



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

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

301 GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGTCTTTGTTTCGTTT

NcoI (560)
BstEII (555)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTACCATGGCCTCGCCCTTTGCTTTACTGATGGTCTGCTGGT KasI (535) AgeI (552)

601 GCTCAGCTGCAAGTCAAGTCTCTCTGGGCTGTGATCTCCCTGAGACCCACAGCCTGGATAACAGGAGCCTTGATGCTCCTGGCACAAATGAGCAGA 1 M A S P F A L L M V L V V

701 ATCTCTCCTTCTCTGTCTGATGGACAGACATGACTTTGGATTTCCCGAGGAGGTTTGTATGGCAACCAGTCCAGAAGGCTCCAGCCATCTCTGTCC 13 L S C K S S C S L G C D L P E T H S L D N R R T L M L L A Q M S R

801 TCCATGAGCTGATCCAGCAGATCTTCAACCTTTACCACAAAAGATTCTGCTGCTGGGATGAGGACCTCTAGACAAATTCTGCACCGAACTCTA 47 I S P S S C L M D R H D F G F P Q E E F D G N Q F Q K A P A I S V

801 TCCATGAGCTGATCCAGCAGATCTTCAACCTTTACCACAAAAGATTCTGCTGCTGGGATGAGGACCTCTAGACAAATTCTGCACCGAACTCTA BglIII (818)

901 CCAGCAGCTGAATGACTTGAAGCCTGTGTGATGCAGGAGGAGAGGGTGGGAGAACTCCCCTGATGAATGCGGACTCCATCTTGCGTGTGAAGAAATAC XmnI (993)

1001 TTCCGAAGAATCACTCTCTATCTGACAGAGAAGAATAACAGCCCTTGTGCTGGGAGGTTGTGAGAGCAGAAATCATGAGATCCCTCTCTTTATCAACAA 113 Q Q L N D L E A C V M Q E E R V G E T P L M N A D S I L A V K K Y

101 TTCCGAAGAATCACTCTCTATCTGACAGAGAAGAATAACAGCCCTTGTGCTGGGAGGTTGTGAGAGCAGAAATCATGAGATCCCTCTCTTTATCAACAA BspHI (1073)

1101 ACTTGCAAGAAAGATTAAGGAGGAAGGAATAACATCTGGTCCAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACA ACTAGA NheI (1143)

1201 ATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCA BstXI (1140) MscI (1149)

1301 TTCATTTTATGTTTCAGGTTTCAGGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATCTAAAATACAGCATAGCA HpaI (1281) MfeI (1292)

1401 AAACCTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTG EcoRI (1377)

1501 CAGCCTCACCTTCTTTTCATGGAGTTTAAGATATAGTGTATTTTCCAAGGTTTGAAGTCTCTTCAATTTCTTTATGTTTTAAATGACTGACCTCCAC SapI (1559)

1601 ATTCCTTTTTAGTAAAATATTCAGAAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTC SspI (1616) SwaI (1630)

1701 ATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTAAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGT 141 N R T Y

1801 ACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAGCAGTCCAGGAGCATAGTCAGAGATGAGCTCTCT SacI (1891)

1901 GCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTG BstXI (1920)

2001 CTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCC StuI (2055)

2101 TGATGGCCGCCCCGACATGGTGTCTGTTGCTCATAGAGCATGGTGTCTTCTCAGTGGCGACTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAA XmnI (2197)

2201 GGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCT BbsI (2201) AseI (2263)

2301 IATCTGACGGTTCACAAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTT SacI (2320)

2401 GGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCAT SpeI (2418)

2501 TGATGTA CTG CCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTA CTG CCAAGTAGGAAAGTCCCATAAGGTCATGTA CTG GGCATA
SnaBI (2546)

2601 ATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTA CTG CCAAGTGGGCAGTTTACCGTAAATAC
NdeI (2651)

2701 TCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGGTCTGTTGGGCGGT CAGCCAG

2801 GCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTG
PstI (2830) **SdaI (2829)** **BspLU11I (2847)** **PacI (2837)**

2901 CTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGG

3001 CGTTTCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGCGCTTTC

3101 TCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTT CAGCCCGACCGCTGCGCTTA
ApaLI (3161)

3201 TCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCG

3301 GTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAG

3401 AGTTGGTAGCTCTTGATCCGGCAAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAA

3501 GATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGG
EagI (3597) **PacI (3577)** **SwaI (3586)** **NotI (3596)**

3601 CCGCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTTGTGTAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAAC

3701 AAAC TAGCAAAATAGGCTGTCCCAAGTCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA