



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
MfeI (82) EcoNI (96)
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) **PvuII (239)** 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCCTACCTGAGGCC
EcoNI (287) **Bsu36I (291)**
301 GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

BspHI (560)
AgeI (552) 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCCTACCTGAGATCACCGGTCATCATGAGAGAACCCTGGAGGCGTTGAAGTTGGCAGACTT
1▶ M R E P L E A L K L A D L

SapI (609) **SfiI (639)** **NcoI (656)** 601 GGATTTGAGGAAGAGCTCTCGGCTTCTGGGTGGAGAATGGCCAGTGGGCGCTTCACCATGGATCAGTCCCTGAATCAGTGACAGAAAACTTTGAGTAC
13▶ D F R K S S L A S G W R M A S G A F T M D Q F P E S V T E N F E Y

StuI (713) **XcmI (785)** 701 GATGATTTGGCTGAGGCTGTTATATTGGGACATCGTGGTCTTTGGGACTGTGTTCTGTCCATATTCTACTCCGTCATCTTTGCCATTGGCCTGGTGG
47▶ D D L A E A C Y I G D I V V F G A T V F L S I F Y S V I F A I G L V
801 GAAATTTGTTGGTAGTGTGGCCCTACCAACAGCAAGAACGCAAGTGTGACCGACATTTACCTCCTGAACCTGGCCTTGTCTGATCTGCTGTTTGT
80▶ G N L L V V F A L T N S K K P K S V T D I Y L L N L A L S D L L F V
901 AGCCACTTTGCCCTTCTGGACTCACTATTTGATAAATGAAAAGGCGCTCCACAATGCCATGTGCAAATCACTACCGCTTCTTCTCATCGGCTTTTT
113▶ A T L P F W T H Y L I N E K G L H N A M C K F T T A F F F I G F F

Acc65I (1037) **RsrII (1078)** 1001 GGAAGCATATTCTTCATACCGTCATCAGCATTGATAGGTACCTGGCCATCGTCTGGCCGCAACTCCATGAACAACCGGACCGTGCAGCATGGCGTCA
147▶ G S I F F I T V I S I D R Y L A I V L A A N S M N N R T V Q H G V

AvrII (1107) 1101 CCATCAGCCTAGGCGTCTGGCAGCAGCCATTTGGTGGCAGCACCCAGTTCATGTTCAAAAAGCAGAAAGAAAATGAATGCCTTGGTACTACCCCGA
180▶ T I S L G V W A A A I L V A A P Q F M F T K Q K E N E C L G D Y P E
1201 GGTCCCTCAGGAAATCTGGCCCGTCTCCGCAATGTGGAACAAATTTCTTGCTTCTACTCCCTGCTCATTATGAGTTATTGCTACTTCAAGATC
213▶ V L Q E I W P V L R N V E T N F L G F L L P L L I M S Y C Y F R I

Psp1406I 1301 ATCCAGACGCTGTTTTCTGCAAGAACCACAAGAAAGCCAAAGCCATTAAGTATCCTTCTGGTGGTATCGTGTTTTTCTCTTCTGGACACCCCTACA
247▶ I Q T L F S C K N H K K A K A I K L I L L V V I V F F L F W T P Y
1401 ACGTTATGATTTTCTGGAGACGCTTAAGCTCTATGACTTCTTCCAGTGTGACATGAGGAAGGATCTGAGGCTGGCCCTCAGTGTACTGAGACGGT
280▶ N V M I F L E T L K L Y D F F P S C D M R K D L R L A L S V T E T V

NsiI (1535) 1501 TGCATTTAGCCATTGTTGCCTGAATCCTCTCATCTATGATTTGCTGGGAGAAAGTTCAGAAGATACCTTACCACCTGTATGGGAAATGCCTGGCTGT
313▶ A F S H C C L N P L I Y A F A G E K F R R Y L Y H L Y G K C L A V

XcmI (1689) 1601 CTGTGTGGCGCTCAGTCCACGTTGATTTCTCCTCATCTGAATCACAAGGAGCAGGCATGGAAGTGTCTGAGCAGCAATTTACTTACCACACGAGTG
347▶ L C G R S V H V D F S S E S Q R S R H G S V L S S N F T Y H T S

NsiI (1706) **NheI (1733)** 1701 ATGGAGATGCATTGCTCCTTCTCTGAAGGGAATGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAA
380▶ D G D A L L L L •

HpaI (1871) **MfeI (1882)** 1801 AAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAAACAAGTTAAACAACAACATTCATTTAT

EcoRI (1967) 1901 GTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACTTTAAC
2001 CTCCAAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACC

SapI (2149) 2101 TTCTTTCATGAGTTTAAGATATAGTGTATTTCCCAAGGTTTGAAGTCTTCTTCTTATGTTTTAAATGCACTGACCTCCACATTCCTTTT

SspI (2206) **SwaI (2220)** 2201 TAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCC

2301 CCAGTTTAGTGTGACTTAGGGAACAAAGAACCTTTAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGG
141▶ • N R T Y K L P

2401 GATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCATCTCAATGAGCACAAGCAGTCAAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCA
133▶ 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 E R C M G
2501 CAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTGTCTCAGCAG
99▶ 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 G N S V A S

StuI (2645) 2601 ACCCAATGGCAATGGCTTCAGCAGACAGTACCTGCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCAGTCTTGGTCTGATGGCCG
66▶ 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 T R I A A

2701 CCCGACATGGTGCTTGTGTCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTTCATG
33 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 N F T K M

2801 GTGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGG
AseI (2853)

2901 TTCACTAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCC

3001 GTTGATTTACTAGTCAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTG
SpeI (3008)

3101 CCAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCCATAAGGTCATGTACTGGGCATAATGCCAGGCC
SnaBI (3136)

3201 GGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGAGTTTACCCTAAATACTCCACCCATT
NdeI (3241)

3301 GACGTCAATGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTACGCCAGGCGGGCCATT

3401 TACCGTAAGTTATGTAACGCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCCTTTT
PacI (3427) PstI (3420) SdaI (3419) BspLU11I (3437)

3501 TCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCC
3601 TGGAAAGTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCA

3701 CGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCCAGCCGACCCTGCGCCTTATCCGGTAACT
ApaLI (3751)

3801 ATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGTACAGA
3901 GTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGC
4001 TCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGA

4101 TCTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAA
EagI (4187) NotI (4186) PacI (4167) SmaI (4176)

4201 ATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAACGAAACAAACAACTAGCAA
4301 AATAGGCTGTCCCGAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA