



PvuI (7)
SgfI (6) 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA MfeI (82) EcoNI (96)

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGCTGTACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCCGCCGCTACCTGAGGCC EcoNI (287)

301 GCCATCCACGCGGTTGAGTGCAGTCTGCCGCTCCCGCTGTGGTGCCTCTGAAGTGCCTCCGCGCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441) **NaeI (441)**
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGTCTTTGTTTCGTTT

KasI (535) **AgeI (552)** **BspLU11I (560)** **Tth111I (575)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTCAACATGTCTTTAAAGAGACATAGTCTGCGAAGGAACGCCTG 1▶ M S L K R H S L R R N A C NdeI (698)

601 TCACCTGGAGACGAGAGCTGGCATTCTACCATCCTTTATAGTGATGCTACAGGACAAAGAGGAATGGATAAAAAATTGGTGAGCAACTCAATAGAGCA
13▶ H L E T R A G I P T I L Y S D A T G Q R G M D K N I G E Q L N R A

Ppu10I (720) **NsiI (720)** **SphI (718)**
701 TATGAAGCCTCCGACAGGCATGCATGGATAGAGATTCAGCAGTAAGAGAGCTACAGCAAAAAGACTGAGAATATGAACAAAGAATACGCGAGCAACAGG
47▶ Y E A F R Q A C M D R D S A V R E L Q Q K T E N Y E Q R I R E Q Q
801 AACAGCTGTCAATTCAACAAAACCTAATTGACAGGCTGAAATCACAGCTACTTCTCGTGATTCTAGTCGAGATAACAGTTATGGCTATGTACCTTTGCT
80▶ E Q L S F Q Q N L I D R L K S Q L L L V D S S R D N S Y G Y V P L L
901 TGAAGACAGTGACAGAAGGAAGAATAATTTGACCTTGATGAACCACATGATAAAGTAAACTAGGAACACTGAGAGATAAGCAATCAAAGGTGAGACGA
113▶ E D S D R R K N N L T L D E P H D K V K L G T L R D K Q S K V R R
1001 CAAGAAGTTTCTTCTGGAAAAGAATCCGCCAAGGGTCTCAACATCCCTCTGCATCACGAAAGGATAATATAGAGAAGACTTTCTGGGACCTTAAAGAAG
147▶ Q E V S S G K E S A K G L N I P L H H E R D N I E K T F W D L K E

NheI (1119) **DraIII (1179)**
1101 AATTTATAGGATTTGCTTGTAGCAAAAGCACAGAAAGATCACTTAAGCAACTTAATATACCAGATATTGCAACTGACACACAGTGTCTGTGCCTAT
180▶ E F H R I C L L A K A Q K D H L S K L N I P D I A T D T Q C S V P I

Eco47III (1230) **AfeI (1230)**
1201 ACAGTGTACTGATAAAACAGAGAAAACAAGAAGCGCTGTTAAGCCCCAGGCTAAAGATGATATAAATAGAGGTATGTCGTGCGTCACAGCTGTACACCA
213▶ Q C T D K T E K Q E A L F K P Q A K D D I N R G M S C V T A V T P
1301 AGAGGACTGGGCGGGATGAGGAAGATACCTCTTTTGAATCACTTTCTAAATCAATGTCAAGTTTCCGCCTATGGACAATGACTCTATTTTTCTACATA
247▶ R G L G R D E E D T S F E S L S K F N V K F P P M D N D S I F L H
1401 GCACTCCAGAGGCCCGAGCATCTTGCCTGCCACACCTGAGACAGTGTGCCAGGACCGATTAAATATGAAAGTCAGAGACAACCCAGGAAACTTTGT
280▶ S T P E A P S I L A P A T P E T V C Q D R F N M E V R D N P G N F V
1501 TAAAACAGAAGAACTTTATTTGAAATTCAGGGAATTGACCCATAAATTCAGCTATACAAAACCTTAAAACAACCTGACAAAACAACCCCTCAATCTT
313▶ K T E E T L F E I Q G I D P I T S A I Q N L K T T D K T N P S N L

DraIII (1627)
1601 AGAGCGACGTGTTTGCAGCTGGAGACCAATGTGTTCTATGTAATAACGTTCCCACTTCAAGACCCGCTGACGCACCTTTTCCCTACTGGATTCCC
347▶ R A T C L P A G D H N V F Y V N T F P L Q D P P D A P F P S L D S

Asp718I (1770) **Acc65I (1770)**
1701 CAGGAAAGGCTGTCCGAGGACCACAGCAGCCCTTTTGGAGCCTTTTCTTAACCAAGACTGACTTAGTGGTACCAAGTGATTCAGACTCAGAGCTCCT
380▶ P G K A V R G P Q Q P F W K P F L N Q D T D L V V P S D S D S E L L

EcoRI (1816)
1801 TAAACCTTAGTGTGTGAATCTGTCAAGAGCTTTTCCACCATCCATTACATCCAGAGGGGATTTCTCCGGCATCTTAATACACACTTTAATGGGGAG
413▶ K P L V C E F C Q E L F P P S I T S R G D F L R H L N T H F N G E

SpeI (1926)
1901 ACTTAAATCAGTTTGAACACAGACAACTAGTCTAGCTCGCATGATAAGATACATTGATGAGTTTGGACAACCAACTAGAATGCAGTGAACAAAA
447▶ T •

HpaI (2095)
2001 TGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAGTTAA

MfeI (2106) **EcoRI (2191)**
2101 CAACAACAATTGCATTCTTTTATGTTTCAGGTTACAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCTAA
2201 AATACAGCATAGCAAACTTTAACTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTGCCAATGT
2301 GCATTAGCTGTTTGCAGCCTCACCTTCTTCATGGAGTTAAGATATAGTGATTTTCCCAAGGTTTGAAGTACTGCTCTTCATTCTTTATGTTTAAATG

SspI (2430) **SwaI (2444)**
2401 CACTGACCTCCACATTCCTTTTGTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGAT
2501 GCTCAAGGCCCTTATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACGCAAGAAAGCGAGCTTCTAGCT

2601 TTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCA
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

BstXI (2734)

2701 GAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGT
107 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 D

StuI (2869)

2801 CCTTCTGCCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCCAGCAGACAGTGCCTGCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTC
74 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 E

2901 CCCAGTCTTGGTCTGATGGCCGCCCGACATGGTCTTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGC
41 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

BspHI (3019) **AseI (3077)**

3001 TGAGAGATGTTGAAGTCTTCTGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGA
74 Q S I N F T K M

3101 TGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTCGCTCAATGGGGCGGAGT

SpeI (3232)

3201 TGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACC

SnaBI (3360)

3300 GCTATCCACGCCATTGATGTAAGTCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTCCAAAGTAGGAAAGTCCCATAAAGT

NdeI (3465)

3400 CATGTAAGTGGCATAATGCCAGGCGGGCCATTTACCGTATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCAAGTGGGCA

3500 GTTTACCGTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTACTATGGAAACATACGTCATTATTGACGTCAATGGGCGGGGTCGT

PstI (3644) **SdaI (3643)** **PacI (3651)** **BspLU11I (3661)**

3600 TGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTTGCAGGTTAAATAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACC

3698 GTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGG

3798 ACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTCG

ApaLI (3975)

3898 GGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCCAGC

3998 CCGACCGTGGCGCTTATCCGGTAACTATCGTCTTGTAGTCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAG

4098 AGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCA

4198 GTTACCTTCGAAAAAGAGTTGGTAGCTCTTGTCCGCAAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAA

PacI (4391)

4298 AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATT

EagI (4411)

Swal (4400) **NotI (4410)**

4398 AACATTTAAATCAGCGGCCCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAA

4498 ACAAACGAAACAAACAAACTAGCAAAATAGGCTGTCCCGTCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA