



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCTTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTCACGCGCCCGCCCTACCTGAGGCC

HindIII (245) 301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

Bsu36I (291)

NgoMIV (441) 401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

BstEII (555) 501 TCTGTTCTGCCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTACCATGGACTGGCCGCACAGCCTCTTCTCCTGGCCAT

AgeI (552) **NcoI (560)** **BstAPI (573)** **SapI (582)** **MscI (593)**
 1► M D W P H S L L F L L A I
 601 CTCCATCTTCTGGCGCAAGCCACCCCGGAACACCAAGGCAAAAGAAAAGGGCAAGGGAGGCCAGTCCCTTGGCCCTGGGCTCATCAGGTGCCG

13► S I F L A P S H P R N T K G K R K G Q G R P S P L A P G P H Q V P

XhoI (713) 701 CTGGACCTGGTGTCTCGAGTAAAGCCCTACGCTCGAATGGAAGAGTATGAGCGGAACCTTGGGGAGATGGTGGCCAGCTGAGGAACAGCTCCGAGCCAG

BsrBI (748) 47► L D L V S R V K P Y A R M E E Y E R N L G E M V A Q L R N S S E P

NcoI (859) 801 CCAAGAAGAAATGTGAAGTCAATCTACAGCTGTGGTTGCCAACAAGAGGAGCCTGTCCCATGGGGCTACAGCATCAACCACGACCCAGCCGATCCC

80► A K K K C E V N L Q L W L S N K R S L S P W G Y S I N H D P S R I P

XmnI (942) 901 TCGGACTTGCCCGAGGCGCGGTGCCTATGTTTGGGTTGCGTGAATCCCTTACCATGCAGGAGGACCGTAGCATGGTGGAGCGTGCCAGTGTTCAGCCAG

113► A D L P E A R C L C L G C V N P F T M Q E D R S M V S V P V F S Q

Bsp120I (1042) 1001 GTGCCGGTGGCCGCGCCTCTGTCTCAACCTCCTCGCCCTGGGCCCTGCCCGAGCGTGTCTCATGGAGACCATCGTGTGGGTTGCACCTGCATCT

EcoO109I (1042) 147► V P V R R R L C P Q P P R P G P C R Q R V V M E T I A V G C T C I

MscI (1155) 1101 TCTGAGCCAACCAACCCGGTGGCCTCTGCAACAACCTCCCTCCCTGTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACA

XcmI (1110) **NheI (1149)** 180► F •

HpaI (1287) **MfeI (1298)** 1201 ACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAAACA

EcoRI (1383) 1301 ATTGCATTCATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAATACAGC

1401 ATAGCAAACTTTAACTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGC

SapI (1565) 1501 TGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAAGATATAGTGTATTTTCCCAAGGTTTGAAC TAGCTCTTCAATTTTATGTTTTAAATGCACTGACC

SspI (1622) **SwaI (1636)** **EcoO109I (1697)** 1601 TCCCACATTCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGG

1701 CCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCC

141► • N R

SacI (1897) 1801 TGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGTAGG

138► 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 S I L

1901 CTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGC

105► 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 D K Q

StuI (2061) 2001 CCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCT

71► 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 E G T K

2101 TGGTCTGATGGCCGCCGACATGGTGTCTTGTCTCATAGAGCATGGTGTCTCTCAGTGGCGACCTCCAGCTCCAGATCCTGCTGAGAGAT

38► 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 Q S I

BbsI (2207) **XmnI (2203)** **AseI (2269)** 2201 GTTGAAGTCTTCATGGTGGCCCTCTATAGTGTGCTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACGCGTGGATGGCGTCT

5► N F T K M

2301 CCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTCGTCATATGGGGCGGAGTTGTTACGA
SacI (2326)

2401 CATTTTGGAAAGTCCCCTTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCAC
SpeI (2424)

2501 GCCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCAATGTACTG
SnaBI (2552)

2601 GGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCCAAGTGGGCAGTTTACCGT
NdeI (2657)

2701 AAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCTGTTGGGCGGTC
PacI (2843)

2801 AGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCC
PstI (2836)
SdaI (2835)
BspLU11I (2853)

2901 GCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGAT
PacI (2843)

3001 ACCAGGCGTTTTCCCCTGGAAGCTCCCTCGTGCGCTCTCTGTTCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGC
PacI (2843)

3101 GCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTTCAGCCCGACCGCTGC
ApaLI (3167)

3201 GCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATG
ApaLI (3167)

3301 TAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGG
ApaLI (3167)

3401 AAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCT
ApaLI (3167)

3501 CAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAAT
PacI (3583) **Swal (3592)**

3601 CAGCGCCGCAATAAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTTGTGTGAATCGTAACATAACGCTCTCCATCAAAACAAAACGAAA
EagI (3603)
NotI (3602)

3701 CAAAACAACTAGCAAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA