



PvuI (7)
SgfI (6)
1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCTGTACTGGCTCCGCCTTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

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

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

AgeI (552) **BspHI [m] (560)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTATCATGATCGCCTGGCGTCTGCCCTGTGCGTGCTCTTGGT
1 M I A W R L P L C V L L V

Tth111I (682)
601 GGCTCCGTCGAGAGCCACCTGGGGCCCTGGGGCCCAAGAAGCTCTCGAGAAAGACGCGGAGTTTGGCGCACCTACGCGGACGACGTCAACAGCGAG
13 A S V E S H L G A L G P K N V S Q K D A E F E R T Y A D D V N S E

DraIII (724) **RsrII (742)**
701 CTGGTCAACATCTACACCTTCAACCAACCGTGACCCGCAACCGGACCGAGGGTGTGCGAGTGTCTGTGAATGTCCTGAACAAGCAGAAAGGGGCGCCTT
47 L V N I Y T F N H T V T R N R T E G V R V S V N V L N K Q K G A P
801 TGGTGTGTGGTCCGCCAGAAGGAGGCTGTGTCTCCAGGTGCCCTAATCCTTCGAGGACTATATCAGCGGAAGTACCTCTACCAAAAAGTGGGA
80 L L F V V R Q K E A V V S F Q V P L I L R G L Y Q R K Y L Y Q K V E
901 ACGAACTCTGTGTCAGCCCCACCAAGAATGAGTCTGAGATCCAGTTTTTCTATGTGGAGTGTCTACCCTGTCACCCGTCAATACCACTTACCAGCTC
113 R T L C Q P P T K N E S E I Q F F Y V D V S T L S P V N T T Y Q L

Scal (1076)
1001 CGAGTCAACCGTGTGGACAATTTGTGCTCAGGACTGGAGAGCTGTTACTTTAATACCACTGCAGCCCAGCCCCAGTACTTCAAATACGAGTTTCTCG
147 R V N R V D N F V L R T G E L F T F N T T A A Q P Q Y F K Y E F P

BstEII (1125)
1101 ATGGTGTGGACTCGGTAATTGTCAAGGTGACCTCAAGAAGGCCTTCCCTGCTCAGTCATCTCCATCCAAGATGTCCTGTGCCCTGTCTATGATCTGGA
180 D G V D S V I V K V T S K K A F P C S V I S I Q D V L C P V Y D L D
1201 CAACAATGTAGCCTTCATTGGCATGTACCAGACGATGACTAAGAAGGCAGCCATCACTGTGCAGCGGAAAGACTTCCCAGCAACAGCTTCTATGTGGTG
213 N N V A F I G M Y Q T M T K K A A I T V Q R K D F P S N S F Y V V
1301 GTGGTAGTGAAGACTGAGGACCAGGCCTGCGGAGGGTCTTGCCTTCTACCTTTTGTGGAAGATGAGCCAGTGGATCAAGGGCACCGTCAGAAAACAC
247 V V V K T E D Q A C G G S L P F Y P F V E D E P V D Q G H R Q K T
1401 TGTGAGTGTGCTCTCAGGCTGTACATCTGAGGCTATGTTGGTGGGATGCTCTTTGCTGGGCATATTCTTGTCTTCTACCTGCTGACTGTGCT
280 L S V L V S Q A V T S E A Y V G G M L F C L G I F L S F Y L L T V L

XmaI (1583)
1501 GCTGGCCTGTTGGGAGAAGTGGAGGCAAGGAAGAAGACCTTGTCTGTTGGCCATAGACCGAGCCTGCCAGAAAGTGGTCACGCCCGGCTTGGCTGAT
313 L A C W E N W R Q R K K T L L L A I D R A C P E S G H A R V L A D
1601 TCATTTCTGGCAGTGCCTTACGAGGGTTACAACATATGGCTCCTTTGAAAATGGTTCGGATCCACTGACGGGTTGGTTGAAAGCGCAGGTTACAGGGG
347 S F P G S A P Y E G Y N Y G S F E N G S G S T D G L V E S A G S G

NcoI (1778)
1701 ACCTCTCTACAGTTACCAGGGGACGACCACTTCAAGCGGCGCCTTCCCTCTGGCCAGATGCGGCAGCTGTGCATTGGCCATGGACCGCTCCTTTGACGC
380 D L S Y S Y Q G H D Q F K R R L P S G Q M R Q L C I A M D R S F D A

BstBI (1892)
1801 AGTGGTCTCGGCCTCGACTGGACTCCATGAGCTCCGTGGAAGAGGATGACTACGACACACTGACTGACATCGACTCAGACAAAAACGTCATTTCGAACC
413 V G P R P R L D S M S S V E E D D Y D T L T D I D S D K N V I R T
1901 AAGCAATACCTCTGTGTGGCTGATCTGGCAGCAAAAGGACAAACGTGTTTTGCGGAAAAAGTACCAGATTTACTTCTGGAACATAGCCACCATTGCGGTCT
447 K Q Y L C V A D L A R K D K R V L R K K Y Q I Y F W N I A T I A V
2001 TCTACGCACTTCTGTGGTGCAGCTGGTGTATCACCTACCAGACGGTGGTGAATGTCACAGGGAACAGGACATCTGCTACTACAACCTCCTCTGTGCCCA
480 F Y A L P V V Q L V I T Y Q T V V N V T G N Q D I C Y Y N F L C A H
2101 CCCGCTGGGCAACCTCAGCGCTTCAACAACATCCTCAGCAACTTGGGTACATCCTGCTGGGCTGCTCTTCTGCTCATCATCCTGCAGCGAGAGATC
513 P L G N L S A F N N I L S N L G Y I L L G L L F L L I I L Q R E I

NcoI (2279)
2201 AATCATAACCGGGCCCTGCTCGGAATGACCTCTATGCTCTGGAGTGTGGATCCCCAACACTTTGGTCTGTTTTACGCCATGGGCACAGCACTGATGA
547 N H N R A L L R N D L Y A L E C G I P K H F G L F Y A M G T A L M

BsrGI (2372) **SphI (2393)**
2301 TGGAGGGCTACTTAGTGCTTACCAGCTGTGCCCAACTACACCAACTCCAGTTTGATACCTCCTTCATGTACATGATTGCTGGCCTCTGCATGCT
580 M E G L L S A C Y H V C P N Y T N F Q F D T S F M Y M I A G L C M L

NdeI (2450)
2401 GAAGCTCTACCAGAAGCGGCACCCAGATATCAACGCCAGTGCCTACAGTGCATAGCTTGGCCATCGTCATCTTCTTCTCCGTTCTGGGCGTGGTG
613 K L Y Q K R H P D I N A S A Y S A Y A C L A I V I F F S V L G V V
2501 TTTGGCAAAGGGAACACGGCCTTCTGGATTGTCTTCTCCGTCACTTCCACATCATCACCCTGCTCCTCAGCACTCAGCTCTATTACATGGGCGCTGGA
647 F G K G N T A F W I V F S V I H I I S T L L L S T Q L Y Y M G R W

RsrII (2681)

2601 AGCTGGACTCCGGGATCTTCGCGCATCTCCATGTGCTCTACACAGACTGCATCCGGCAGTGCAGCGGGCCCTTTACACGGACCGCATGGTGCTTCT
680▶ K L D S G I F R R I L H V L Y T D C I R Q C S G P L Y T D R M V L L
2701 GGTTCATGGCAACATTATCAACTGGTGGTGGTGCATACGGACTCATCATGCCCAATGACTTTGCTTCTACTTGTGGCAATTGGCATCTGCAAC
713▶ V M G N I I N W S L A A Y G L I M R P N D F A S Y L L A I G I C N

BspHI (2828)

BstAPI (2876)

2801 CTGCTGCTTTATTTGCGCTTCTACATCATCATGAAGCTCCGGAGCGGGAGAGGATCAAGCTCATCCCTCTGCTCTGCATCGTCTGCACCTCCGTGGTCT
747▶ L L L Y F A F Y I I M K L R S G E R I K L I P L L C I V C T S V V

BbrPI (2937)

2901 GGGGCTTCGCGCTCTTCTTCTTCCAGGGACTGAGCACGTGGCAGAAAACCCCGCAGAGTCCAGGGAGCACAACCGGACTGCATCCTCCTCGACTT
780▶ W G F A L F F F F Q G L S T W Q K T P A E S R E H N R D C I L L D F
3001 CTTTGATGACCACGATATCTGGCACTTCTGTCTCCATTGCCATGTTGGGTCCTTCTGGTTTTGCTGACGTTGGATGACACTTGGACACAGTACAG
813▶ F D D H D I W H F L S S I A M F G S F L V L L T L D D D L D T V Q

BglIII (3107)

NheI (3141)

3101 CGGGACAAGATCTATGCTTCTAGCAGCATCTGTGGTCCAGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAAGTGAAT
847▶ R D K I Y V F •

HpaI (3279)

3201 GCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACCAAGTTAACAAACAATTGCATT

EcoRI (3375)

3301 CATTATGTTTCAGGTTAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAA

3401 ACTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGA

3501 GCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCAAGTGTGAACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACAT

SspI (3614)

Swal (3628)

3601 TCCCTTTTAGTAAAATATTAGAAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCAT

3701 AATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTAC

3801 TTGAGGGGATGAGTTCTCAATGGTGGTTTTGACCAGCTTGCATTCAATGAGCACAAGCAGTCCAGGAGCATAGTCAGAGATGAGCTCTCTGC
135▶ 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 C

BstXI (3918)

3901 ACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCT
102▶ 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 S

4001 CACAGCAGACCAATGGCAATGGCTTACGACAGACAGTGGACCTGCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGCTCTG
69▶ 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 R

4101 ATGGCCGCCCCGACATGGTGTGTTGCTCTCATAGAGCATGGTGTCTTCTAGTGGCGACTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGG
35▶ 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 T

AseI (4261)

4201 TCTTCATGGTGGCCCTCTATAGTGAGTGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGATGGCGTCTCCAGCTTA
2▶ K M

4301 TCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGG

SpeI (4416)

4401 AAAGTCCCCTGTTGATTTACTAGTCAAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTG

SnaBI (4544)

4501 ATGTACTGCCAAAACCGCATCATCATGTAATAGCGATGACTAATACGTAGATGTAAGTCCCAAGTAGGAAAGTCCCATAAAGTTCATGTAAGTGGCATAAT

NdeI (4649)

4601 GCCAGCGGGCCATTTACCGTCAATTGACGTCAATAGGGGGGCTACTTGGCATATGATACACTTGTACTGCAAGTGGGAGTTTACCGTAAATACTC

4701 CACCCATTGACGTCAATGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGACCCAGGC

PacI (4835)

SdaI (4827)

BspLU11I (4845)

4801 GGGCATTACCGTAAGTTATGTAACGCTGCAGGTTAATAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTCT

4901 GCGTTTTTCCATAGGCTCCGCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGGC

5001 TTTCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCTGCCGTTACCGGATACCTGTCGCTTTCTCCCTCGGGAAGCGTGGCGCTTTCTC

ApaLI (5159)

5101 ATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCAGCCGACCGCTGCGCTTATC

5201 CGGTAACATCGTCTTGTAGTCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGCT

5301 GCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAG

5401 TTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTCGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGA

5501 TCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCC

EagI (5595)
PacI (5575) SwaI (5584) NotI (5594)

5601 GCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAA

5701 ACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA