System Biology: identifying immune markers contributing to the host immune responses to SARS-CoV-2 infection and their correlations with clinical and virological outcomes





Leads



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Key Objectives of WP5

- Develop a combination of complementary OMICS-based approaches to characterize the molecular mechanisms of coronaviruses/host cell interactions, to understand and characterize the host response during the course of infection, and decipher how coronaviruses manipulate/hijack some of these responses
- Conduct longitudinal immunological and virological analysis on samples obtained from the COVID-19 cohorts
- Provide a comprehensive platform of assays and technologies to monitor and fully characterize the innate and adaptive immune responses induced by the novel therapeutics developed under CARE
- Perform data integration of phenotypic, serum, genetic, clinical, virological and immunological parameters to identify signatures of the infection predictive of clinical profiles or prognosis, as well as immune correlates associated with treatment efficacy

CONNECTIONS



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with other work packages

Work packages 1 and 2

Identification of essential cellular pathways for replication which may lead to novel inhibitors of virus replication

Work package 4

Provision of guidance for selection of SARS-CoV-2 patient cohorts for antibody isolation from B cells

Work package 7

CoV-2

Transcriptomic analyses on samples from CARE clinical trial

OMICS approaches used



Human proteins 1,143 interacting with SARS-CoV-2 proteins identified Deregulated proteins 83 identified Proviral genes identified in 392 RNAi screening for SARS-

Antiviral genes identified in 403 RNAi screening for SARS-CoV-2

Variants of concern studied



2020	Identification of CD177 as specific neutrophil activation marker and thus as a hallmark of COVID-19 severe disease
2022	Identification of a "core gene signature" associated with a history of

COVID-19 Observation that CoV infection leads 2024 to increased nucleotide levels and

rewiring of glycolysis

Identification of several lipid pathway modifying cellular proteins as pan-coronavirus host factors



Publication of **web application to** visualize genes linked to human genetic associations to COVID-19

