



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAGGTGGCGCGGGTAAACTGGAAAAGTGTCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACCGCGCCCGCCCTACCTGAGGCC

HindIII (245) 301 GCCATCCACGCCGGTTGAGTCGGTCTGCGCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

Bsu36I (291)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

NgoMIV (441)

501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCATGGCTTGGCTCCTGAGAGGGCAGCCCCACGCGTGTCT

NcoI (560)
BstEII (555)
AgeI (552) BstXI (560) 1▶ M A L A P E R A A P R V L

601 GTTCGGAGAGTGGCTCCTTGAGAGATCAGCAGCGGCTGCTATGAGGGGTGCACTGGCTGGACGAGGCCCGCACCTGTTTCCGCGTGCCTGGAAGCAC

BstAPI (629) 13▶ F G E W L L G E I S S G C Y E G L Q W L D E A R T C F R V P W K H

PstI (649)

701 TTCGCGCAAGGACCTGAGCGAGGCCGACGCGCATCTTCAAGGCTGGCTGGCCCGCGGAGGTGGCCGCTAGCAGAGGGGAGGTGGCCCGC

StuI (743) 47▶ F A R K D L S E A D A R I F K A W A V A R G R W P P S S R G G G P

801 CCCCCGAGGCTGAGACTGCGGAGCGCGCGGCTGGAACCAACTTCCGCTGCGCACTGCGCAGCAGCGTCTGCTGATGCTGCGAGATAACTCGGG

NgoMIV (826) 80▶ P P E A E T A E R A G W K T N F R C A L R S T R R F V M L R D N S G

SandI (899)

EagI (905) 901 GGACCCGCGGACCCGCAAGGTGTACGCGCTCAGCCGGAGCTGTGCTGGCGAGAAGGCCAGGCACGGACCAGACTGAGGAGAGGCCCCCGCAGCT

113▶ D P A D P H K V Y A L S R E L C W R E G P G T D Q T E A E A P A A

SfiI (1019)
Bsp120I (1018) 1001 GTCCCACCACAGGGTGGGCCCCAGGGCCATTCTGGCACACACATGCTGGACTCCAAGCCCCAGGCCCCCTCCCTGCCCCAGCTGGTGACAAGG

147▶ V P P P Q G G P P G P F L A H T H A G L Q A P G P L P A P A G D K

1101 GGGACCTCCTGCTCCAGGCACTGCAACAGAGCTGCCTGGCAGACCATCTGTGACAGCGTATGGGGGAGATCCAGTCCCAACCAAGGCTCCTGGAGA

Tth111I (1152) 180▶ G D L L L Q A V Q Q S C L A D H L L T A S W G A D P V P T K A P G E

1201 GGGACAAGAAGGGCTTCCCTGACTGGGCCTGTGCTGGAGGCCAGGGCTCCTGCTGGGGAGTGTACGGTGGGAGTAGAGACGACCCCGAGCCCC

XmaI (1297) 213▶ G Q E G L P L T G A C A G G P G L P A G E L Y G W A V E T T P S P

1301 GGGCCCCAGCCCGGCACTAACGACAGGCGAGGCCGCGGCCAGAGTCCCCGACAGGCAGGCGTACCTGTACCCTCCCAAGCGCTGCACCG

Bsp120I (1300) 247▶ G P Q P A A L T T G E A A A P E S P H Q A E P Y L S P S P S A C T

1401 CGGTGCAAGACCTGGCTGTGCCGAGTGCACCTAGAGGGCACGAGCGTGTGCTTCCCTGGATAGCAGCAGCCTCAGCCTCTGCCTGTCCAG

ApaLI (1426) 280▶ A V Q E P W L C R V H L E G T Q R E G V S S L D S S S L S L C L S S

BbsI (1458)

1501 CGCCAACAGCCTCTATGACGACATCGAGTGCTTCTTATGGAGCTGGAGCAGCCCGCTAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTG

MscI (1566) 313▶ A N S L Y D D I E C F L M E L E Q P A •

1601 GACAAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGT

HpaI (1698)

1701 TAAACAACAATAATTCATTCTTTATGTTTCAGGTTCCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTC

MfeI (1709)

EcoRI (1794)

1801 TAAATACAGCATAGCAAACTTAACTCCAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAA

1901 TGTGATTAGCTGTTGCAGCCTCACCTCTTTCATGGAGTTAAGATATAGTGTATTTTCCAAGTTTGAAGTCTCTCATTCTTTATGTTTTAA

SapI (1976)

2001 ATGCACTGACCTCCACATTCCCTTTTTAGTAAATATTCAGAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCA

SspI (2033) **Swal (2047)**

2101 GATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTA

2201 GCTTTAGTTCCTGGTACTTGGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTTCATCTCAATGAGCACAAGCAGTCAGGAGCATAG

141▶ • N R T 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

2301 TCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAA
108 D S I L E R 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

2401 AGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTACAGACAGACAGTACCCTGCCAATGTAGGCCCTCAATGTGGACAGCAGAGATGAT
75 D K Q G N 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

2501 CTCCTCAGTCTTGGTCTGATGGCCGCCGACATGGTGTCTTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCAGCTCCACCAGCTCCAGATCC
42 E G T K T 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

BspHI (2622)
2601 TGCTGAGAGATGTTGAAGTCTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGT
8 Q Q S I N F T K M

BbsI (2618) **AseI (2680)**

2701 GGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTCGCTCAATGGGGCGG
SacI (2737)

2801 AGTTGTTACGACATTTTGAAAGTCCCCTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCTGAGTCAAA
SpeI (2835)

2901 CCGCTATCCAGCCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAG
SnaBI (2963)

3001 GTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGG
NdeI (3068)

3101 CAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGCGGGGGTC

3201 GTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACC
PacI (3254) PstI (3247) SdaI (3246) BspLU11I (3264)

3301 GTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGG
BspLU11I (3264)

3401 ACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACTGTCCGCTTTCTCCCTTGC

3501 GGAAGCGTGGCGCTTTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTGAGC
ApaLI (3578)

3601 CCGACCGTGGCGCTTATCCGGTAACTATCGTCTTGTAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAG
ApaLI (3578)

3701 AGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCA
ApaLI (3578)

3801 GTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGCAAGCAGCAGATTACGCGCAGAA
ApaLI (3578)

3901 AAAAAAGATCTCAAGAAGATCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATT
PacI (3994)

EagI (4014)
4001 AACATTTAAATCAGCGGCCGAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTAATCGTAACTAACATACGCTCTCCATCAA
Swal (4003) NotI (4013)

4101 ACAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCAAGTCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA