



PvuI (7)
SgfI (6) **MfeI (82)**
1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203)
HindIII (245)
Bsu36I (291)
PvuII (239)
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCAGCTTTGCTGACCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

AgeI (552) **BspLU11I (560)**
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCTACCTGAGATCACCGTCAACATGTTGTTTGCCTGTGCTCTCCTTGCCTCCTGGGTCT
1▶ M L F A C A L L A L L G L

PstI (609)
601 GGCAACCTCCTGCAGTTTCATCGTGCCCGCAGTGAGTGGAGGGCCCTGCCATCCGAGTGCTCTAGCCGCTGGGGCACCCAGTTCGCTACGTGGTGATC
13▶ A T S C S F I V P R S E W R A L P S E C S S R L G H P V R Y V V I

BstAPI (713) **NgoMIV (709)**
701 TCACACACAGCCGGCAGCTTCTGCAACAGCCCGGACTCCTGTGAACAGCAGGCCCGCAATGTGCAGCATTACCACAAGAATGAGTGGGCTGGTGCGATG
47▶ S H T A G S F C N S P D S C E Q Q A R N V Q H Y H K N E L G W C D

BstEII (865)
801 TAGCCTACAATTCTTATTGGAGAGGACGGTTCATGTCTATGAAGGCCGAGGCTGGAACATCAAGGGTGACCACACAGGGCCATCTGGAATCCCATGTC
80▶ V A Y N F L I G E D G H V Y E G R G W N I K G D H T G P I W N P M S

Acc65I (936)
901 TATTGGCATCACCTTCATGGGAACTTCATGGACCGGTACCCGCAAAGCGGGCCCTCCGTGCTGCCATAAATCTTCTGGAATGTGGGGTGTCTCGGGGC
113▶ I G I T F M G N F M D R V P A K R A L R A A L N L L E C G V S R G

BstEII (1060)
1001 TTCCTGAGATCCAATATGAAGTCAAAGGACACCGGATGTGCAAAGCACTCTCTCCAGGTGACCAACTCTATCAGGTCATCAAAGCTGGGAACACT
147▶ F L R S N Y E V K G H R D V Q S T L S P G D Q L Y Q V I Q S W E H

MscI (1146)
NheI (1140)
1101 ACCGAGAGTGAGAGACCTTGAGACCTAGTGAGAATCCCCCGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGACAAACCACAAC TAGAATG
180▶ Y R E •

HpaI (1278) **MfeI (1289)**
1201 CAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACATTGCATTC

EcoRI (1374)
1301 ATTTTATGTTTCAGGTTCAAGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAAA
1401 CTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGATTAGCTGTTTGCAG

SapI (1556)
1501 CCTCACCTTCTTTCATGGAGTTAAGATATAGTGATTTTTCCAAAGTTTGAAGTCTCTCATTCTTTATGTTTTAAATGCACTGACCTCCACATT

SspI (1613) **Swal (1627)**
1601 CCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATA
1701 ATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACT
141▶ • N R T Y K

SacI (1888)
1801 TGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCA
135▶ 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 S I L E R C

BstXI (1917)
1901 CATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTC
102▶ 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 K Q G N S

StuI (2052)
2001 ACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGA
68▶ 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 G T K T R I

BbsI (2198)
XmnI (2194)
2101 TGCCGCCCGACATGGTGTGTTGTCTCATAGAGCATGGTGTCTTCTAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGT
35▶ 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 Q S I N F T

2201 CTT**CATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAA**AACAGCGTGGATGGCGTCTCCAGC**TTAT**
2 K M ← AseI (2260)

2301 CTGACGGTTCAC**TAAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGG**A
SacI (2317)

2401 AAGTCCC**GTTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCAGCCCAT**TGA
SpeI (2415)

2501 TG**TACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAAT**G
SnaBI (2543)

2601 CCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCC
NdeI (2648)

2701 ACCCATTGACGTCAATGGAAAGTCCCTATTGGCGT**TACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGT**CAGCCAGGCG

2801 GGCCATTTACCGTAAGTTATGTAAC**GCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCTT**GCTG
PacI (2834)
PstI (2827)
SdaI (2826) BspLU11I (2844)

2901 GCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGT
3001 TTCCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGCGCTTTCTCA

3101 TAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTT**CAGCCCACCGCTGCGCCTTATCC**
ApaLI (3158)

3201 GGTA**ACTATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTG**
3301 CTACAGAGTTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGT
3401 TGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGAT

3501 CCTTTGATCTTTTCTACGGG**CTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCG**
PacI (3574) SmaI (3583) NotI (3593)

3601 CAATAAAATATCTTTATTTT**CATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAAA**
3701 CTAGCAAATAGGCTGTCC**CCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA**