



PvuI (7)
SgfI (6)

1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203)

201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCCGCCCTACCTGAGGCC

301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTAAAGCTCAGGTGAGACC

HindIII (245)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCCTGCTTGTCAACTCTACGTCTTTGTTTCGTTT

NgoMIV (441)

501 TCTGTTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCATCATGAGGACGCTGCTGACCATCTTGACTGTGGGATCCCT

BspHI (560)

AgeI (552)

BamHI (592)

BbrPI (640)

601 GGCTGCTCACGCCCTGAGGACCCCTCGGATCTGCTCCAGCACGTGAAATTCAGTCCAGCAACTTTGAAAACATCCTGACGTGGGACAGCGGGCCGGAG

13▶ A A H A P E D P S D L L Q H V K F Q S S N F E N I L T W D S G P E

Tth111I (709)

BsiWI (737)

701 GGCACCCAGACACGGTCTACAGCATCGAGTATAAGACGTACGGAGAGGGACTGGGTGGCAAAGAAGGGCTGTCAGCGGATCACCCGGAAGTCTGCA

47▶ G T P D T V Y S I E Y K T Y G E R D W V A K K G C Q R I T R K S C

801 ACCTGACGGTGGAGACGGCAACCTCACGGAGCTACTATGCCAGGGTACCCTGTGAGTCCGGGAGGGCGGTGAGCCACCAAGATGACTGACAGGTT

80▶ N L T V E T G N L T E L Y Y A R V T A V S A G G R S A T K M T D R F

ClaI (960)

901 CAGCTCTCTGAGCACACTACCCTCAAGCCACCTGATGTGACCTGTATCTCCAAAGTGAAGTGCATTGATGATTGTTTCATCTACCCACGCCCATC

113▶ S S L Q H T T L K P P D V T C I S K V R S I Q M I V H P T P T P I

MscI (1011)

1001 CGTGACGGCGATGGCCACCGCTAACCCCTGGAAGACATCTCCATGACCTGTTCTACCACTTAGAGCTCCAGGTCAACCCGACCTACCAAATGCACCTTG

147▶ R A G D G H R L T L E D I F H D L F Y H L E L Q V N R T Y Q M H L

BspHI (1163)

1101 GAGGGAAGCAGAGAGAATATGAGTTCTTCGGCCTGACCCCTGACACAGAGTTCCTTGGCACCATCATGATTTGCGTTCACCTGGGCCAAGGAGAGTGC

180▶ G G K Q R E Y E F F G L T P D T E F L G T I M I C V P T W A K E S A

BspLU11I (1205)

BspEI (1255)

NcoI (1274)

ScaI (1293)

1201 CCCCTACATGTGCCGAGTGAAGACACTGCCAGACCGGACATGGACCTACTCCTTCTCCGGAGCCTTCTGTTCTCCATGGGCTTCTCTGTCGAGTACTC

213▶ P Y M C R V K T L P D R T W T Y S F S G A F L F S M G F L V A V L

1301 TGCTACCTGAGCTACAGATATGTACCAAGCCGCTGCACCTCCCAACTCCCTGAACGTCCAGCGAGTCTGACTTCCAGCCGCTGCGCTTCATCCAGG

247▶ C Y L S Y R Y V T K P P A P P N S L N V Q R V L T F Q P L R F I Q

ScaI (1460)

SdaI (1495)

1401 AGCACGTCTGATCCCTGTCTTTGACCTCAGCGGCCCCAGCAGTGTGCCCAGCTGTCCAGTACTCCAGATCAGGGTGTCTGGACCCAGGGAGCCTGC

280▶ E H V L I P V F D L S G P S S L A Q P V Q Y S Q I R V S G P R E P A

1501 AGGAGTCCACAGCGGCATAGCTGTCCGAGATCACCTACTTAGGGCAGCCAGACATCTCCATCTCCAGCCCTCCAACTGCCACCTCCCAGATCCCTC

313▶ G A P Q R H S L S E I T Y L G Q P D I S I L Q P S N V P P P Q I L

Bsp120I (1639)

1601 TCCCCACTGCTCTATGCCCAAACGCTGCCCTGAGGTGGGGCCCCATCCTATGCACCTCAGGTGACCCCCGAAAGCTCAATTCCCATTCTACGCCCCAC

347▶ S P L S Y A P N A A P E V G P P S Y A P Q V T P E A Q F P F Y A P

BspEI (1746)

NsiI (1776)

1701 AGGCCATCTAAGTCCAGCCTTCTCTATGCCCTCAAGCCACTCCGGACAGCTGGCCTCCCTCTATGGGGTATGCATGGAAGTTCTGGCAAAGA

380▶ Q A I S K V Q P S S Y A P Q A T P D S W P P S Y G V C M E G S G K D

1801 CTCCCCACTGGGACACTTTCTAGTCTTAAACCTTAGGCCTAAAGTCAAGTTCAGAAAGACCCAGCTGGAAGTGCATGTTAGTGGCCTTTCT

413▶ S P T G T L S S P K H L R P K G Q L Q K E P P A G S C M L G G L S

1901 CTGCAGGAGTGACTCCTTGGCTATGGAGGAATCCCAAGAAGCAAAATCATTGCACCCAGCCCTGGGGATTTCACACAGACAGACATCTGACCCAAATG

447▶ L Q E V T S L A M E E S Q E A K S L H Q P L G I C T D R T S D P N

2001 TGCTACACAGTGGGGAGGAAGGGACACCACAGTACCTAAAGGGCCAGCTCCCCCTCCTCTCCTCAGTCCAGATCGAGGGCCACCCATGTCCTCCCTTT

480▶ V L H S G E E G T P Q Y L K G Q L P L L S S V Q I E G H P M S L P L

PshAI (2131)

2101 GCAACCTCCTTCCCGTCCATGTTCCCCCTCGGACCAAGGTCAAAGTCCCTGGGGCCTGCTGGAGTCCCTGTGTGTCCCAAGGATGAAGCCAAGGCCCA

513▶ Q P P S R P C S P S D Q G P S P W G L L E S L V C P K D E A K S P

2201 GCCCCTGAGACCTCAGACCTGGAGCAGCCACAGAAGTGGATTCTTTTTAGAGGCCTGGCCCTGACTGTGAGTGGGAGTCTGAGGGGAATGGGAAA

547▶ A P E T S D L E Q P T E L D S L F R G L A L T V Q W E S •

MscI (2306)

NheI (2300)

2301 GCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATCGAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTA

HpaI (2438)

MfeI (2449)

2401 TTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAAACAACAACAATTGCAATTCATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGTTTT

EcoRI (2534)

2501 TTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAAATCTAAATAACAGCATAGCAAACTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCT

2601 GAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTGCGAGCCTCACCTTCTTTCATGGAGTTTAAAGATATAGTGTATTTT

2701 **SapI (2716)** **SspI (2773)** **Swal (2787)**
 CCCAAGGTTTGAAGCTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCCACATTCCCTTTTTAGTAAAAATTCAGAAATAATTTAAATACATC
 2801 ATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGA
 2901 ACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTT
 141 • N R T Y K L P I L E E I T T K V L K
 3001 GCCATTCACTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGTGACCACCTGATGGATCTGTCCACC
 122 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 R D V
 3101 TCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGA
 88 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 V T V
 3201 CCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAAGTCTTGGTCTGATGGCCGCCCGACATGGTCTTGTGTCCCTCATAGAGCAT
 55 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 Y L M
XmnI (3354)
 3301 GGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTAT
 22 T I K E T A V E V L E L D Q Q S I N F T K M
AseI (3420)
 3401 GCGGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCC
SpeI (3575)
 3501 CACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCCTTGATTACTAGTCAAAACAAACTCCCATTGA
 3601 CGTCAATGGGGTGGAGACTTGAAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGAC
SnaBI (3703)
 3701 TAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGC
NdeI (3808)
 3801 GTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCGAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTA
SdaI (3986) PacI (3994)
 3901 TGGGAACATACGTCATTATTGACGTCAATGGCGGGGGTCTGTTGGCGGTCAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAACGCCTGCAGGTTAATT
BspLU11I (4004)
 4001 AAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCGTTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACA
 4101 AAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGAC
 4201 CCTGCCGCTTACCGGATACTGTCCGCCTTCTCCCTTCGGAAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTT
ApaLI (4318)
 4301 CGCTCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGTAAGACACGACT
 4401 TATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACAC
 4501 TAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCCGCTGGTAGC
 4601 GGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACG
EagI (4754)
PacI (4734) Swal (4743) NotI (4753)
 4701 AAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGT
 4801 TTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCA
 4901 GAACATTTCTCTATCGAA