

Manual Genefinding

Start codon: **ATG**
 Stop codons: **TAA, TAG, TGA**
 Donor splice site: **^GT[AG]AG**
 Acceptor splice site: **[CT]AG^**

>U70368 (950 bp)

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1  CTCCCTTAGA AGACTCCAGC AAGTTATTTG AAGAGGTCTT TGGAGACATG
51  GTGAGTTCTC TTCCTTCCC AGAAGGTAAG TCTCACTGTA AGGTCTTTAT
101 GTCTTGTGTG TCCCCCAGCA GCCTTGTTCAT CTCCGGCTGC CCTAGACCTG
151 CATAAGGACA GATTGAGTGT GCTGGGATAG ACTTTTGTG ACAAAGGGGC
201 TGCTCTGCCC TTCTAAGAGG TTGAGTCTCA TCATAAGGCC TTTTGCAGCT
251 TGCATGTGTA GTGCCAGGAA AGAGTAGTCA TCCCCCAAAA CCAGACAGGA
301 ACTGACGAGA TGCAATCACT GTGTGGACTT TTTACCAGCT AGCTAGGGCA
351 CTACCATGAG CCACTGTCTA GCAGGGAGGC TTTGGGGATG GTGTGCCCCG
401 AATATCTCTC AGGGTAAGAG TTTACAGTAA GCAGCAAGCA GAGGGGTGTG
451 GGTGAGTGTG CAAGTATCTA ATTGGCTAGT TTTTGTGGCC TGTAACATAT
501 TGGTGGGTGT TGGGAGTCAT AAGCTAAATG TTTGCTTTCC TCTGCATTGG
551 TGGTCATTAG GGAGGGGGCA GATTATGAAC CTAGGTTGCA GATCTGTTGG
601 AGTAATAACA AGACACTGGT CTTGTTGGGG GTATAACCTA GAGACTCGAT
651 TTATGTTTCAT GTTTGGTTTG GGATGGGTTT TATGTGAGTG TTTTCTTTTT
701 TGGGGAGGGG GTCGGTTAAC TTGGAAAGTA ATGCTAGGTA CTGTCCTGTT
751 CATTTCCCTG AGGTGAAAGT TAGGTCAGGT TTTCTAGAAT GGAGTCTGAA
801 GGTA AACAT TTGGCCACTG GCATGCCCTA AAGTCTTTTT GTGTTCTTGT
851 CCCCTAGCAG ATCCAGCCCT ATCATCTCCT GGTGCCCAAC AGCTGCATCA
901 GGATGAAGCT CAGGTAGTGG TGGAGCTAAC TGCCAATGAC AAGCCCAGTC

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Find, mark and
count all ATGs

How many ATGs do you
expect?