# Identification and prioritisation of drug targets in the SARS-CoV-2 HMOX1 pathway

## Background

Both vaccines and anti-viral agents have been successful in reducing the danger from infection by SARS-CoV-2, but there remains a need to find novel therapeutic agents. An interaction has been observed between the SARS-CoV-2 protein ORF3a and the human protein HMOX1, which has a known role in platelet aggregation, thrombosis and inflammation. In this project we propose you use the existing disease map and other resources to create a model of the HMOX1 response to ORF3a and explore the gene regulatory network sensitivity to drug action.

## Suggested aims

* Build a network of heme metabolism in COVID-19, either de novo or derived from the relevant pathway in the disease map project.
* Study the static network in CellDesigner and Cytoscape
* From the literature, identify the key genes and their expected role in inflammation, thrombosis and others in the disease state using a Boolean or multistate model (i.e. generate a specification to test model correctness). Identify which genes are expected to determine the danger
* Convert to BMA format with CASQ and test and refine the network by altering target functions, gene interactions using stability testing for steady state analysis
* Once the specification is matched, use insights from different network analyses to identify and test the impact of inhibiting or activating individual genes to identify putative drug targets.
* Note their location in the pathway, including their relationship to other genes, and cross compare with biological knowledge to assign priority

## Relevant resources

<https://biomodelanalyzer.org/>

<https://fairdomhub.org/models/718>

## Relevant review

<https://pubmed.ncbi.nlm.nih.gov/32899231/>