



## Programming Persistence of a Parasitic Infection

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Apicomplexans have coevolved with their animal hosts for half a billion years, developing the complex adaptations that support their obligate parasitic lifecycle. This protist phylum includes deadly and prevalent human infections like malaria and toxoplasmosis. Our work seeks to uncover the cellular adaptations that enable this form of parasitism. Using *Toxoplasma gondii* as a model organism for the phylum, we have integrated a variety of systematic approaches to assess gene function, including CRISPR-based genetic screens, quantitative proteomics, and single-cell transcriptional profiling. Together these methods provide new perspectives on the critical molecular events that govern the invasion of host cells, the regulation of gliding motility, and the establishment of chronic infections. Evidence points to conserved functions throughout the phylum for several of the pathways we have uncovered, including essential steps in the erythrocytic cycle of *Plasmodium falciparum*, which causes the most lethal form of malaria in humans. Beyond uncovering novel avenues for therapeutic intervention, our results inform our understanding of eukaryotic diversity.



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**Host:** Dr. Aaron Reinke

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