



PvuI (7)
SgfI (6)
1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) **PvuII (239)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACCGCGCCGCCGCCCTACCTGAGGGC
301 GCCATCCACGCGGTTGAGTCGCGTCTGCCGCTCCCGCCTGTGGTGCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGTCTTTGTTTCGTTT

BspHI (566)
EcoRV (558) **BsaBI (558)** **EcoRI (570)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCCCTACCTGAGATCACCGGAGATATCCATCATGAATTCCACAGAGTCCTACTTTGGAACGGA
1 M N S T E S Y F G T D

NcoI (639)
601 TGATTATGACAACACAGAGTATTATTCTATTCTCCAGACCATGGCCATGCTCCCTAGAAGAGGTCAGAAAATTCCACCAAGTATTTGTCCAAATTGCC
11 D Y D N T E Y Y S I P P D H G P C S L E E V R N F T K V F V P I A

PshAI (783)
701 TACTCCTTAATATGTGCTTTGGCCTCCTGGCAACATTATGGTGGTGATGACCTTTGCCTTCTACAAGAAAGCCAGATCCATGACTGACGTCTACCTGT
45 Y S L I C V F G L L G N I M V V M T F A F Y K K A R S M T D V Y L

MscI (806)
801 TGAACATGGCCATCACAGACATACTCTTTGTCCCTACCCTACCGTTCTGGGCAGTTACTCATGCCACCAACACTTGGGTTTTACGCGATGCACGTGTGTA
78 L N M A I T D I L F V L T L P F W A V T H A T N T W V F S D A L C K

NdeI (914) **AgeI (968)**
901 ACTGATGAAAGGCACATATGCGGTCAACTTTAACTGTGGGATGCTGCTCCTGGCCTGTATCAGCATGGACCGGTACATTGCCATCGTCCAGGCAACAAAA
111 L M K G T Y A V N F N C G M L L L A C I S M D R Y I A I V Q A T K
1001 TCTTTCCGGGTACGCTCCAGAACACTGACGCACAGTAAGGTCATCTGTGTGGCAGTGTGGTTCATCTCCATCATCATCTCAAGCCCTACATTTATCTTCA
145 S F R V R S R T L T H S K V I C V A V W F I S I I I S S P T F I F

BbrPI (1167)
1101 ACAAGAAATACGAGCTGCAGGATCGTGATGCTGTGAGCCACGGTACAGGCTGTCTCAGAGCCATCACGTGGAAGCTGCTGGGTATGGGACTGGAGCT
178 N K K Y E L Q D R D V C E P R Y R S V S E P I T W K L L G M G L E L
1201 GTTCTTTGGGTTCTTACCCTTTGCTGTTTATGGTGTCTGTATCTGTTTATTATCAAGACCTTGGTGCAGGCCAGAACTCCAAGAGGCACAGAGCC
211 F F G F F T P L L F M V F C Y L F I I K T L V Q A Q N S K R H R A

PshAI (1371)
1301 ATCCGAGTCGTGATCGCTGTGGTCTCGTGTCTCCTGGCTTGTGATCCCTCACAAATGGTCTCCTCGTACTGCGGTCAACACGGGCAAAGTGGGCC
245 I R V V I A V V L V F L A C Q I P H N M V L L V T A V N T G K V G

BstXI (1433) **EcoO109I (1448)**
1401 GGAGCTGCAGCACCGAGAAAGTCCCTCGCTACACCAGGAACGTGGCCGAGGTCCTGGCTTTTCTGATTGCTGCTCAACCCCGTGTGTATGCGTTTAT
278 R S C S T E K V L A Y T R N V A E V L A F L H C C L N P V L Y A F I

BspHI [mj] (1530) **XmaI (1589)**
1501 TGGACAGAAATTCAGAACTACTTCATGAAGATCATGAAGATGTGTGGTGTATGAGAAGGAAGAATAAGATGCCTGGCTTCTGTGCCCCGGGTTTAC
311 G Q K F R N Y F M K I M K D V W C M R R K N K M P G F L C A R V Y

NsiI (1649) **NheI (1690)** **MscI (1696)**
1601 TCGGAAAGCTACATCTCCAGGCAGACCAGTGAGACCGTCAAAAATGATAATGCATCGTCTTTACCATGTAACACGAGAGCACAAAGCAAGCTAGCTGGC
345 S E S Y I S R Q T S E T V E N D N A S S F T M • -
1701 CAGACATGATAAGATACATTGATGAGTTTGACAAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATT

HpaI (1828)
1801 TGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACAAATTGCATTCAATTTATGTTTCAGGTTTCAGGGGAGGTGTGGAGGTTTTTAAAGCAAG

EcoRI (1924)
1901 TAAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAA
2001 TAAGGCATAGGCATCAGGGGCTGTTGCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTTCATGGAGTTTAAAGATATAGTGTATTTTCCAAGTGT

SapI (2106) **SspI (2163)** **SwaI (2177)**
2101 GAACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTGTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGA

EcoO109I (2238)
2201 AAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAGGAACCTTTAATA

2301 GAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTTCATC
141 • N R T Y K L P I L E E I T T K V L K G N M

SacI (2438) **BstXI (2467)**
2401 TCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGT
118 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 E D S Y

2501 AGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAAT
85 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 R G I
StuI (2602)

2601 GTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTCTTGTGCTCCATAGAGCATGGTATCTTC
52 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 T I K
BbsI (2748)

2701 TCAGTGGCGACCTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATAC
18 E T A V E V L E L D Q Q S I N F T K M
XmnI (2744)

2801 TATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCCACCGTACAC
AseI (2810) SacI (2867)

2901 GCCTACCGCCATTTCGCTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCCATTGACGTCAATGGG
SpeI (2965)

3001 GTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAG
SnaBI (3093)

3101 ATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCA
NdeI (3198)

3201 TATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCTATTGGCGTTACTATGGGAACATA

3301 CGTCATTATTGACGTCAATGGCGGGGGTCTGTTGGCGGTGTCAGCCAGGCGGGCCATTACCGTAAGTTATGTAACGCCCTGCAGGTTAATTAAGAACATGT
SdaI (3376) PacI (3384) BspLU111 (3394)

3401 GAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACG
3501 CTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGCTT
3601 ACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCATAGCTCACGCTGTAGGTATCTCAGTTCCGGTGTAGGTGCTTCGCTCCAAGC
ApaLI (3708)

3701 TGGGCTGTGTGCACGAACCCCCGTTTCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACT
3801 GGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCCTGAAGTGGTGGCTAACTACGGCTACACTAGAAGAACA
3901 GTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTTTGATCCGGCAAACAACCCGCTGGTAGCGGTGGTTTTT
4001 TTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACG
EagI (4144)

4101 TTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTGTGTG
PacI (4124) SmaI (4133) NotI (4143)

4201 AATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCGAGTGCAAGTGCAGGTGCCAGAACATTTCT
4301 CTATCGAA