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Structural Work On Potential Drug Targets From Tropical Parasites. T Arakaki^{1,2}, M Holmes^{1,2}, I Le Trong^{1,2}, J Caruthers^{2,3}, E Boni^{1,2}, E Phizicky^{2,4}, E Quarterly^{2,4}, G DeTitta^{2,5}, J Luft^{2,5}, A Lauricella^{2,5}, O Kalyuzhniy^{1,2}, J Ross^{1,2}, F Buckner^{2,6}, W Van Voorhis^{2,6}, C L M J Verlinde^{1,2}, W G J Hol^{2,7}, E A Merritt^{1,2}, Depts of ¹Biochemistry and ⁶Medicine, Univ. of Washington, Seattle, ²Structural Genomics of Pathogenic Protozoa Consortium, ³Stanford Univ., ⁴Univ. of Rochester School of Medicine, ⁵Hauptman Woodward Inst., ⁷Howard Hughes Medical Inst., UW.

Diseases caused by eukaryotic pathogens such as *Plasmodium spp.*, *Leishmania spp.*, and *Trypanosoma* afflict billions of people in the poorest developing countries. The Structural Genomics of Pathogenic Protozoa Consortium is studying selected proteins from these protozoans, seeking potential targets for drugs to mitigate these diseases. Target proteins include phosphatases, lipid binding proteins, and enzymes from the pentose phosphate and pyrimidine biosynthesis pathways. Several structures will be presented, including that of a tyrosine phosphatase from *L. major*, a phosphatidylethanolamine-binding protein from *P. vivax*, and the *T. brucei* dihydroorotate dehydrogenase (DHODH), from the pyrimidine biosynthetic pathway. DHODH oxidizes dihydroorotate to orotate and comparison with other DHODH structures offers insights for the development of a broad, general inhibitor of trypanosomatid DHODHs.

