



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

1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
PvuII (239)
Bsu36I (291)

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCGCCCTACCTGAGGGC

301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

AgeI (552)
NeoI (568)
EcoRI (576)

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTAGGAGGGCCACCATGGGAGAATTCAAGGTGGATAAGTTCAAC

1► M G E F K V D K F N

BglII (620)
SphI (649)

601 ATTGAAGATTTCTTCAGTGGAGATCTTGATATTTCAATTATAGCTCTGGCATGCCCTTATTCTGCCAGATGCTGTCCCATGCCACTCAGAGAACCTGG

11► I E D F F S G D L D I F N Y S S G M P S I L P D A V P C H S E N L

701 AAATCAACAGTTATGCTGTGGTGTAAATATACGTCCTGGTACTCTGCTGAGCCTTGTTGGGAACTCCTTGGTGTGCTGGTCATCTTATACAACCGGAG

44► E I N S Y A V V V I Y V L V T L L S L V G N S L V M L V I L Y N R S

801 CACCTGCTGTACCCGATGTCTACCTGCTGAACCTGGCATTGCTGACCTGTTCTTTGCCCTGACCTGCTGTGGGCTGCATCTAAAGTAAATGGA

77► T C S V T D V Y L L N L A I A D I G F A L T L P V W A A S K V N G

BstEII (947)

901 TGGACTTTTGGCTCAACCCTGTGCAAGATATTCTCATACTGGAAGGAGTTACCTTCTACAGCAGTGTCTGCTACTAGCCTGCATCAGCATGGACCGCT

111► W T F G S T L C K I F S Y V K E V T F Y S S V L L L A C I S M D R

BsrGI (1010)

1001 ACCTGGCATTGTACATGCCACAAGTACACTGATCCAGAAGAGACACTTGGTCAAGTTTGTGTGCATAGCCATGTGGTACTATCAGTAATTCTGGCCCT

144► Y L A I V H A T S T L I Q K R H L V K F V C I A M W L L S V I L A L

1101 GCCCATCTTAATTCTACGAAATCCTGTTAAGGTAACCTTTCTACCTTAGTCTGCTATGAGGATGTAGGTAACAATACATCCCGTTTGGGGTCTGACTG

177► P I L I L R N P V K V N L S T L V C Y E D V G N N T S R L R V V L

FspI (1270)

1201 CGTATCCTGCCTCAGACTTTTGGCTTCTCGTGCCGCTGCTCATCATGCTGTTCTGCTACGGTTTCACTGCGCACCTCTTTAAGGCCACATGGGGC

211► R I L P Q T F G F L V P L L I M L F C Y G F T L R T L F K A H M G

BspHI (1393)

1301 AGAAGCACCGGGCCATGCGGGTTCATCTTCGCTGTCGTCCTTGTCTTCTGCTCTGCTGGTGCCTACAACCTGGTTCTGTTACAGACACCCCTCATGAG

244► Q K H R A M R V I F A V V L V F L L C W L P Y N L V L F T D T L M R

PvuII (1484)

1401 AACCAAGCTGATCAAGGAGACCTGTGAGCGCCGCGATGACATTGACAAGGCCCTGAATGCTACGGAGATTCTTGGCTTCTCCACAGCTGCCTTAACCCC

277► T K L I K E T C E R R D D I D K A L N A T E I L G F L H S C L N P

NcoI (1532)
XmnI (1597)

1501 ATCATCTATGCCTTTATTGGCCAGAAATTTGCGCATGGACTTCTCAAGATCATGGCTACTTATGGCCTGTGACAGAAAGGAGTCTTAGCCAAGGAGGAA

311► I I Y A F I G Q K F R H G L L K I M A T Y G L V S K E F L A K E G

1601 GGCCTTCTTTTGTAGCTCGTCTTCAGCAAACCTCTACTACCCTCTAAAGACTGTTACCTAAACGGTGGCCCTCGGGTTCCTTCTTGTCTTTGAG

344► R P S F V S S S S A N T S T T L •

NheI (1717)

1701 CATGGCATCATTACCAGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTG

HpaI (1855)
MfeI (1866)

1801 TGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACAATTGCATTATTTTATGTTTCAGGTTTCAGGGG

EcoRI (1951)

1901 GAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCCAAATCAAGCCTC

2001 TACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTGCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTT

SapI (2133)
SspI (2190)

2101 AAGATATAGTGTATTTTCCCAAGTTTGAAGTACTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCCACATTCCTTTTATGAAAAATTCAGAA

SwaI (2204)
EcoO109I (2265)

2201 AATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGG

2301 ACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGTTGACTTGGAGGGGATGAGTTCCTCAATG

141► • N R T Y K L P I L E E I

SacI (2465)
BstXI (2494)

2401 GTGGTTTTGACCAGTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCC

127► 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 V V R

2501 TGATGGATCTGTCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGC
 94 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 A I A
 2601 TTCAGCACAGACAGTGCCTGCCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCCAAGTCTTGGTCTGATGGCCGCCCGACATGGTGGCTTG
 61 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 H K
 XmnI (2771)
 2701 TTGTCCTCATAGAGCATGGTGTCTTCTCAGTGGCAGCTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGGCTTTCATGGTGGCCCTCTATAGT
 27 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 (2837) SacI (2894)
 2801 GAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTC
 SpeI (2992)
 2901 TGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAAGTCCCGTTGATTTACTAGTCA
 3001 AAACAACTCCCATGACGTCAATGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATC
 SnaBI (3120)
 3101 ATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCCATAAAGTCAATGACTGGGCATAATGCCAGGCGGGCCATTTACCGTCAT
 NdeI (3225)
 3201 TGACGTCAATAGGGGGCTACTTGCCATATGATACACTTGATGACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGT
 3301 CCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGGTCTGTTGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTA
 PacI (3411)
 PstI (3404)
 SdaI (3403) BspLU11I (3421)
 3401 ACGCCTGCAGGTTAATAAGAACATGTGAGCAAAGGCCAGAAAAGGCCAGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCC
 3501 CCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTG
 3601 CGCTCTCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTCTCATAGCTCAGCTGTAGGTATCTCA
 ApaLI (3735)
 3701 GTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAA
 3801 CCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGTACAGAGTCTTGAAGTGGTGG
 3901 CCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAC
 4001 AAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTC
 EagI (4171)
 Pacl (4151) SwaI (4160) NotI (4170)
 4101 TGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCAT
 4201 TACATCTGTGTGGTTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAG
 4301 TGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA