

Computing the Similarity and the Diversity in the Species Based on Cronobacter Genome

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Abstract : The purpose of computing the similarity and the diversity in the species is to trace the process of evolution and to find the relationship between the species and discover the unique, the special, the common and the universal proteins. The proteins of the whole genome of 40 species are compared with the cronobacter genome which is used as reference genome. More than 3 billion pairwise alignments are performed using blastp. Several findings are introduced in this study, for example, we found 172 proteins in cronobacter genome which have insignificant hits in other species, 116 significant proteins in the all tested species with very high score value and 129 common proteins in the plants but have insignificant hits in mammals, birds, fishes, and insects.

Keywords : genome, species, blastp, conserved genes, Cronobacter

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