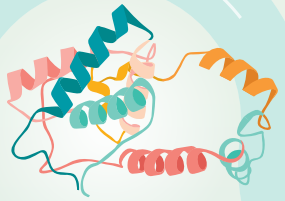
Immunologists struggling to understand COVID-19 ARE IN IT FOR THE LONG HAUL

Researchers and clinicians from fifteen institutions across the country are working together to enroll nearly 2000 COVID-19 patients in a clinical trial examining acute and long-term immune responses to the virus. The goal of the study, dubbed Immunotyping Assessment in a COVID-19 Cohort (IMPACC), is to characterize immune signatures to differentiate infection severity and explore long-term effects. Understanding immune response heterogeneity in COVID-19 patients could improve treatment and help "long-haulers" combat lingering effects.

IMPACC is part of the Human Immunology Project Consortium (HIPC) established by the NIAID. The HIPC will develop a publicly available resource detailing varied immune responses to infections, treatments, and vaccines.

IMPACC researchers and clinicians hope to help clinicians predict which patients may have the most severe infections, what treatment is best, and when the treatment should be administered.

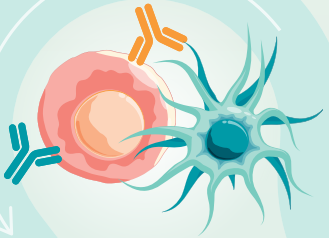
Patients with severe COVID-19 infection have an intense extrafollicular B-cell response akin to that found in autoimmune disorders such as systemic lupus erythematosus.[1,2]

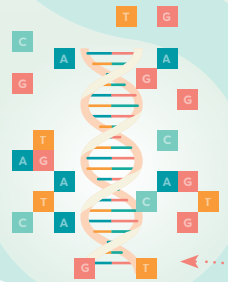


Clinicians collect nasal swabs and blood samples from patients throughout their hospitalization and at follow-up visits once every three months. They also collect lower airway secretions from patients using ventilators.

COVID-19 infected patients develop autoantibodies against the following:

- Phospholipids and carbohydrates[3, 4, 5]
- Rheumatoid factor[3]
- Blood plasma proteins important for blood clotting[3,6]
- Cytokines, chemokines, and complement components[7, 8]





Researchers will collect cells from individual patients to quantify the population of immune cells and immune related proteins such as cytokines and interferons in the patient samples at the collected time points. The researchers will use several approaches, including cytometry by time of flight, next generation sequencing, and proteomics to analyze the samples.

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