



PvuI (7)
SgfI (6) **MfeI (82)**
1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTGTCTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) **PvuII (239)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACCGCGCCGCCCTACCTGAGGGCC
301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

AgeI (552) **BspLU11I (568)**
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCTACCTGAGATCACCGGTAGGAGGGCCAACATGTTCCAGATCCAGAGTTTGAGCCGAGT
1► M F Q I P E F E P S

PstI (619) **Bsu36I (661)** **StuI (695)**
601 GAGCAGGAAGACTCCAGCTCTGCAGAGAGGGGCTGGGCCAGCCCGCAGGGGACGGGCCCTCAGGCTCCGGCAAGCATCATCGCCAGGCCCCAGGCC
11► E Q E D S S S A E R G L G P S P A G D G P S G S G K H H R Q A P G **XcmI (693)**
701 TCCTGTGGGACGCCAGTACCAGCAGGAGCAGCAACAGCAGCCATCATGGAGGCGCTGGGCTGTGGAGATCCGGAGTCGCCACAGCTCCTACCC **SacII (799)**
44► L L W D A S H Q Q E Q P T S S S H H G G A G A V E I R S R H S S Y P

BsrBI (854) **Eco47III (892)**
801 CGCGGGGACGGAGGACGACGAAGGGATGGGGGAGGAGCCAGCCCTTTCGGGGCCGCTCGCGCTCGGCGCCCCCAACTCTGGGCAGCACAGCGCTAT
77► A G T E D D E G M G E E P S P F R G R S R S A P P N L W A A Q R Y

SapI (965)
901 GGCCGCGAGCTCCGGAGGATGAGTGACGAGTTTGTGGACTCCTTAAAGAGGGACTTCTCGCCCCGAAGAGCGGGCACAGCAACGCAGATGCCGCAAA
111► G R E L R R M S D E F V D S F K K G L P R P K S A G T A T Q M R Q **MscI (1099)**

PvuII (1004) **NheI (1093)**
1001 GCTCCAGCTGGACGCGAGTCTTCCAGTCTTGGTGGGATCGGAACTTGGGCAGGGGAAGCTCCGCCCTCCAGTGACCTTTCGCTCCACATCCGCTAGCT
144► S S S W T R V F Q S W W D R N L G R G S S A P S Q •
1101 GGCAGACATGATAAGATACATTGATGAGTTTGACAAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTT

HpaI (1231) **MfeI (1242)**
1201 ATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTATTTATGTTTCAGGTTTCAGGGGAGGTGTGGAGTTTTTAAAGC

EcoRI (1327)
1301 AAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGAT
1401 GAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGAGCCTCACCTTCTTTCATGGAGTTTAAAGATATAGTGATTTTCCCAAGG

SapI (1509) **SspI (1566)** **SwaI (1580)**
1501 TTTGAACTAGCTTTCATTTCTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAAATATTCAGAAAATAATTTAAATACATCATTGCAA
1601 TGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTA
1701 ATAGAAATTTGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTC
141► • N R T Y K L P I L E E I T T K V L K G N **BstXI (1870)**

1801 ATCTCAATGAGCACAAGCAGTCAAGGAGCATAGTCAGAGATGAGTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAG
119► 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 S
1901 AGTAGGGGTCCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTTCAGCACAGACAGTACCCTGCC
86► 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 G

StuI (2005)
2001 AATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCGAGTCTTGGTCTGTATGGCCGCCCGACATGGTGTCTGTTGCTCCTCATAGAGCATGGTATC
53► 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

XmnI (2147)
2101 TTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATA
19► K E T A V E V L E L D Q Q S I N F T K M

AseI (2213)
2201 TACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTA

SpeI (2368)
2301 CACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAAT

2401 GGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTA
SnaBI (2496)
 2501 TAGATGTAAGTCCCAAGTAGGAAAGTCCATAAGGCATGTAAGTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTG

2601 GCATATGATACACTTGATGTAAGTGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAAC
NdeI (2601)

2701 ATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATTAAGAACA
PacI (2787)
PstI (2780)
SdaI (2779)
BspLU11I (2797)

2801 TGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCG
 2901 ACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGTCCCTCGTGGCTCTCCTGTTCCGACCCTGCCG
 3001 CTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGTTGCTCCCA

3101 AGCTGGGCTGTGTGCACGAACCCCGTTCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCC
ApaLI (3111)
 3201 ACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGA
 3301 ACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTT
 3401 TTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACTC

3501 ACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGT
EagI (3547)
PacI (3527) **SwaI (3536)** **NotI (3546)**
 3601 GTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATT
 3701 TCTCTATCGAA