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Structural and Functional Implications of Tcru010945AAA, An Arginase Superfamily Protein.

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The mission of Structural Genomics of Protozoan Parasites (SGPP) is to determine crystal structures of proteins from major eukaryotic tropical pathogenic protozoa, specifically *Trypanosoma brucei* (African Sleeping Sickness), *Trypanosoma cruzi* (Chagas Disease), *Leishmania spp* (Leishmaniasis), and *Plasmodium falciparum* (Malaria). One protein of focus is Tcru010945AAA, a 315-residue protein from *Trypanosoma cruzi*, which belongs to the arginase superfamily, and was isolated, purified and crystallized in both native and Se-Met incorporated forms. Native crystals of Tcru010945AAA diffract to better than 1.5Å and molecular replacement using homologous structures failed to yield a structure. The Se-Met crystals diffract to 1.9Å and the structure was solved using SAD-phasing. Autobuilding tools such as Resolve and ARP/wARP produced an initial model trace followed by manual autobuilding and loop building by Robetta. The current model contains 298 of 315 residues with R = 0.182 and Rfree = 0.204. The structure of Tcru010945AAA has an α/β fold similar to other members of the arginase superfamily. Further studies to identify the substrate of Tcru010945AAA are in progress and include soaking and co-crystallization with arginine.