATTGG
EagI (4591)

4401 TAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCT
EagI (4591)

4501 TTGATCTTTTCTACGGGCTGACGCTCAGTGGAACGAAAACCTACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAA
PacI (4571) SwaI (4580) **NotI (4590)**

4601 TAAAAATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTA
EagI (4591)

4701 GCAAAATAGGCTGTCCCCAGTGAAGTGCAAGTGCCAGATGCCAGAACATTTCTCTATCGAA