



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA **MfeI (82)**

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTACTGGCTCCGCCTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCCGCCCTACCTGAGGCC **HindIII (245)**

301 GCCATCCACGCGGGTTGAGTCGCGTTTTCGCCGCCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGCTTTTGTTCGTTT **NgoMIV (441)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCCTACCTGAGATCACCGGTACCATTGGGGTACTGCTCACACAGAGGACGCTGCTCAGTCT **NcoI (560)**
BstEII (555)
AgeI (552) 1▶ M G V L L T Q R T L L S L

601 GGTCTTGCACTCCTGTTTCCAAGCATGGCGAGCATGGCGGTATAGGACGCTGCTCGAAAGAGTACCGCGTGTCTTGGCCAGCTCCAGAAGCAGACA **MscI (678)** **BglII (699)**
13▶ V L A L L F P S M A S M A A I G S C S K E Y R V L L G Q L Q K Q T

701 GATCTCATGCAGGACACCAGCAGACTCCTGGACCCTATATACGTATCCAAGGCTGGATGTTCTAACTGAGAGAGCACTGCAGGGAGCGCCCGGGG **XcmI (716)** **SnaBI (740)** **StuI (750)** **XmaI (793)**
47▶ D L M Q D T S R L L D P Y I R I Q G L D V P K L R E H C R E R P G
801 CCTCCCCAGTGAGGAGCCCTGAGGGGCTGGCAGGCGGGCTTCTCGAGACCCTCAATGCCACACTGGGCTGCGTCCTGCACAGACTGGCCGACTT
80▶ A F P S E E T L R G L G R R G F L Q T L N A T L G C V L H R L A D L
901 AGAGCAGCGCTCCCAAGGCCAGGATTTGGAGAGGCTGGGCTGAACATCGAGGACTTGGAGAAGTGCAGATGGCGAGGCCGAACATCCTCGGGCTC
113▶ E Q R L P K A Q D L E R S G L N I E D L E K L Q M A R P N I L G L
1001 AGGAACAACATCTACTGCATGGCCAGCTGCTGGACAACCTCAGACACGGCTGAGCCACGAAGGCTGGCCGGGGGCTCTCAGCCGCCACCCACCC
147▶ R N N I Y C M A Q L L D N S D T A E P T K A G R G A S Q P P T P T

1101 CTGCTCGGATGCTTTTACGCGAAGCTGGAGGCTGCAGGTTCTGCATGGCTACCATCGCTTTCATGCACTCAGTGGGGCGGGTCTTTCAGCAAGTGGGG **DraIII (1168)** **BbsI (1183)**
180▶ P A S D A F Q R K L E G C R F L H G Y H R F M H S V G R V F S K W G

1201 GGAGAGCCGAACCGGAGCCGAGACACAGCCCCACCAGGCCCTGAGGAAGGGGTGCGCAGGACCAGACCCTCCAGGAAAGCAAGAGACTCATGACC **FspI (1256)** **BspHI (1292)**
213▶ E S P N R S R R H S P H Q A L R K G V R R T R P S R K G K R L M T

1301 AGGGGACAGCTGCCCCGTAGCTCGAGAGCACCCCTTGCCTGGTGAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGACAAACCACAAC **BstAPI (1329)** **MscI (1353)**
247▶ R G Q L P R •

1401 TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAGTTAACAAACAAT **HpaI (1485)** **MfeI (1496)**

1501 TGCATTCATTTTATGTTTCAGGTTCAAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTCTAAAATACAGCAT **EcoRI (1581)**

1601 AGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTG

1701 TTTGAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCAAGTTTTGAAGTCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTC **SapI (1763)**

1801 CCACATTCCTTTTTAGTAAAAATTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCC **SspI (1820)** **SwaI (1834)**

1901 CTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTCTG **SacI (2095)**

2001 GTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCT **BstXI (2124)**
137▶ 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 S I L E

2101 CTCTGCATGCCACAGGGGCTGACCACCTGATGGATCTGCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCC **StuI (2259)**
104▶ 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 K Q G

2201 GTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGCACCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTG **BbsI (2405)**
71▶ 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 G T K

2301 GTCCTGATGGCCGCGCCGACATGGTGTGTTGCTCATAGAGCATGTTGATCTTCTCAGTGGCGACCTCCACAGCTCCAGATCCTGCTGAGAGATGT **XmnI (2401)** **AseI (2467)**
37▶ 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 Q S I N

2401 TGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCC **SacI (2524)**
4▶ F T K M

2501 AGCTTATCTGACGGTTCACATAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACA

2601 TTTTGAAAGTCCC GTT GATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGC
SpeI (2622) ←

2701 CCATTGATGACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGG
SnaBI (2750)

2801 CATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAA
NdeI (2855)

2901 ATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTCAG

3001 CCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAGGCCAGAAAAGGCCAGGAACCGTAAAAAGGCCGC
SdaI (3033) Pacl (3041) BspLU11I (3051) ←

3101 GTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGTAC

3201 CAGGCGTTTTCCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGC

3301 TTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGC
ApaLI (3365)

3401 CTTATCCGGTAACTATCGTCTTGAGTCCAAACCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTA

3501 GCGGTGCTACAGAGTTCTGAAGTGGTGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAA

3601 AAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCA

3701 AGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC A
Pacl (3781) SwaI (3790)

EagI (3801)
NotI (3800)

3801 GCGGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACA
3901 AAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA