ANALOGOUS ENZYMES IN THE AMINO ACID METABOLISM OF *LEISHMANIA MAJOR*: PUTATIVE TARGETS FOR DRUG DEVELOPMENT.

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Proteins with the same enzymatic function but no detectable sequence similarity are considered as analogous enzymes, and are the result of independent evolutionary events. The criteria used for the search of new drug targets take into account the absence of the enzyme in humans. We developed AnEnπ, a tool that groups proteins based on sequence similarity of enzymatic function that allows the search of analogies between organisms. Here, we used AnEnπ to find putative analogies of enzymatic functions between *Homo sapiens* and *Leishmania major*, using as model the biochemical pathways for amino acid metabolism. A preliminary analysis of a dataset composed of 624 enzymatic activities revealed 394 enzymatic functions with at least one protein sequence associated. Also, we determined a subset of enzymatic functions shared by *L. major* and *H. sapiens*. In 109 cases, the sequences from these organisms were grouped in the same cluster, indicating a common origin for these enzymes. Four enzymatic functions were identified where the sequences from *L. major* and *H. sapiens* were placed in different clusters, representing putative analogies and possible candidates for the development of new drugs. Studies to determine and compare the 3D-structures of these analogous enzymes will be conducted aiming to screen potential drug targets. Financial Support: CNPq, PDTIS-FIOCRUZ.