

## ***IN SILICO* STUDY OF CORONINS AS PUTATIVE FLAGELLAR PROTEINS IN *LEISHMANIA SPP.***

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Coronins constitute an evolutionarily conserved family of WD-repeat actin-binding proteins involved in cell locomotion, phagocytosis and cytokinesis. The coronins have a conserved basic N-terminal motif and three to ten WD repeats clustered in one or two core domains. The WD40 motif is found in a large number of eukaryotic proteins involved in a variety of cellular processes. Using a combination of Bioinformatics tools, we identified coronins in four species of *Leishmania* (*L. major*, *L. infantum*, *L. donovani* and *L. braziliensis*). The proteins were determined *in silico* through different types of data from multiple databases (NCBI, GeneDB, PDB, Uniprot and Swiss-Prot). Therefore, sequences and structural analyses were obtained of *Leishmania spp* coronins and the functional assignment of these proteins was inferred using the BLAST search tool against conserved domain databases. For global alignments of protein sequences, we used CLUSTALW and MODELLER software was used to generate 3D models. The results display sequences with high similarity between coronins from different species of *Leishmania* and well-conserved domains/motifs. These putative coronins sequences contribute to improve knowledge on protein databases, specially, to predict its relevant role in flagellar activities, as available in FlagelLink (<http://nugen.lcc.uece.br/lpgate/?p=flagdb>).

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