



PvuI (7)
SgfI (6) 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
MfeI (82)
101 GAGAAAGTGGCGCGGGGTAAACTGGAAAAGTGTCTGTACTGGCTCCGCCTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGCC
PvuII (239)
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCTGACCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

XcmI (560)
BstEII (555)
AgeI (552) NcoI (560)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCCGCTACCTGAGATCACCGGTACCATGGATAAATTGGACAGATCATCAAGTTAGCCAGCT
1 M D K L G Q I I K L G Q L

BstAPI (666)
ApaLI (664)
601 CATCTATGAC_CAGTGTGAAAAGATGAAATACTGCCGAAACAATGCCAGCGTCTAGGAAACCGTGTGCACGGCTGTACAGCCTCTCCAGAGACTCCAG
13 I Y D Q C E K M K Y C R K Q C Q R L G N R V H G L L Q P L Q R L Q
701 GCCCAAGGAAAGAAGAACTGCCGATGACATTACTGCTGCCCTGGCCGTTTTGATGAAGTCTGAAGGAGGCTAACAGCAGATAGAAAAGTTCAGCA
47 A Q G K K N L P D D I T A A L G R F D E V L K E A N Q Q I E K F S
801 AGAAGTCCCATATTTGGAAGTTTGTGAGTGTGGCAATGATAAGATCCTTCCATGAAGTGAATGAGAAGCTGAGAGACGTCTGGGAGGAGCTGTTGCT
80 K K S H I W K F V S V G N D K I L F H E V N E K L R D V W E E L L L
901 GCTGCTTCAGGTTTATCATTGGAATACCGTTTCAGAC_GTCAGCCAGCCAGCATCCTGGCAGCAGGAAGATCGACAGGATGCAGAGGAAGACGGAAATGAA
113 L L Q V Y H W N T V S D V S Q P A S W Q Q E D R Q D A E E D G N E

BglII (1098)
1001 AATAGGAAAGTTATCCTGATGCGAGTTGCAAATTAGCGTGAAGAAATCAACAAAACCTGAAGCAATGCTCACTAAAACCCACACAGGAGATCCCACAAG
147 N T K V I L M Q L Q I S V E E I N K T L K Q C S L K P T Q E I P Q

BglII (1198)
1101 ATCTCAAATCAAGGAGATTCAAAGGAACATCTTGGACCTCCGTGGACCAAACCTGAAGACAAGTAAATGAGCACCATTTATAGAGGAGAGTATCACAG
180 D L Q I K E I P K E H L G P P W T K L K T S K M S T I Y R G E Y H R

XmnI (1290)
1201 ATCTCCAGTTACCATCAAAGTATCAACAACCCCGAGCCGAAAGTGTGGAATAGTGAAGTTCACCTTCAATGACGAGATCAAACCATGAAGAAATTC
213 S P V T I K V F N N P Q A E S V G I V R F T F N D E I K T M K K F

ScaI (1379)
1301 GATTCTCCAACATCTTGCATATATTTGGGATTTGCATTGATCAAACAGTGAAGCCCCCTGAGTTCTCATTGTCATGGAGTACTGTGAACCTGGAACCC
247 D S P N I L R I F G I C I D Q T V K P P E F S I V M E Y C E L G T

FspI (1442)
1401 TGAGGAACTGCTGGATAGAGAAAAAGACCTCACAAATGAGTGTGCGCAGCCTCCTAGTCTGAGGGCAGCCAGAGGCTTATACAGGCTACACCATTGCGGA
280 L R E L L D R E K D L T M S V R S L L V L R A A R G L Y R L H H S E

HindIII (1558) **EcoRI (1590)**
1501 AACACTCCACAGAAACATCAGCAGCTCCAGTTTCTCGTAGCCGAGGCTACCAAGTAAAGCTTGACAGATTTGAGTTAAGCAAAAACAGAAATCCATC
313 T L H R N I S S S S F L V A G G Y Q V K L A G F E L S K T Q N S I
1601 AGCCGGACAGCAAAGAGCACTAAAGCAGAGAGATCCAGTTCAACGATATATGTCTCCCCTGAGAGACTGAAAAATCCATTTTGCCTTTATGACATAAAAG
347 S R T A K S T K A E R S S S T I Y V S P E R L K N P F C L Y D I K
1701 CTGAAATATATAGCTTTGGAATTGTACTCTGGGAAATTGCCACTGAAAGATCCCATTGAAAGCTGTGATTCTAAGAAGATCCGGGAGCTGGTGGCTGA
380 A E I Y S F G I V L W E I A T G K I P F E G C D S K K I R E L V A E

AseI (1855)
1801 GGACAAGAAGCAGGAACAGTGGGTGAGGATTGCCCTGAGTTGTTGCGGAAATCATTAAATGAGTGTGTCGTCATGAGCCCTCCAACGGCCCTCTGTG
413 D K K Q E P V G Q D C P E L L R E I I N E C R A H E P S Q R P S V

MseI (1965)
NheI (1959)
1901 GACGGAATCTTGAGAGACTGTCTGCGGTTGAAGAATCCACGGACAAGAAGGTGTAAGAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTGG
447 D G I L E R L S A V E E S T D K K V

HpaI (2097)
2001 ACAAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAAACAAGTT

MfeI (2108) **EcoRI (2193)**
2101 AACAAACAATTCATTATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTCT
2201 AAAATACAGCATAGCAAACTTAACTCCAATCAAGCCTCTACTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAAT

2301 GTGCATTAGCTGTTTGCAGCCTCACCTCTTTTCATGGAGTTTAAAGATATAGTGATTTTTCCCAAGGTTTGAAGCTAGCTCTTCATTTCTTTATGTTTTAAA
SapI (2375)

2401 TGCAGTACCTCCACATTCCCTTTTTAGTAAAAATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAG
SspI (2432) **SwaI (2446)**

2501 ATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTAAATAGAAATTGGACAGCAAGAAAAGCGAGCTTCTAG
EcoO109I (2507)

2601 CTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGT
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 (2707)

2701 CAGAGATGAGCTCTGACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAA
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 (2871)

2801 GTCCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATC
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
2901 TCCCAGTCTTGGTCTGATGGCCGCCGACATGGTCTTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCT
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
XmnI (3013) **AseI (3079)**

3001 GCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACGCGTG
8 Q S I N F T K M

3101 GATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGA
SacI (3136)

3201 GTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCGTGAGTCAAAC
SpeI (3234)

3301 CGCTATCCAGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGG
SnaBI (3362)

3401 TCATGTAAGTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCCAAGTGGGC
NdeI (3467)

3501 AGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATTTGACGTCAATGGGGCGGGGTGC
PacI (3653)

3601 TTGGCGGTGACCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCG
PstI (3646) **SdaI (3645)** **BspLU11I (3663)**

3701 TAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCTGACGAGCATCAGAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGA
PacI (4393)

3801 CTATAAAGATACCAGGCTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGG
ApaLI (3977)

3901 GAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTCAGCC
EagI (4413)

4001 CGACCGCTGCGCTTATCCGGTAACTATCGTCTTGTAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGA
SwaI (4402) **NotI (4412)**

4101 GCGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAG
EagI (4413)

4201 TTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAA
PacI (4393)

4301 AAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTA
EagI (4413)

4401 ACATTTAAATCAGCGGCCCAATAAAAATATCTTTATTTTATTACATCTGTGTGGTTTTTTGTGTGAATCGTAACATAACATACGCTCTCCATCAAAA
SwaI (4402) **NotI (4412)**

4501 CAAAACGAAACAAACAAACTAGCAAATAGGCTGCCCCAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA