



PvuI (7)
SgfI (6) 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA MfeI (82)

101 GAGAAAGTGGCGGGGTAACGGAAAGTGTGCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **PvuII (239)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCAGAGGGCTCGCATCTCTCTTTCACGCGCCCGCCCTACCTGAGGGCC

301 GCCATCCACGCGGGTTGAGTCGCGTTCTGCGCCCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGTCTTTGTTTCGTTT

NcoI (560)
BstEII (555)
AgeI (552) 501 TCTGTTCTGCGCGGTACAGATCCAAGCTGTGACCGCGCCCTACCTGAGATCACCGGTACCATTGGATCTGGTCGGAGTGTCTTCGCTGAGCCAGGGCC **Bsp120I (595)**
1 M D L V G V S S P E P G P

SauI (612) **NcoI (628)**
601 CGCAGCAGCTTGGGACCCAGTAAAGTGCCTATGGGCTACCCCTCAAACACAGATCCTGTTCACTGACCGAGGTGATGAGTGGAGACTGGCTAAAGAG
13 A A A W G P S K C P W A T P Q N T V S C S L T E V M S E E L A K E

PstI (700)
701 CTGCAGTTGGAAGAAGAAGCGGCTGCTTCCCTGAAGTGTGTTGCTGAAGGACCATTCATTCTGGAGAAAACATTGACACTTCCAGTGACCTAATGC
47 L Q L E E A A A F P E V V V A E G P F I S G E N I D T S S D L M
80 TGGCTCAGATGCTACAGATGGAATTTGACAGAGAATATGATGCACAGCTTAGGCGTGAGGAAAAGAAGTTCAATGGTGATAGCAAAGTTTCCATTTCGTT
80 L A Q M L Q M E F D R E Y D A Q L R R E E K K F N G D S K V S I S F

XhoI (971)
901 TGAAAACATCGCAAAGTTCATCCTTTGAAGACAGTGACAGCTCTGAAGACGAGGTTGACTGGCAGGACACTCGAGACGATCCCTACAGACCAGCAAAG
113 E N Y R K V H P F E D S D S E D E V D W Q D T R D D P Y R P A K
1001 CCAATTCCTACTCCAAAAGGGTTTTATTGAAAAGGAAAAGACATCACCAAGCATGATGAAGTAGTATGTGAAAGAAAGAACACAGCAAGAATGG
147 P I P T P K K G F I G K G K D I T T K H D E V V C G R K N T A R M

SapI (1198)
1101 AAAATTTGCCCTGGCTTTAGGTTAGGGATGGAATGGAATGGATTTGAAACTATCCAACCACGTTTTTAATGCCTTAAACACACGCTACTCAGA
180 E N F A P G F Q V G D G I G M D L K L S N H V F N A L K Q H A Y S E
1201 AGAGCGTCGGAGTGCCGCTACACGAGAAGAAGAACATTCTACCGTGAAAAGCAGTTGATCCTAAGACACGCTTACTTATGTATAAAATGGTCAAC
213 E R R S A R L H E K K E H S T A E K A V D P K T R L L M Y K M V N

NdeI (1364)
NsiI (1361)
1301 TCTGGAATGTTGGAGACAATCACTGGCTGTATTAGTACAGGAAAGAACTGTGTTGCTTTTCATGCATATGGAGGGAGCCTGGAGGATGAAAAGGAAGTG
247 S G M L E T I T G C I S T G K E S V V F H A Y G G S L E D E K E D
1401 GTAAGCTATACCAACAGAAATGTCCATCAAGGTATTTAAAACACCCTTAATGAGTTTAAAGAATCGTACAAGTACATTAAGATGATTTTCAGGTTTAA
280 G K A I P T E C A I K V F K T T L N E F K N R D K Y I K D D F R F K

EcoRI (1589)
1501 AGATCGTTCAGTAAACTAAATCCACGTAAGATCATCCGCATGTGGGAGAGAAAAGAAATGCACAATCTTACAAGAATGCAGAAGGCTGGAATTCCTGT
313 D R F S K L N P R K I I R M W A E K E M H N L T R M Q K A G I P C

