



PvuI (7)
SgfI (6)
1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGTGTCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCCGCCCTACCTGAGGCC
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

BstEII (555)
AgeI (552)
501 TCTGTTCTGCCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTACCATTGGATGTATGCGTCCGCTTGGCCCTGTGGCTCCTCTG
1 M D V C V R L A L W L L W
601 GGGACTCCTCTGCACCAGGGCCAGAGCCTCAGCCATAGTCACAGTGAGAAGGCGACAGGAACAGCTCGGGGGCCAACTCTGAGGAGTCCACTGCAGCA
13 G L L L H Q G Q S L S H S H S E K A T G T S S G A N S E E S T A A
701 GAGTTTTGCCGAATTGACAAGCCCTGTGTACAGTGAGGATGAGAACTCAGCTTCGAGGCAGTCCGTAACATCCACAACTGATGGACGATGATGCCA
47 E F C R I D K P L C H S E D E K L S F E A V R N I H K L M D D D A

BbsI (841)
Bsu36I (834)
801 ATGGTGATGTGGATGTGGAAGAAAGTGTGAGTTCCTGAGGGAAGACCTCAATTACCATGACCCAACAGTGAACACAGCACCTTCCATGGTGAGGATAA
80 N G D V D V E E S D E F L R E D L N Y H D P T V K H S T F H G E D K

Bst1107I (946) **NdeI (989)**
901 GCTCATCAGCGTGGAGGACCTGTGGAAGGCATGGAAGTCATCAGAAGTATACAATTGGACCGTGGATGAGGTGGTACAGTGGCTGATCACATATGTGGAG
113 L I S V E D L W K A W K S S E V Y N W T V D E V V Q W L I T Y V E

BspEI (1022)
1001 CTGCCTCAGTATGAGGAGACCTTCGGAAAGCTGCAGCTCAGTGGCCATGCCATGCCAAGGCTGGCTGTACCAACACCACCATGACAGGGACTGTGCTGA
147 L P Q Y E E T F R K L Q L S G H A M P R L A V T N T T M T G T V L

PshAI (1108)
1101 AGATGACAGACCGGAGTCAATCGGCAGAAAGTGCAGCTGAAGGCTCTGGATACAGTGTCTTTGGGCTCCTCTTACTCGCCATAATCACCTCAAGGA
180 K M T D R S H R Q K L Q L K A L D T V L F G P P L L T R H N H L K D
1201 CTTTCATGCTGGTGGTGTCTATCGTTATTGGTGTGGGCGGCTGCTGTTTGCCTATATCCAGAACCCTTACTCCAAGGAGCAGATGAAGAAGATGATGAAG
213 F M L V V S I V I G V G G C W F A Y I Q N R Y S K E H M K K M M K
1301 GACTTGGAGGGTTACACCGAGCTGAGCAGAGTCTGCATGACCTTCAGGAAAGGCTGCACAAGGCCAGGAGGAGCACCCGACAGTGGAGTGGAGAAGG
247 D L E G L H R A E Q S L H D L Q E R L H K A Q E E H R T V E V E K

BsrBI (1489)
1401 TCCATCTGAAAAGAAGCTGCGCGATGAGATCAACCTTGTAAAGCAGGAAGCCAGCGGCTGAAGGAGCTGCGGGAGGGTACTGAGAATGAGCGGAGCCG
280 V H L E K K L R D E I N L A K Q E A Q R L K E L R E G T E N E R S R

StuI (1538)
1501 CCAAAAATATGCTGAGGAGGAGTTGGAGCAGGTTTCGGGAGGCTTGGAGAAAGCAGAGAAGGAGCTAGAATCTCACAGCTCATGGTATGCTCCAGAGGCC
313 Q K Y A E E E L E Q V R E A L R K A E K E L E S H S S W Y A P E A
1601 CTTCAGAAGTGGTGCAGCTGACACATGAGGTGGAGGTGCACTATTACAACATCAAGAAGCAAAATGCTGAGAAGCAGCTGCTGGTGGCAAGGAGGGGG
347 L Q K W L Q L T H E V E V Q Y Y N I K K Q N A E K Q L L V A K E G

BbrPI (1744) **SapI (1757)**
1701 CTGAGAAGATAAAAAAGAAGAGAAACACACTCTTTGGCACCTTCCAGTGGCCACAGCTCTTCCCTGGATGATGTAGATCATAAAATTCTAACAGCTAA
380 A E K I K K K R N T L F G T F H V A H S S S L D D V D H K I L T A K
1801 GCAAGCACTGAGCGAGGTGACAGCAGCATTGCGGGAGCGCTGCACCCTGGCAACAGATCGAGATCCTCTGTGGCTCCAGATTGTCAACAACCTGGC
413 Q A L S E V T A A L R E R L H R W Q Q I E I L C G F Q I V N N P G

