



PvuI (7)
SgfI (6) 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA MfeI (82)

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

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

301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTAAAGTCAAGTGCAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGTCTTTGTTTCGTTT

BssHII (595)
501 TCTGTTCTGCGCGGTTACAGATCCAAGCTGTGACCGCGCGCTACCTGAGATCACCGGTAGGAGGGCCACCATGGCGGGAACTGTGGGCCCCGCGCGCGC **SacII (590)**
1 M A G N C G A R G A **Bsp120I (586)**

BstAPI (608) **BssHII (679)**
601 CTGTGCGGCACACGCTGCTGTTGACCTGCCGCCGCGCTGCTCGGAGAGCTCTGCGTGTCTGGACAGCTGCGAGCGCGCTGGCTGGCGCGGCC
11 L S A H T L L F D L P P A L L G E L C A V L D S C D G A L G W R G

XcmI (758)
701 TGGCAGAGAGACTTTCAAGCAGCTGGCTGGATGTTCTGTCATATTGAAAAGTATGTAGACCAAGGTAAGTGAACAAGAGAATTACTTTGGTCTGGGC
44 L A E R L S S S W L D V R H I E K Y V D Q G K S G T R E L L W S W A

BstEII (819) **Tth111I (850)**
801 ACAGAAAAACAAGACCATCGGTGACCTTTACAGGTCCTCCAGGAGATGGGACATCGTCGAGCTATTCATTTAATTACAACTATGGAGCAGTGTGAGT
77 Q K N K T I G D L L Q V L Q E M G H R R A I H L I T N Y G A V L S

XcmI (958)
901 CCTTCAGAGAAGAGTTATCAGGAAGGTGGATTTCCAAATATATTATTCAAGGAAACAGCCAATGTCCCGTGGATAATGTTCTTATTCTGAACATAATG
111 P S E K S Y Q E G G F P N I L F K E T A N V T V D N V L I P E H N

ScaI (1007)
1001 AAAAAGGAGTACTGCTTAAATCTCCATCAGCTTTCAAATATCATAGAAGGAACTAGAAATTTCCACAAAGACTTCTAATTGGAGAAGGAGAGATTTT
144 E K G V L L K S S I S F Q N I I E G T R N F H K D F L I G E G E I F

Bst1107I (1104) **NdeI (1132)**
1101 TGAGGTATACAGAGTGGAGATTCAAACCTAACATATGCTGTCAAATATTTAAACAGGAGAAAAAATGCAGTGAAGAAGCATTGGAAGAGGTTTTTA
177 E V Y R V E I Q N L T Y A V K L F K Q E K K M Q C K K H W K R F L

1201 TCTGAGCTTGAAGTTTTACTACTGTTTCATCACCACAAACATACTAGAGTTGGCTGCATATTTACAGAGACTGAGAAGTTCTGTCTGATTATCCATACA
211 S E L E V L L L F H H P N I L E L A A Y F T E T E K F C L I Y P Y

BstBI (1366)
1301 TGAGAAATGGAACACTTTTTGACAGATTGCAGTGTGTAGGTGACACGGCCCACTCCCTTGGCACATTGCAATCGGTATATTAATAGGAATATCCAAAGC
244 M R N G T L F D R L Q C V G D T A P L P W H I R I G I L I G I S K A

Psp1406I (1416)
1401 CATTCACTACCTGCACAACGTTCAACCATGCTCGGTCTGTGGCAGTATATCAAGTCAAACATCCTTTTGGATGATCAGTTTCAACCCAACTAACT
277 I H Y L H N V Q P C S V I C G S I S S A N I L L D D Q F Q P K L T

NcoI (1507)
1501 GATTTTGCATGGCACACTTCCGGTCCACCTAGAACATCAGAGTTGTACCATAAATATGACCAGCAGCAGCAGTAAACATCTGTGGTACATGCCAGAAG
311 D F A M A H F R S H L E H Q S C T I N M T S S S S K H L W Y M P E

1601 AGTACATCAGACAGGGGAACTTTCCATTAACAGATGTCTACAGCTTTGGAATTGTAATAATGGAAGTTCTAACAGGATGTAGAGTAGTGTAGATGA
344 E Y I R Q G K L S I K T D V Y S F G I V I M E V L T G C R V V L D D

XbaI (1775)
1701 TCCAAAACATATCCAGCTGCGGGATCTCCTTAGAGAATTGATGGAGAAGAGAGCCTGGATTGATGCTCTCTCATTCTAGATAAAGTGCCTCCCTGC
377 P K H I Q L R D L L R E L M E K R G L D S C L S F L D K K V P P C

