Phosphoproteomic Analysis of Adult *Schistosoma mansoni*

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This study employed phosphoproteomics to unravel the phosphorylation status of the adult *Schistosoma mansoni* proteome to provide insight into which proteins and pathway(s) are activated in the mature worms. We identified 3,710 unique proteins containing either serine, threonine or tyrosine phosphorylation sites. Motif analysis of these sites revealed the majority of those over-represented to be classified either as proline-directed or basic; further analysis of the motifs revealed that they were likely phosphorylation sites for a number of upstream kinases including CAMKII, CK1/2, PKA and PKC. Gene ontology (GO) analysis of the dataset found the majority of proteins were classified under the molecular function category (52%), with 27% under biological process and 15% as cellular component. Protein–protein interaction analysis found 24,868 potential interactions in the dataset at high confidence (>0.7). Proteins with high numbers of putatively interacting partners included ubiquitins, heat shock proteins and DNA topoisomerases. Future work aims to hone in on signalling hubs of interest and use tools including RNAi to further understanding of the functional cell biology of *S. mansoni*.