MscI (1647)
1601 CCAACAGTTGACTGCTTAAGAAGCACATTTTAGTTATGTCTTTCATTGGCCATGATCAAGTTCAGCCCTAAATTAAGAAGTAAAGCTTAGTAATG
347 P T V V L L K K H I L V M S F I G H D Q V P A P K L K E V K L S N

SphI (1770) **BspLU11I (1793)**
1701 AAGAAATGAAAGATGCCTACTATCAGACTCTTTCATTTGATGCAGCAATATATAACGAATGTACCCTTGTGCATGCTGACCTCAGCGAGTATAACATGTT
380 E E M K D A Y Y Q T L H L M Q Q L Y N E C T L V H A D L S E Y N M L

SphI (1803) **PshAI (1828)**
1801 GTGGCATGCTGGGAAGGTCTGGTTGATTGACGTGAGTCAAGTGGTAGAGCCAACCCATCCTCATGGCCTGGAGTCTTATTCCGTGACTGTAGGAATGTT
413 W H A G K V W L I D V S Q S V E P T H P H G L E F L F R D C R N V
1901 TCACAGTCTCCAGAAAAGGAGGAGTAAACGGAAGCCCTCAATGAACGGGAGCTGTTCAATGCTGTTTCTGGCCTGAACATCTCGGCAGACAATGAAGCTG
447 S Q F F Q K G G V T E A L N E R E L F N A V S G L N I S A D N E A
2001 ATTTCTTAGCTGAGATAGAAGCTTTGGAGAAGATGAAGATCAGATTGAGAAGAGGAGGAAAGCAGCTGCTTCTGAAAAGATGATGGAAGCCC
480 D F L A E I E A L E K M N E D H I Q K N G R K A A S F L K D D G S P

MscI (2131)
2101 ACCTGTGCTGTCTGCCGACTAGTACGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGC
513 P V L S A D •

HpaI (2263) **MfeI (2274)**
2201 TTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAAACAGTTAAACAACAACAATTCATTCTTTATGTTTCAGG

EcoRI (2359)
2301 TTCAGGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAATACAGCATAGCAAACTTTAACCTCAAAT

2401 CAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTGCGCCTCACCTTCTTTCA

SapI (2541) **SspI (2598)**
2501 TGGAGTTTAAAGATATAGTATTTTCCCAAGTTTGAAGTACTGCTTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTATAGTAAA

Swal (2612)
2601 TATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTA
2701 GTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTT
141 • N R T Y K L P I L E
SacI (2873)
2801 CCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCT
130 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 M G C P S
2901 GACCAACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCACAGCAGACCCAATG
97 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 V A S G I
StuI (3037)
3001 GCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCGAGTCTTGGTCTGTATGGCCGCCCGACAT
63 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 I A A G V H
XmnI (3179)
3101 GGTGCTTGTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCT
30 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 K M
AseI (3245)
3201 CCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAA
SacI (3302)
3301 ACGAGCTCTGCTTATATAGACCTCCCACGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCCTTGATTT
SpeI (3400)
3401 ACTAGTCAAAACAAACTCCATTGACGTC AATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACC
SnaBI (3528)
3501 GCATCATCATGGTAATAGCGATGACTAATACGTAGATGTA CTGCAAGTAGGAAAGTCCCATAGGTCATGTA CTGACTGGGCATAATGCCAGGCGGGCCATTT
NdeI (3633)
3601 ACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTA CTGCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAA
3701 TGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGGCGGGTCTGTTGGCGGTG CAGCCAGGCGGGCCATTTACCGTAA
PacI (3819)
PstI (3812)
SdaI (3811) BspLU11I (3829)
3801 GTTATGTAACGCCGTCAGGTTAA TTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAGGCCGCTTGGCTGGCGTTTTTCCATAGG
3901 CTCCGCCCCCTGACGAGCATC AAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCT
4001 CCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAG
ApaLI (4143)
4101 GTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTT CAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT
4201 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGA
4301 AGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTTTGATC
4401 CGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT
EagI (4579)
PacI (4559) Swal (4568) NotI (4578)
4501 ACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGAATAAAAATATCTTT
4601 ATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCT
4701 GTCCCGAGTCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA