



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

1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTGTCGTGACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)

Psp1406I (203)
PvuII (239)

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCTGACCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

NcoI (560)
BstEII (555)
AgeI (552) BstXI (560)

501 TCTGTTCTGGCGCTTACAGATCCAAGCTGTGACCGCGCTACCTGAGATCACCGGTACCATTGGTATGGAGAAGCTAGTCCCCTGCTGGTCGGGCG

1 ▶ M V M E K P S P L L V G R

NcoI (684)

601 GGAATTTGTGAGACAGTATTACACACTGCTGAACAGGCCAGACATGCTGCATAGATTTTATGAAAGAAGCTCTTCTTATGTCATGGGGATTGGAT

13▶ E F V R Q Y Y T L L N Q A P D M L H R F Y G K N S S Y V H G G L D

701 TCAAATGGAAAGCCAGCAGATGCAGTCTACGGACAGAAAGAAATCCACAGGAAAGTATGTCACAAAATTCCACAACTGCCACCAAGATTTCGCCATG

47▶ S N G K P A D A V Y G Q K E I H R K V M S Q N F T N C H T K I R H

Psp1406I (891)

801 TTGATGCTCATGCCACGCTAAATGATGGTGTGGTAGTCCAGGTGATGGGGCTTCTCTAACAACAACCAGGCTTTGAGGAGATTTCATGCAAACGTTTGT

80▶ V D A H A T L N D G V V V Q V M G L L S N N N Q A L R R F M Q T F V

EcoRV (946)

901 CCTTGCTCCTGAGGGTCTGTTGCAAATAAATCTATGTTACAATGATATCTTCAGATACCAAGATGAGGTCTTTGGTGGGTTTGTCACTGAGCCTCAG

113▶ L A P E G S V A N K F Y V H N D I F R Y Q D E V F G G F V T E P Q

Acc65I (1056)

1001 GAGGAGTCTGAAGAAGAAGTAGAGGAACCTGAAGAAAGACAGCAAACCTGAGGTGGTACCTGATGATTCTGGAACCTTCTATGATCAGGCAGTTGTCA

147▶ E E S E E E V E E P E E R Q Q T P E V V P D D S G T F Y D Q A V V

1101 GTAATGACATGGAAGAACATTTAGAGGAGCCTGTTGCTGAACCAGAGCCTGATCCTGAACCAGAACCAGAACAAGAACCTGTATCTGAAATCCAAGAGGA

180▶ S N D M E E H L E E P V A E P E P D P E P E Q E P V S E I Q E E

PstI (1265)

1201 AAAGCCTGAGCCAGTATTAGAAGAACTGCCCTGAGGATGCTCAGAAGAGTCTTCTCCAGCACCTGCAGACATAGCTCAGACAGTACAGGAAGACTTG

213▶ K P E P V L E E T A P E D A Q K S S S P A P A D I A Q T V Q E D L

DraIII (1340)

1301 AGGACATTTTCTGGGCATCTGTGACCAGTAAGAATCTCCACCCAGTGGAGCTGTTCCAGTACTGGGATACCACCTCATGTTGTTAAAGTACCAGCTT

247▶ R T F S W A S V T S K N L P P S G A V P V T G I P P H V V K V P A

SspI (1486)

1401 CACAGCCCCGTCCAGAGTCTAAGCCTGAATCTCAGATTCACCCACAAAGACCTCAGCGGGATCAAAGAGTGCAGAAACAACGAATAAATATTCCTCCCA

280▶ S Q P R P E S K P E S Q I P P Q R P Q R D Q R V R E Q R I N I P P Q

SmaI (1503) **XcmI (1581)**

1501 AAGGGGACCCAGACCAATCCGTGAGGCTGGTGAAGGATGACATTGAACCCGAAGAATGGTGAAGACCCCTGACAGTACCAACTCTTATTGGCAAC

313▶ R G P R P I R E A G E Q G D I E P R R M V R H P D S H Q L F I G N

BspHI (1605) **FspI (1667)**

1601 CTGCCCTCAGAGTGGACAAATCAGAGCTTAAAGATTTCTTTCAAAGTTATGGAAACGTGGTGGAGTTGCGCATTAACAGTGGTGGGAAATTACCCAATT

347▶ L P H E V D K S E L K D F F Q S Y G N V V E L R I N S G G K L P N

1701 TTGGTTTTGTTGTTTGTGATGATTCTGAGCCTGTTAGAAAAGTCTTAGCAACAGGCCATCATGTTGAGAGTGGGTCGCTGATGTCGAAGAGAA

380▶ F G F V V F D D S E P V Q K V L S N R P I M F R G E V R L N V E E K

1801 GAAGACTCGAGTCCAGGGAAGGCGACCGACGAGATAATCGCCTTCGGGACCTGGAGGCCCTCGAGGTGGGCTGGTGGTGAATGAGAGGCCCTCCC

413▶ K T R A A R E G D R R D N R L R G P G G P R G G L G G G M R G P P

NheI (1995)

1901 CGTGGAGGCATGGTGCAGAAACCAGGATTTGGAGTGGGAAAGGGGCTTGCACCAGGAGTGAATCTTCATGGATCTTCATGCAGCCATACAAACGCTAG

447▶ R G G M V Q K P G F G V G R G L A P R Q •

MscI (2001)

2001 CTGCCAGACATGATAAGATACATTGATGAGTTTGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCT

HpaI (2133) MfeI (2144)

2101 TTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTTTATGTTTCAGGTTACAGGGGAGGTGTGGGAGTTTTTTAAA

EcoRI (2229)

2201 GCAAGTAAACCTCTACAAATGTGGTATGGAATCTAAATACAGCATAGCAAACCTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGG

2301 ATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTGCAGCCTCACCTTCTTTCAGGAGTTAAGATATAGTGATTTTCCCAA

2401 **SapI (2411)** SspI (2468) SwaI (2482)
 GGTTTGAACTAGTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCCACATTCCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGC

2501 AATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGACCTT

2601 TAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCAT

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

2701 TCATCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATC

120 SacI (2743) BstXI (2772)

2801 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 I S R D V E D
 AGAGTAGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGCACCTG

87 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 E A C V T V R

2901 **StuI (2907)**
 CCAATGTAGGCCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGTCTGTTGCTCATAGAGCATGGTGA

53 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 N D E Y L M T I

3001 **XmnI (3049)**
 TCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGA

20 K E T A V E V L E L D Q Q S I N F T K M

3101 **AseI (3115)** SacI (3172)
 TATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCCACCG

3201 TACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAAAAAACCTCCATTGACGTCA

SpeI (3270)

3301 ATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATGTTAATAGCGATGACTAATA

SnaBI (3398)

3401 CGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACT

3501 **NdeI (3503)**
 TGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGA

3601 ACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAACGCCTGCAGGTTAATTAAGAA

PacI (3689) PstI (3682) **SdaI (3681)** **BspLU11I (3699)**

3701 CATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAAT

3801 CGACGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGC

3901 CGCTTACCGGATACCTGTCCGCTTTCTCCCTCGGGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCCGTTGAGTGGTTCGCTC

4001 **ApaLI (4013)**
 CAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGTGCCTTATCCGGTAACTATCGTCTTGTAGTCCAACCCGTAAGACACGACTTATCG

4101 CCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAA

4201 GAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTATCCGCAAAACAAACCACCGCTGGTAGCGGTGG

4301 TTTTTTGTTCGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAAAAC

4401 **EagI (4449)** PacI (4429) SwaI (4438) **NotI (4448)**
 TCACGTTAAGGGATTTGGTTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGTTTTT

4501 GTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAAACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACA

4601 TTTCTCTATCGAA