





AgeI (2837)

2801 tctttcctctcctgacagGTGTGAAACAGGAAGAGAACCGGTAGGAGGGCCATCATGGAAATCAAGGTGCTGTTTGCCTCATCTGTATTGCTGTTGCTG  
1 ▶ M E I K V L F A L I C I A V A

BglIII (2968)

2901 AGGCCAAAACCACTGAAATCAATGAAGACCTCAATATAGCTGTGTGGCTCCAACCTTGGCCACCACAGATCTTGAGACTGACCTGTTCAACCAACTGGGA  
16 ▶ E A K P T E I N E D L N I A A V A S N F A T T D L E T D L F T N W E  
3001 GACCATGAATGTGATTAGCACTGACACAGAGCAGGTGAACACAGATGCTGACAGGGGCAAGCTGCCTGGCAAAAACTCCCCCAGATGCTCTGAGGGAG  
49 ▶ T M N V I S T D T E Q V N T D A D R G K L P G K K L P P D V L R E  
3101 CTGGAGGCCAATGCCAGAAGGGCTGTTGCACAAGAGGCTGCCTCATTGCTCTCCACATTAAGTGCACCCCTAAGATGAAGAAATTTATCCCTGGCA  
83 ▶ L E A N A R R A G C T R G C L I C L S H I K C T P K M K K F I P G  
3201 GGTGCCACACTTATGAAGGTGAAAAGGAGTCTGCTCAGGGAGGGATTGGAGAGGCAATTGTTGATATCCCAGAGATTCCTGGCTTCAAGGATAAGGAGCC  
116 ▶ R C H T Y E G E K E S A Q G G I G E A I V D I P E I P G F K D K E P  
3301 ACTGGACCAAGTTTATTGCTCAAGTGGACCTCTGTGCTGATTGCACCACTGGCTGTCTGAAAGGGCTTGCCAATGTCCAGTGCTGACCTCCTGAAGAAG  
149 ▶ L D Q F I A Q V D L C A D C T T G C L K G L A N V Q C S D L L K K

NheI (3487)

3401 TGGCTTCCCAGAGGTGTACCACCTTTTCCAGCAAGATTCAGGGTAGGGTGGACAAAATCAAGGGTCTGGCTGGGGACAGATGATAGCTAGCTGGCCAGA  
183 ▶ W L P Q R C T T F A S K I Q G R V D K I K G L A G D R •  
3501 CATGATAAGATACATTGATGAGTTTGGACAAACCACAACACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTA

3601 ACCATTATAAGCTGCAATAAACAAAGTTAACAAACAATTGCATTCAATTTATGTTTCAGGTTTCAGGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAA

3701 ACCTCTACAAATGTGGTATGGAATTAATTCTAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAA

3801 TAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAGATATAGTGATTTTTCCAAGGTTT

SapI (3914)

3901 GAAGTACTCTTCATTTCTTTATGTTTTAAATGCAGTACCTCCACATTCCTTTTTAGTAAAATATTCAGAATAATTTAAATACATCATTGCAATGA  
4001 AAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAAGGAACCTTTAATA  
4101 GAAATTTGACAGCAAGAAAGCGAGCTTCTAGCTTATCTCAGTCTGCTCCTCTGCCACAAAGTGCACGAGTTGCCGCGGGTCCGCGAGGGCGAACT

125 ▶ • D Q E E A V F H V C N G A P D R L A F E

4201 CCCGCCCCACGGCTGCTCGCCGATCTCGGTGATGGCCGGCCGGAGGCGTCCCGGAAGTTCGTGGACACGACCTCCGACCACTCGGCGTACAGCTCGTC  
104 ▶ R G W P Q E G I E T M A P G S A D R F N T S V V E S W E A Y L E D

SgrAI (4394)

4301 CAGGCCGCGCACCCACACCCAGGCCAGGGTGTGTCCGGCACCACTGGTCTGGACCGCGTGTGAACAGGGTACGTCGTCGCGGACCAACCCGGC  
71 ▶ L G R V W V W A L T N D P V V Q D Q V A S I F L T V D D R V V G A  
4401 AAGTCGCTCCACGAAGTCCCGGGAGAACCCGAGCCGTCGTTCCAGAACTCGACGCTCCGGCGACGTCGCGCGGGTGAACCCGGAACCGCACTGG

37 ▶ F D D E V F D R S F G L R D T W F E V A G A V D R A T L V P V A S T  
4501 TCAACTTGGCCATGATGGCTCCTCTGTGAGGAGGAAAGAGAAGAAGGTTAGTACAATTGCTATAGTGAGTTGATTATACTATGCAGATATACTATG  
4 ▶ L K A M

4601 CCAATGATTAATTGTCAAAGTAGGGCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGCTGCC

4701 GTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTT

4801 CCCCTGGAAGCTCCCTCGTGCCTCTCTGTCCGACCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCATA

4901 GCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTGTTGCTCCAAGTGGGCTGTGTGCACGAACCCCGTTACGCCGACCGCTGCGCTTATCCGG

5001 TAACTATCGTCTTGTAGTCCAACCCGTAAGACACGACTTATGCCACTGGCAGCAGCCACTGTTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCT

5101 ACAGAGTTCTTGAAGTGGTGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTG

5201 GTAGCTCTTATCCGGCAAAACAAACCCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCC

5301 TTTGATCTTTTACGGGCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCA