Malaria is caused by apicomplexan parasites of the genus *Plasmodium*. Our understanding of the biology of the malaria parasite is hampered by the large proportion of the cell's proteome that is of unknown cellular location or function. Apicomplexans, as for all of Myzozoa, have developed new cell compartments and structures along with great proteomic novelty, and this hinders interpretation of these cells from classical organism models. To address this problem, we are generating comprehensive high-resolution maps of protein subcellular localisation for the blood stages of the life cycle of *Plasmodium falciparum*. To achieve this, we have used the spatial proteomics technique hyperplexed Localisation of Organelle Proteins by Isotopic Tagging (hyperLOPIT) and generated data for 3916 *P. falciparum* proteins in the schizont stage and 3508 *P. falciparum* proteins in the trophozoite stage. We have also recently generated data on extracellular merozoites. With these data, we have performed high-resolution mapping of the subcellular localisations of these proteins. A curated list of marker proteins with experimentally validated localisation reveals that our hyperLOPIT maps clearly resolve numerous compartmental proteomes across the asexual developmental stages, including some sub-compartmental resolution. In addition to resolving the structures within the parasite, these maps also resolve parasite-derived structures exported into the host erythrocyte and parasite proteins that target to the host's plasma membrane. Furthermore, we find evidence of proteins from the host cell that map to compartments within the parasite, providing further insight into the interactions between parasite and host. Using supervised machine-learning classification methods we have attributed proteins of unknown localisation to the known cellular niches, providing localisation assignments to approximately 60% of the proteins analysed in our datasets. We are currently experimentally validating the results of these analyses through epitope tagging of a number of assignments of uncharacterised proteins. At least a half of the proteins in our data are uncharacterised or hypothetical proteins, and information about the localisation of these proteins across different developmental stages offers a major advance in our understanding of the organisation and biology of the malaria parasite.