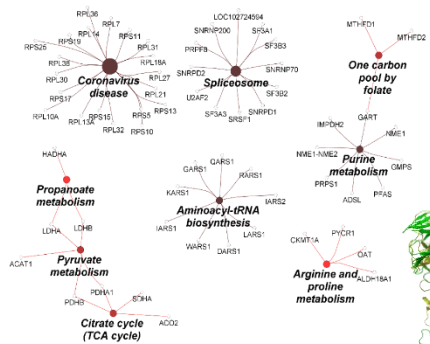




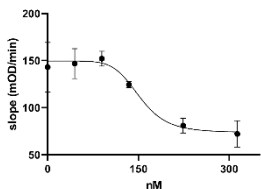
Second year activity

SARS-CoV-2

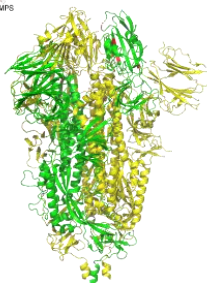
SARS-CoV-2 is the causative agent of COVID-19 disease; its genome encodes 4 structural proteins, including Spike (S). To elucidate the molecular mechanisms in which the Spike protein is involved, a functional proteomics approach was performed. Among the Spike interactors, we found LDHB, and their interaction was studied in detail.



Functional enrichment analysis of 121 putative Spike interactors.



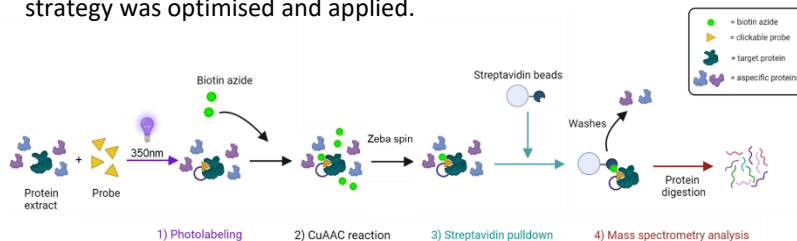
Spike inhibits LDHB protein



Pymol representation of Lip-MS experiments spike alpha and NAD+

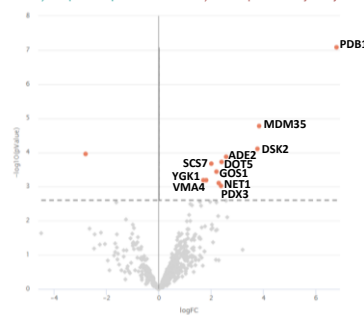
Plasmodium falciparum

P. falciparum is one of five different species of Plasmodium that cause malaria infection in humans. Among all antimalarial drugs, Plasmodione are redox-active agents that are highly effective. To identify the protein targets of plasmodium, an activity-based protein profiling (ABPP) strategy was optimised and applied.



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11 proteins were found to be statistically more abundant in the ABPP than in the control, with an FDR < 5%.



Ph.D. Student:
Vittoria Monaco

Title
Study of the molecular mechanisms relevant to the interactions between pathogens and hosts