

## W0655

**Structural Genomics of Malaria Parasites and Other Apicomplexan Organisms.** A. Dong, J. Lew, Y. Zhao, J. Artz, M. Amani, M. Vedadi, T. Hills, W. Qiu, S. Brokx, G. Wasney, M. Melone, Z. Alam, A. Wernimont, A.M. Edwards, C.H. Arrowsmith, J. Weigelt, M. Sundstrom, A. Bochkarev, R. Hui, Structural Genomics Consortium (SGC), Univ. of Toronto, 100 College St., Toronto, Ontario, M5G1L5, Canada.

Advances in vaccine development and drug discovery are urgently needed to control malaria and other diseases caused by Apicomplexan parasites. This can be facilitated by production of purified recombinant proteins from Apicomplexan genomes and determination of their 3D structures. Using a combination of novel and established high throughput techniques in structural genomics, the Structural Genomics Consortium has been able to express over 200 soluble Apicomplexan proteins and obtain over 30 distinct 3D protein structures by means of crystallography, all of which are deposited in the Protein Data Bank.

In obtaining these results, we have been able to demonstrate that (a) it is difficult but not impossible to express Plasmodium proteins on a high throughput E. coli based platform; (b) contrary to literature reports, Plasmodium proteins are not generally more toxic to E. coli hosts than others; (c) Plasmodium vivax and Plasmodium knowlesi proteins tend to be more soluble than Plasmodium falciparum proteins.

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