



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA **MfeI (82)**
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACACGCCGCCGCCCTACCTGAGGCC **PvuII (239)** **Bsu36I (291)**
301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCCTCCCGCCTGTGGTGCCCTCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

KasI (535) 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCCTACCTGAGATCACCGGTCATCATGAGAAATAAGAAAATTCTCAAGGAGGACGAGCTCTT **AgeI (552)** **BspHI (560)**
1 M R N K K I L K E D E L L

BstBI (646)
Bsp119I (646) 601 GAGTGAGACCCAACAAGCTGCTTTTACCAAATGCAATGGAGCCTTTTCAAATCAATGTTCCAAAGCCCAAGAGGAGAAATGGGGTGAACCTTCCCTA
13▶ S E T Q Q A A F H Q I A M E P F E I N V P K P K R R N G V N F S L
701 GCTGTGGTGGTCACTACCTGATCCTGCTCACCCTGGCGCTGGGCTGCTGGTGGTCCAAAGTTCTGAATCTGCAGGCGCGGCTCCGGGTCCTGGAGATGT
47▶ A V V V I Y L I L L T A G A G C L L V V Q V L N L Q A R L R V L E M
801 ATTTCTCAATGACACTCTGGCGGCTGAGGACGCCCTGCTCTCTGCTGAGTACAGCACCCCTGGAGAACACCTGGCTCAGGTCGAGGCT
80▶ Y F L N D T L A A E D S P S F S L L Q S A H P G E H L A Q G A S R L
BstAPI (900) 901 GCAAGTCTGCAGGCCAACTCACCTGGGTCCGCGTCAGCCATGAGCACTTGTGTCAGCGGGTAGACAACCTCACTCAGAACCAGGGATGTTCAGAATC
113▶ Q V L Q A Q L T W V R V S H E H L L Q R V D N F T Q N P G M F R I **BstAPI (945)**

KasI (1012) 1001 AAAGGTGAACAAGGCGCCCGCAGGCTTCAAGGTCAACAAGGGGGCCATGGGCATGCCTGGTGCCCTGGCCCGCCGGGACCACCTGCTGAGAAGGGAGCCA
147▶ K G E Q G A P G L Q G H K G A M G M P G A P G P P G P P A E K G A **NeoI (1043)** **XcmI (1097)**
SmaI (1137) 1101 AGGGGGCTATGGGACGAGATGGAGCAACAGGCCCTCGGGACCCCAAGGCCACCGGGAGTCAAGGGAGAGGGCGGCTCCAAGGACCCAGGGTGTCTCC
180▶ K G A M G R D G A T G P S G P Q G P P G V K G E A G L Q G P Q G A P
1201 AGGGAAGCAAGGACCACTGGCACCCAGGACCCCAAGGAGAGAAGGGCAGCAAAGGGGATGGGGTCTCATTGGCCAAAAGGGGAACTGGAATAAG
213▶ G K Q G A T G T P G P Q G E K G S K G D G G L I G P K G E T G T K
PshAI (1312) 1301 GGAGAGAAAGGAGACCTGGGTCTCCAGGAAGCAAAGGGGACAGGGGCATGAAAGGAGATGCAGGGGTCTGGGGCTCTGGAGCCAGGGGAGTAAG
247▶ G E K G D L G L P G S K G D R G M K G D A G V M G P P G A Q G S K
SphI (1049) 1401 GTGACTTCGGGAGGCCAGGCCACAGGTTTGGCTGTTTTCTGGAGCTAAAGGAGATCAAGGACAACCTGGACTGCAGGGTGTTCGGGCCCTCCTGG
280▶ G D F G R P G P P G L A G F P G A K G D Q G Q P G L Q G V P G P P G **Bsp120I (1488)**
XmaI (1576) 1501 TGCACTGGGACACCCAGGTGCCAAGGGTGAGCCTGGCAGTGTGGTCCCTGGGCGAGCAGGACTTCCAGGGAGCCCGGGAGTCCAGGAGCCACAGGC
313▶ A V G H P G A K G E P G S A G S P G R A G L P G S P G S P G A T G **StuI (1596)**
1601 CTGAAAGGAAGCAAAGGGGACACAGGACTTCAAGGACAGCAAGGAAGAAAAGGAGAATCAGGAGTTCAGGCCCTGCAGGTGTGAAGGGAGAACAAGGGA
347▶ L K G S K G D T G L Q G Q Q G R K G E S G V P G P A G V K G E Q G
MscI (1740) 1701 GCCCAGGGCTGGCAGGTCCCAAGGGAGCCCTGGACAAGTGGCCAGAAGGGAGACCAGGGAGTGAAGGATCTTCTGGGGAGCAAGGAGTAAAGGGAGA
380▶ S P G L A G P K G A P G Q A G Q K G D Q G V K G S S G E Q G V K G E
Acc65I (1882) 1801 AAAAGGTGAAAGAGGTGAAAACCTCAGTGTCCGTCAGGATTGTCCGCGAGTAGTAACCGAGCCGGGCTGAAGTTTACTACAGTGGTACCTGGGGACAATT
413▶ K G E R G E N S V S V R I V G S S N R G R A E V Y Y S G T W G T I **BsrGI (1973)**
SphI (1943) 1901 TGCGATGACGAGTGGCAAAATTCTGATGCCATTGTCTTCTGCCGATGCTGGGTTACTCAAAGGAAGGGCCCTGTACAAAGTGGGAGCTGGCACTGGCC
447▶ C D D E W Q N S D A I V F C R M L G Y S K G R A L Y K V G A G T G **Bsp120I (1967)**
BglIII (2000) 2001 AGATCTGGCTGATAATGTTTCAGTGTGCGGGCAGGAGAGTACCTGTGGAGCTGCACCAAGAATAGCTGGGGCCATCATGACTGCAGCCACGAGGAGGA
480▶ Q I W L D N V Q C R G T E S T L W S C T K N S W G H H D C S H E E D **BspHI (2076)**
MscI (2132) 2101 CGCAGGCGTGAGAGTGCAGCGTCTGAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATG
513▶ A G V E C S V • **NheI (2126)**

HpaI (2264) 2201 CTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAAATTGCATTTCATTTATGTTTCAG
MfeI (2275)

EcoRI (2360) 2301 GTTCAGGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCCAAA
MscI (2132) 2401 TCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTCTTTC

2501 ATGGAGTTAAGATATAGTGTATTTTCCAAGTTTGAAGTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCCACATTCCCTTTTTAGTAAA
SapI (2542) SspI (2599)

2601 ATATTCAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTT
Swal (2613)

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

2801 TCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGC
130 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 S
BstXI (2903)

2901 TGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAAT
97 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

3001 GGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCCGACA
64 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 V
StuI (3038)

3101 TGGTGCTTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCC
30 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
XmnI (3180)

3201 TCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTA
AseI (3246)

3301 AACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCATTGCGTCAATGGGGCGGAGTTGTTACGACATTTGGAAAGTCCCGTTGATT

3401 TACTAGTCAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAAC
SpeI (3401)

3501 CGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTCATGACTGGGCATAATGCCAGGCGGGCCATT
SnaBI (3529)

3601 TACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGACTGCCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCA
NdeI (3634)

3701 ATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCAATGGGGCGGGTCTGTTGGGGCGTACAGCCAGGCGGGCCATTACCGTA

3801 AGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCCTTTTCCATAG
PacI (3820) BspLU11I (3830)

3901 GCTCCGCCCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGC

4001 TCCCTCGTGCGCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTA

4101 GGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCT
ApaI (4144)

4201 TGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGATTCTTG

4301 AAGTGGTGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGAT

4401 CCGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTGTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTC

4501 TACGGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGAATAAAATATCTT
PacI (4560) Swal (4569) EagI (4580) NotI (4579)

4601 TATTTTCATTACATCTGTGTGTTGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGC

4701 TGCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA