



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

MfeI (82)
101 GAGAAGGTGGCGCGGGTAAACTGGGAAAGTATGTCGTGACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACCGCGCCCGCCCTACCTGAGGCC

HindIII (245)
301 GCCATCCACGCCGGTTGAGTCGGTCTTCCGCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

BstEII (555)
501 TCTGTTCTGGCGGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCATGGTGCCTCCAGCCAGCGGTGGAGAAGCAGGTGCC

AgeI (552) **NcoI (560)** **XcmI (572)**
601 CGTGAACCTGGGCTGACCCGAGCTCCGGTCTGGCGGCGCTCGTGTGCTACCTTGTCTACGGCTTCATGGCGCAGATACGGCCAGGGGAGAGC
13▶ M V P S S P A V E K Q V P
13▶ V E P G P D P E L R S W R R L V C Y L C F Y G F M A Q I R P G E S

Bsp120I (721) 701 TTCATACCCCTACCTCCTGGGCCCCACAAGAACTTACGCGGGAGCAGGTACGAACGAGATCACGCCGTGCTGCTACTCCTACCTGCGCGTGC
47▶ F I T P Y L L G P D K N F T R E Q V T N E I T P V L S Y S Y L A V

SgrAI (767)
801 TGGTGCCCGTGTCTGCTCACCAGTACTGCGCTACACGCGGTGCTGCTGTCAGGGGCTCAGCTTCGTGTCGGTGTGGTGTGCTGCTGCTGGG
80▶ L V P V F L L T D Y L R Y T P V L L L Q G L S F V S V W L L L L L G

SapI (930) **NcoI (947)**
901 CCACTCGGTGGCGCACATGCAGCTCATGGAGCTTCTACAGCTCACCATGGCCGCGCATCGCCTATTCCTACATCTTCTCTCGTGGCGCC
113▶ H S V A H M Q L M E L F Y S V T M A A R I A Y S S Y I F S L V R P

XcmI (1058)
1001 GCGCGTACCAGCGTGTGGCCGCTACTCGCGCTGCGGTGCTGCTGGCGTGTCCAGCTCCGTGCTGGCCAGCTGCTGGTCACTGTGGCCGAG
147▶ A R Y Q R V A G Y S R A A V L L G V F T S S V L G Q L L V T V G R
1101 TCTCCTTCCACGCTCAACTACATCTCGTGGCCTTCTCACCTTACGCTGGTCCCTCGCCCTTCTCTGAAGCGCCCAAGCGCAGCCTTCTTCAA
180▶ V S F S T L N Y I S L A F L T F S V V L A L F L K R P K R S L F F N
1201 CCGCGACGACCGGGGGCGGTGCGAACTCGGCTTCCGAGCTGAGCGCATGAATCCCGGCCAGGCGGAAGCTGGACACGCCCTGCGGGTGGCCTGT
213▶ R D D R G R C E T S A S E L E R M N P G P G G K L G H A L R V A C

NotI (1350)
1301 GGGGACTCAGTGTGGCGGGATGCTGCGGGAGCTGGGGACAGCCTGCGCGGCCGAGCTGCGCCTGTGGTCCCTCTGGTGGGTCTTCAACTCGGCCG
247▶ G D S V L A R M L R E L G D S L R R P Q L R L W S L W V F N S A

ApaLI (1423) **BstAPI (1486)**
1401 GCTACTACCTGGTGTACTACTGTCACATCTGTGGAACGAGGTGGACCCACCACCAACAGTGCAGCGGGTCTACAACGGCGGGCAGATGCTGCCTC
280▶ G Y Y L V V Y Y V H I L W N E V D P T T N S A R V Y N G A A D A A S
1501 CACGCTGCTGGCGCCATCACGTCTTCCGCGGGGCTTCTGGAAGATCCGCTGGGCGCGTGGTCCAAGTCTCATCGCGGGCTCACGGCCACGCAG
313▶ T L L G A I T S F A A G F V K I R W A R W S K L L I A G V T A T Q
1601 GCGGGCTGGTCTTCTTCTTGGCGCACACCGGACCCGAGCAGCATGTGCTATCGGGCTTCTGCTGTTCCGCGGGCTCCTACAGTCTCTCG
347▶ A G L V F L L A H T L R H P S S I W L C Y A A F V L F R G S Y Q F L
1701 TGCCCATCGCCACCTTTCAGATTGCATCTTCTGTCTAAAGAGCTCTGTGCCTGGTCTTCCGGGTCAACACGTTCTTTCACCATCGTCAAGACCAT
380▶ V P I A T F Q I A S S L S K E L C A L V F G V N T F F A T I V K T I