BspHI (1976)
1901 ATCCACTCACTGGTGGCTGCCCTCAACATAGACCCAGCTGGATGGGAGTACACGCCCAACCTGCTCACTTCATCATGACTGACGACGTGGATGACA
447 I H S L V A A L N I D P S W M G S T R P N P A H F I M T D D V D D
2001 TGGATGAGGAGATTGTGTCTCCCTTGTCCATGCAGTCCCCTAGCCTGCAGAGCAGTGTTCGGCAGCGCCTGACGGAGCCACAGCATGGCCTGGGATCTCA
480 M D E E I V S P L S M Q S P S L Q Q S S V R Q R L T E P Q H G L G S Q
2101 GAGGATTTGACCAATCCGATTCCGAGTCCCTCCCTCAGTACAGTACCGCCAGCGTGTGGCCCCAACCTCCTCAGATGAGCCGCTGCTGCAGACGAG
513 R D L T H S D S E S S L H M S D R Q R V A P K P P Q M S R A A D E
2201 GCTCTCAATGCCATGACTTCCAATGGCAGCCACCGGCTGATCGAGGGGTCCACCCAGGCTCTGTTGGAGAAACTGCCTGACAGCCCTGCCCTGGCCA
547 A L N A M T S N G S H R L I E G V H P G S L V E K L P D S P A L A

DraIII (2372)
2301 AGAAGGCATTACTGGCGCTGAACCATGGCTGGACAAGGCCACAGCCTGATGGAGCTGAGCCCTCAGCCCCACCTGGTGGCTCTCCACATTTGGATTC
580 K K A L L A L N H G L D K A H S L M E L S P S A P P G G G S P H L D S
2401 TTCCGTTCTCACAGCCAGCTCCCCAGACACACACCTCCTCAGTTGGGACAGCCGAGCCCTGCAAGCCGAAACACACGATTCCCCAC
613 S R S H S P S S P D P D T P S P V G D S R A L Q A S R N T R I P H
2501 CTGGCTGGCAAGAAGGCTGTGGCTGAGGAGGATAATGGCTCTATTGGCAGGAAACAGACTCCAGCCAGGCCGGAAGAAGTTTCCCTCAAATCTTTA
647 L A G K K A V A E E D N G S I G E E T D S S P G R K K F P L K I F

2601 AGAAGCCTCTTAAGAAGTAGGCAGGATGGGGTGGCAGTAAAGGACAGCTTGTCTTCCGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGG
680 ▶ K K P L K K •

2701 ACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT
HpaI (2797)

2801 AACAAACAACATTCATTTCATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAATGTGGTATGGAATTCT
EcoRI (2893)

2901 AAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAAT

3001 GTGCATTAGCTGTTTGCAGCCTCACCTCTTTCATGGAGTTTAAAGATAGTGTATTTTCCCAAGTTTGAAGCTAGCTCTTCATTTCTTTATGTTTTAAA
SapI (3075)

3101 TGCACTGACCTCCACATTCCCTTTTTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAG
SspI (3132) SwaI (3146)

3201 ATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAG

3301 CTTTAGTTCCTGGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGT
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 D
SacI (3407)

3401 CAGAGATGAGCTCTGACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAA
108 ◀ 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
StuI (3571)

3501 GTCCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATC
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

3601 TCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTCTTGTGTCCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCT
41 ◀ 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 Q
BbsI (3717)

3701 GCTGAGAGATGTTGAAGGCTTCATGGTGGCCCTCTATAGTGAAGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGGTG
8 ◀ Q S I N F T K M
XmnI (3713) AseI (3779)

3801 GATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTGCGTCAATGGGGCGGA
SacI (3836)

3901 GTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCGTGAGTCAAAC
SpeI (3934)

4001 CGCTATCCAGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGG
SnaBI (4062)

4101 TCATGTAAGTGGCATAATGCCAGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGC
NdeI (4167)

4201 AGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATATTGACGTCAATGGGCGGGGGTGC

4301 TTGGGCGTCCAGCCAGCGGGCCATTTACCGTAAAGTATGTAACGCTGCAGGTTAATAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCG
SdaI (4345) PacI (4353) BspLU11I (4363)

4401 TAAAAAGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAATAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGA
BspLU11I (4363)

4501 CTATAAGATACCAGCGTTTTCCCTGGAAGTCCCTCGTGCCTCTCTGTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGG

4601 GAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTCCAGCC
ApaLI (4677)

4701 CGACCCTGCGCCTTATCCGGTAACTATCGTCTTGTAGTCAACCCGGTAAAGACACGACTTATCGCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGA
BspLU11I (4363)

4801 GCGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAG
BspLU11I (4363)

4901 TTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCCGCTGGTAGCGGTGTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAA
BspLU11I (4363)

5001 AAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTA
PacI (5093)

5101 ACATTTAAATCAGCGGCCGAATAAAATATCTTTATTTTATTACATCTGTGTGGTTTTTTGTGTAATCGTAACTAACATACGCTCTCCATCAAAA
EagI (5113) SwaI (5102) NotI (5112)

5201 CAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCAGTGCAAGTGACGGTCCAGAACATTTCTATCGAA