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The First High Resolution Crystal Structure of an Editosome Enzyme from *Trypanosoma brucei*: RNA Editing ligase I. Junpeng Deng, Achim Schnauffer, Reza Salavati, Kenneth D. Stuart, Wim G.J. Hol, Howard Hughes Medical Institute, Univ. of Washington, Seattle WA 98195, USA.

The crystal structure of the adenylation domain of *Trypanosoma brucei* RNA editing ligase 1 (TbREL1), in complex with ATP and magnesium, is reported at 1.2 Å resolution. ATP makes extensive direct and indirect interactions with the ligase via essentially all its atoms extending its base into a deep pocket. The magnesium ion is almost perfectly octahedrally coordinated and interacts with the β- and γ-phosphates in this ternary complex. The Mg:ATP interacts extensively with surrounding residues that occur in conserved nucleotidyl transferase motifs. In addition, the ATP has extensive interactions with residues that are conserved in the editing ligases only. TbREL1 contains a distinctive loop composed of residues that are highly conserved among trypanosomatids and may play a role in RNA and/or protein binding in the editosome. The distinct characteristics of the adenine-binding pocket, and the absence of any close homolog in the human genome, bode well for the design of selective inhibitors that will block the essential RNA ligase function in a number of devastating protozoan pathogens.