

Introduction to Gene Hunting Prokaryotic Genes

Below is a hypothetical sequence of DNA that may be found in a prokaryotic genome. "Hidden" in this genome are two genes; sequences regulating the expression of and coding for the primary structure of a protein.

With the help of your instructor, identify these two protein sequences by first writing out the mRNA sequence and then the resulting amino acid sequence. This should help you understand the two processes we call transcription and translation!

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3'- 1 aagcttcaaa ttaagtcagc tccttaaagt aaagataata aagtgtagtt caagaactat
5'-   ttcgaagttt aattcagtcg aggaatttac tttctattat ttcacatcaa gttcttgata

61 atgaatgatg tgttttgaca taacccaaaat ggggaaaata taattaaagt cagcatattt
   tacttactac acaaaaactgt attgggtttta ccccttttat attaatttca gtcgtataaa

121 ttggaaaatt gatgacgtca tactgacgtc gttttgatga caaatcttat tataagcgaa
   aaccttttaa ctactgcagt atgactgcag caaaactact gtttagaata atattcgctt

181 gaggggtgaag gtgatgcaac attcggaaaa cttacccccc agcccgcatt agacgcccgga
   ctcccacttc cactacgttg taagcctttt gaatgggggg tcgggcgtaa tctgcgggct

241 aaaaaaactt gtttcaggat aacaaagatg agtaaaggag aagaactttt cactggagtt
   tttttttgaa caaagtccta ttgtttctac tcatttcctc ttcttgaaaa gtgacctcaa

301 gtcccaattc ttgttgaatt agatgggtgat gttaatgggc acaaattctc tgtcagtgga
   cagggttaag aacaacttaa tctaccacta caattaccgc tgtttaagag acagtcacct

361 agatgggtgat acaaattctc aacacttgtc actactttct cttatggtgt tcagtaagtg
   tctaccacta tgtttaagag ttgtgaacag tgatgaaaga gaataccaca agtcattcac

421 cattttatac ttaaacaagt tttttttcgg gcgtctaata cgggctggga cttttaatat
   gtaaaatatg aatttgttca aaaaaagcc cgcagattac gcccgacctt gaaaattata

481 tattgggtgca attctagtca aattattgcg tttttttacc caaatgtta atgttaaact
   ataaccacgc taagatcagt ttaataacgc aaaaaaatgg gttttacaat tacaatttga

541 gaaatttggc aacttgcgc aaatatatac aggttatttt gaaaaaaagt tacaggatga
   ctttaaacgc tgtgaacgcg tttatatatg tccaataaaa ctttttttca atgtcctact

601 taaaagttgc acagaaactt atctcaagat ttaccgcgag aaagatggta taaaaattga
   attttcaacg tgtctttgaa tagagttcta aatgggcgtc tttctacat atttttaact

661 tatttgacag agcaaacct gccccattat acaattagtt gtttgacttg tgtcaatggg -5'
   ataaactgtc tcgttttgga cggggtaata tgaaaatcaa caaactgaac acagttacca -3'
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