RsrII (1841)
1801 CATCACTTTCATTGTCTCGGACGTGCGGGGCTGGGCTCCCGGTCCGCAAGCAGTTCAGATTATACTCCGTGTAATCCTGATCCTGTCCATCATCTAC
413▶ I T F I V S D V R G L G L P V R K Q F Q L Y S V Y F L I L S I I Y
1901 TTCTTGGGGCCATGCTGGATGGCCTGCGGCACTGCCAGCGGGCCACCACCCGCGGAGCCCGGGCCAGGGCCTGAGGAGTGCAGCGGAGGAGAAGG
447▶ F L G A M L D G L R H C Q R G H H P R Q P P A Q G L R S A A E E K

SfiI (2029) **StuI (2037)**
2001 CAGCACAGGCACTGAGCGTGCAGGACAAGGGCCTCGGAGGCTGCAGCCAGCCAGAGCCCGCGCTTTCCCGAGAAGACAGCCTGGGGGCTGTGGGGCC
480▶ A A Q A L S V Q D K G L G G L Q P A Q S P P L S P E D S L G A V G P

EcoRI (2164) **BstAPI (2198)**
2101 AGCCTCCCTGGAGCAGAGACAGAGCACCATACTGGCCAGGCCCCGGCCCCGAGGCAGTGAATTCCTGAGCCAGTGAACCCCTTCCCTCCCTGC
513▶ A S L E Q R Q S D P Y L A Q A P A P Q A A E F L S P V T T P S P C
2201 ACTCTGTGCTCCGCCAAGCCTCAGGCCTGAGGCTGCAGATGAGACTTGTCCCGAGCTGGCTGTCCATCCTCCTGGTGTGAGCAAGCTGGGTTTGCAGT
547▶ T L C S A Q A S G P E A A D E T C P Q L A V H P P G V S K L G L Q

MscI (2350) **NheI (2344)**
2301 GTCTTCAAGCGACGGTGTTCAGAAATGTGAACCAGTGACTCTCGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAAGT
580▶ C L P S D G V Q N V N Q •

HpaI (2482) **MfeI (2493)**
2401 AATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGC

2501 ATTCATTTTATGTTTCAGGTTCAAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGC
EcoRI (2578)
2601 AAAACTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTT

2701 GCAGCCTCACCTTCTTTCATGGAGTTTAAAGATATAGTGATTTTTCCCAAGTTTGAAGCTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCCA
SapI (2760)

2801 CATTCCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTT
SspI (2817) SwaI (2831)

2901 CATAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAAGGAACCTTAAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTG
141 • N R T

3001 TACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTC
136 Y K L 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

3101 TGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTT
103 C M 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

3201 GCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTC
70 S V 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
StuI (3256)

3301 CTGATGGCCGCCCGACATGGTCTTGTGTCCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGA
36 R I A 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
XmnI (3398)

3401 AGGTCTTCATGGTGGCCCTCTATAGTGAAGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGC
3 T K M
AseI (3464)

3501 IATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCCTACCGCCATTGCGTCAATGGGGCGGAGTTGTTACGACATTT

3601 TGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCGTGAGTCAAACCGCTATCCACGCCCA
SpeI (3619)

3701 TTGATGTAAGTCCAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCACTGTAAGTGGGCAT
SnaBI (3747)

3801 AATGCCAGGCGGGCCATTTACCGTCAATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCCAAGTGGGCAGTTTACCGTAAATA
NdeI (3852)

3901 CTCCACCCATTGACGTCAATGAAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGGTCTTGGGCGGTGACGCCA

4001 GCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGAACCGTAAAAAGCCGCGTT
SdaI (4030) PacI (4038) BspLU11I (4048)

4101 GCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAG

4201 GCGTTTTCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTT

4301 CTCATAGCTCACGCTGTAGTATCTCAGTTCGGTGTAGTTCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTAGCCCGACCGCTGCGCCTT
ApaLI (4362)

4401 ATCCGGTAACTATCGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGA
4501 GGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGA
4601 GAGTTGGTAGCTCTTATCCGGCAAACAAACCCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGA
PacI (4778) SwaI (4787) NotI (4797)

4701 AGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTATGGCTAGTTAATTAACATTTAAATCAGCG
4801 GCCGCAATAAAAATATCTTTATTTTATTACATCTGTGTGTTGTTTTTTGTGTGAATCGTAACATAACGCTCTCCATCAAAAACAAACGAAACAAAA
4901 CAAACTAGCAAAATAGGCTGTCCCAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA