Integrating Genomic, Functional, Proteomic, and Structural Data of Macromolecular Complexes of Trypanosomes.

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Kinetoplastid parasites have developed specific variations of common eukaryote mechanisms, such as splicing and translation. The characteristics of these variations are determined, at least partly, by their protein components and the nature of their RNA molecules, particularly in the case of the ribosomes.
Protein-protein interaction maps of the salk components of the large subunit of the *Trypanosoma cruzi* ribosome revealed parasite-specific pattern of interaction for these ribosomal protein and prepared an initial cryo-election microscopy (cryo-EM) analysis that allowed to obtain the first 3 D images of *T.cruzi* ribosomes at a resolution of 12 A. Integration of genomic and proteomic data supported particle reconstruction and allowed to distinguish the conserved eukaryotic rRNA core structure, together with novel features of this macromolecular complex. Remarkably, a novel helical structure appears in the small subunit, in the vicinity of the mRNA exit channel. The putative functional role of this specific feature will be discussed in the context of our effort to construct a protein-protein interaction map of the spliceosome of trypanosomes.