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In silico reconstruction of the amino acid metabolic pathways of *Trypanosoma cruzi*

A.C.R. Guimarães[1], T.D. Otto[1,2], M. Alves-Ferreira[1], A.B. Miranda[1] and W.M. Degrave[1]

[1]Laboratório de Genômica Funcional e Bioinformática,
Instituto Oswaldo Cruz, Fiocruz, Rio de Janeiro, RJ, Brasil
[2]Fundação Ataulpho de Paiva, Rio de janeiro, RJ, Brasil

Corresponding author: A.C.R. Guimarães
E-mail: carolg@fiocruz.br

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ABSTRACT. *Trypanosoma cruzi* is the epidemiological agent of Chagas' disease, affecting most of Central and South America, constituting a significant health and socio-economic problem. The parasite has a metabolism largely based on the consumption of amino acids, which participate in a diversity of metabolic pathways, leading to many crucial compounds for the survival of this parasite. Study of its enzymes has the potential to disclose new therapeutic targets and foster the development of new drugs. In this study, we employed computational approaches to reconstruct *in silico* the amino acid metabolic pathways of *T. cruzi*, aiming to link genomic information with functional information. For that, protein sequences from 570 EC classes belonging to 25 different

pathways in general amino acid metabolism were downloaded from KEGG. A subset of 471 EC classes had at least one sequence deposited. Clustering of the proteins belonging to each EC class was performed using a similarity-based approach implemented in the tool AnEnPi. Reconstruction of the metabolic pathways comprising the amino acid metabolism of *T. cruzi* was performed by analyzing the output of BLASTP, using as query the dataset of predicted proteins of *T. cruzi* against all sequences of each individual cluster. This approach allowed us to identify 764 *T. cruzi* proteins probably involved in the metabolism of amino acids as well as the identification of several putative cases of analogy. Furthermore, we were able to identify several enzymatic activities of *T. cruzi* that were not previously included in KEGG.

Key words: Amino acid; Metabolism; *Trypanosoma cruzi*; Analogy

