

To get the full story you need to know the motifs

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Genome sequencing alone provides researchers with only limited information on the organism works because it neither reveals how the system is regulated nor does it indicate the role of each specific DNA sequence or RNA transcript. For that, scientists need to identify the system's regulatory and functional molecules, which are the ones calling the shots.

A very well-established concept in [molecular biology](#) predicts that sequence conservation among species indicates similarity in function. Identification of these sequences, known as motifs, may lead to the discovery of functionally relevant regions within the DNA. But how to find motifs in a highly divergent genomic landscape? A group led by Dr Angela Cruz at the University of São Paulo, in Brazil, may have a solution when it comes to Trypanosomatids, a group of parasites that includes the causing agents of leishmaniasis and Chagas disease.

While in most [organisms](#) genomic regulation occurs at the transcriptional level, in Trypanosomatides the whole genome is first transcribed and then regulated at later stages. This unique feature grants these organisms, which have a complex life cycle that may include passages through more than one host, the ability to switch into very distinct forms very dynamically, allowing their survival in different hostile environments.

By using a combination of computational tools the group led by Dr Angela Cruz developed an in silico-based pipeline containing the complete genome sequences of three species of *Leishmania* (*Leishmania*

Leishmania major, *Leishmania infantum*, and *Leishmania Viannia braziliensis*). Through this pipeline, scientists will be able to easily check whether their favorite gene or gene family carries a conserved sequence of potential regulatory function.

"The pipeline offers a novel and readily available resource for searching functional and regulatory elements in *Leishmania*" says Dr Cruz. Besides its value as a rich repository of sequences, the in-silico-based pipeline developed by Dr Cruz's group represents an innovative approach in which bioinformatics tools are used to pinpoint potentially functional and regulatory sequences that can be further tested by experimental validation, rather than the other way around.

The resource, named LeischCICS, comprises a sequence database that can be searched by labs worldwide interested in finding functional sequences in *Leishmania*, the causing agents of diseases affecting more than 380 million people in 88 countries. The ingenuity of Dr. Cruz's group may pave the way into a better understanding of the regulation of these organism's genomes and may provide new insights into how these pathogens work.

More information: The article entitled 'In silico Identification of Conserved Intercoding Sequences in Leishmania Genomes: Unraveling Putative cis-Regulatory Elements' has been published in the journal *Molecular and Biochemical Parasitology* and is available at www.sciencedirect.com/science/.../ii/S0166685112000515

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