SapI (1820)
1801 CCTCGGAATTTCTCTGCCAAGCTTCTGTTTGGCAGGCCGGTGTGCTGCAACGCGGGCAAAGTTAAGACCATCAATGGATGAAGTTTTAAATACTCTTG
411 P R N F S A K L F C L A G R C A A T R A K L R P S M D E V L N T L

ScaI (1902)
1901 AAAGTACTCAAGCCAGCTTGTATTTTGGTGAAGATCCTCCACATCACTAAAGTCTTTCAGGTGTCCTTCTCCTTATTCTGGAGAATGTACCAAGTAT
444 E S T Q A S L Y F A E D P P T S L K S F R C P S P L F L E N V P S I

Bsu36I (2054)
2001 TCCAGTGGAAAGATGATGAAAAGCCAGAATAACAATTTACTACCTTCTGATGAAGGCTGAGGATAGACAGAATGACTCAGAAAACCTCTTTTGAATGCAGC
477 P V E D D E S Q N N N L L P S D E G L R I D R M T Q K T P F E C S

HindIII (2158)
2101 CAGTCTGAGGTTATGTTTCTGAGCTTGGACAAAAAGCCAGAGAGCAAGAGAAATGAGGAAAGCTTGAACATGCCAGTCTTCTTGTGAAGAAAGTTGGT
511 Q S E V M F L S L D K K P E S K R N E E A C N M P S S S C E E S W

2201 TCCCAAAGTATATAGTTCCATCCAGGACTTAAGGCCCTATAAGGTAATATAGATCTTCTCAGAAGCTCCAGGGCATTCTTGCAGGAGCAGGCCAGT
544 F P K Y I V P S Q D L R P Y K V N I D P S S E A P G H S C R S R P V

XmnI (2355) **BstAPI (2386)**
2301 GGAGAGCAGCTGTTCTCCAAATTTTCTGGGATGAATATGAACAGTACAAAAAGAATAAATTTCTACCAGAAGATAAAGAAAAAGCAAGTATTGCATA
577 E S S C S S K F S W D E Y E Q Y K K E •

MscI (2415)
NheI (2409)
2401 GGCACCTGAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTAAAAAATGCTTTATTTGTGAAATTT

2501 **HpaI (2547)** MfeI (2558)
 GTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACAAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGGAGGTGTG

2601 **EcoRI (2643)**
 GGAGGTTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACCTTTAACCTCCAATCAAGCCTCTACTTGAA

2701 TCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTCATGGAGTTTAAGATATA

2801 **SapI (2825)** **SspI (2882)** SwaI (2896)
 GTGTATTTTCCCAAGTTTGAAGTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAATAATTT

2901 AAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGG

3001 AACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTT
 141 • N R T Y K L P I L E E I T T K

3101 **BstXI (3186)**
 GACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGAT

125 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 R I S

3201 CTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCAC

91 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 A E A C

3301 AGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGCTTGTGTCTCCT
 58 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 N D E

BbsI (3467)
XmnI (3463)

3401 ATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTTCATGGTGGCCCTCTATAGTGAGTCGTA
 25 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 (3529)

3501 TTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATA

SpeI (3684)

3601 TAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAAC

3701 TCCATTGACGTCAATGGGGTGGAGACTTGAATCCCGTGAGTCAAACCGTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAAT

SnaBI (3812)

3801 AGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCA

NdeI (3917)

3901 ATAGGGGGCGTACTTGGCATATGATACACTTGTATGTAAGTGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATGAAAAGTCCCTATTG

PstI (4096)
SdaI (4095)

4001 GCGTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGCGGTCAGCCAGGCGGGCCATTTACCCTAAGTTATGTAACGCTCG

PacI (4103) **BspLU11I (4113)**

4101 AGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACG

4201 AGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCCTGGAAGCTCCCTCGTGCGCTCTCC

4301 TGTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAGCGTGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTG

ApaLI (4427)

4401 TAGGTCGTTTCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAA

4501 GACACGACTTATCGCACTGGCAGCAGCCACTGGAACAGGATTAGCAGAGCGAGGTATGAGCGGTGCTACAGAGTCTTGAAGTGGTGGCTAACTA

4601 CGGTACTACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAACCACC

4701 GCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTC

EagI (4863)
NotI (4862)

4801 **PacI (4843)** **SwaI (4852)** **NotI (4862)**
 AGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCCAATAAAATATCTTTATTTTTCATTACATCTG

4901 TGTGTTGGTTTTTTGTGTGAATCGTAACATACGCTCTCCATCAAAACAACGAAACAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTG

5001 CAGGTGCCAGAACATTTCTCTATCGAA