Global mapping of protein subcellular location illuminates the function and evolution of apicomplexan cells.

Konstantin Barylyuk[1], Ludek Koreny[1], Huiling Ke[1], Simon Butterworth[1], Imen Lassadi[1], Tobias Mourier[2], Laurent Gatto[1], Arnab Pain[2], Kathryn S. Lilley[1], Ross F. Waller[1]

1. Department of Biochemistry, University of Cambridge, UK
2. Biological and Environmental Science and Engineering Division, King Abdullah University of Science and Technology, Saudi Arabia

Our appreciation of the complexity and evolution of protist cells is highly constrained by our limited knowledge of the locations and functions of most of the cell's proteome. Typically, few, if any, proteins have been located in a given taxon, and even the better studied protists, such as some human pathogens, have only a very small fraction of proteins' locations experimentally determined. At best, many protein locations are predicted based on studies of homologues from distant relatives. But, more often, proteins predicted from protist genomes or transcriptomes are 'hypotheticals' unique to a taxon's lineage, stymying even predictions of location or function by comparative biology. To address this deficit in our basic understanding of the compositional organisation of the cell, we have used a spatial proteomics method called LOPIT to simultaneously capture the steady-state subcellular association of thousands of proteins in the apicomplexan *Toxoplasma*. We have resolved almost 4000 proteins to locations including endosymbiotic organelles, secretory compartments related to invasion, discrete cytoskeletal structures, sub-nuclear compartments and large molecular complexes. These protein atlases reveal: protein associations throughout the cell providing testable hypotheses of their function; coordinated transcriptional control of discrete cell compartments; conservation and novelty of compartment proteomes both between apicomplexans, and other eukaryotes; different paces of evolution across the different cell compartments and structures in *Toxoplasma*; and clear instances of protein relocation from one organelle or structure to a different one over evolutionary time. This new, global view of the cell proteome provides a much more complete framework for understanding the mechanisms of function and evolution of these cells.