

## COVID-19-related publications utilizing SomaScan® Technology

### Peer reviewed

Abdel-Aziz, M. I., et al. (2021). "Association of endopeptidases, involved in SARS-CoV-2 infection, with microbial aggravation in sputum of severe asthma." *Allergy* **76**(6): 1917-1921.

<https://doi.org/10.1111/all.14731>

Aid, M., et al. (2020). "Vascular Disease and Thrombosis in SARS-CoV-2-Infected Rhesus Macaques." *Cell* **183**(5): 1354-1366 e1313. <https://doi.org/10.1016/j.cell.2020.10.005>

The COVID-19 pandemic has led to extensive morbidity and mortality throughout the world. Clinical features that drive SARS-CoV-2 pathogenesis in humans include inflammation and thrombosis, but the mechanistic details underlying these processes remain to be determined. In this study, we demonstrate endothelial disruption and vascular thrombosis in histopathologic sections of lungs from both humans and rhesus macaques infected with SARS-CoV-2. To define key molecular pathways associated with SARS-CoV-2 pathogenesis in macaques, we performed transcriptomic analyses of bronchoalveolar lavage and peripheral blood and proteomic analyses of serum. We observed macrophage infiltrates in lung and upregulation of macrophage, complement, platelet activation, thrombosis, and proinflammatory markers, including C-reactive protein, MX1, IL-6, IL-1, IL-8, TNFalpha, and NF-kappaB. These results suggest a model in which critical interactions between inflammatory and thrombosis pathways lead to SARS-CoV-2-induced vascular disease. Our findings suggest potential therapeutic targets for COVID-19.

AlGhatrif, M., et al. (2021). "Age-associated difference in circulating ACE2, the gateway for SARS-CoV-2, in humans: results from the InCHIANTI study." *Geroscience* **43**(2): 619-627.

<https://doi.org/10.1007/s11357-020-00314-w>

Levels of angiotensin-converting enzyme 2 (ACE2), the gateway for COVID-19 virus into the cells, have been implicated in worse COVID-19 outcomes associated with aging and cardiovascular disease (CVD). Data on age-associated differences in circulating ACE2 levels in humans and the role of CVD and medications is limited. We analyzed data from 967 participants of the InCHIANTI study, a community-dwelling cohort in the Chianti region, Italy. Relative abundance of ACE2 in plasma was assessed using a proteomics platform. CVD diagnoses, use of renin-angiotensin-aldosterone system (RAAS) antagonists: ACEi, ARBs, and aldosterone antagonists, were ascertained. Multiple linear analyses were performed to examine the independent association of ACE2 with age, CVD, and RAAS antagonist use. Age was independently associated with lower log (ACE2) in persons aged  $\geq 55$  years (STD beta = - 0.12, p = 0.0002). ACEi treatment was also independently associated with significantly lower ACE2 levels, and ACE2 was inversely associated with weight, and positively associated with peripheral artery disease (PAD) status. There was a trend toward higher circulating ACE2 levels in hypertensive individuals, but it did not reach statistical significance. In a stratified analysis, the association between log (ACE2) and log (IL-6) was more evidenced in participants with PAD. Circulating ACE2 levels demonstrate curvilinear association with age, with older individuals beyond the sixth decade age having lower levels. ACEi was associated with greater circulating ACE2 levels. Interestingly, ACE2 was elevated in PAD and positively associated with inflammatory markers, suggesting compensatory upregulation in the setting of chronic inflammation. Further studies are needed to comprehensively characterize RAAS components with aging and disease, and assess its prognostic role in predicting COVID-19 outcomes.

Anisul, M., et al. (2021). "A proteome-wide genetic investigation identifies several SARS-CoV-2-exploited host targets of clinical relevance." *Elife* **10**. <https://doi.org/10.7554/elife.69719>

**Background:** The virus SARS-CoV-2 can exploit biological vulnerabilities (e.g. host proteins) in susceptible hosts that predispose to the development of severe COVID-19.

**Methods:** To identify host proteins that may contribute to the risk of severe COVID-19, we undertook proteome-wide genetic colocalisation tests, and polygenic (pan) and cis-Mendelian randomisation analyses leveraging publicly available protein and COVID-19 datasets. Results: Our analytic approach identified several known targets (e.g. ABO, OAS1), but also nominated new proteins such as soluble Fas (colocalisation probability > 0.9,  $p = 1 \times 10^{-4}$ ), implicating Fas-mediated apoptosis as a potential target for COVID-19 risk. The polygenic (pan) and cis-Mendelian randomisation analyses showed consistent associations of genetically predicted ABO protein with several COVID-19 phenotypes. The ABO signal is highly pleiotropic and a look-up of proteins associated with the ABO signal revealed that the strongest association was with soluble CD209. We demonstrated experimentally that CD209 directly interacts with the spike protein of SARS-CoV-2, suggesting a mechanism that could explain the ABO association with COVID-19.

**Conclusions:** Our work provides a prioritised list of host targets potentially exploited by SARS-CoV-2 and is a precursor for further research on CD209 and FAS as therapeutically tractable targets for COVID-19.

Arthur, L., et al. (2021) "Cellular and plasma proteomic determinants of COVID-19 and non-COVID-19 pulmonary diseases relative to healthy aging." *Nat Aging* 1: 535–549. <https://doi.org/10.1038/s43587-021-00067-x>

We examine the cellular and soluble determinants of coronavirus disease 2019 (COVID-19) relative to aging by performing mass cytometry in parallel with clinical blood testing and plasma proteomic profiling of ~4,700 proteins from 71 individuals with pulmonary disease and 148 healthy donors (25–80 years old). Distinct cell populations were associated with age (GZMK<sup>+</sup>CD8<sup>+</sup> T cells and CD25<sup>low</sup> CD4<sup>+</sup> T cells) and with COVID-19 (TBET<sup>+</sup>EOMES<sup>-</sup> CD4<sup>+</sup> T cells, HLA-DR<sup>+</sup>CD38<sup>+</sup> CD8<sup>+</sup> T cells and CD27<sup>+</sup>CD38<sup>+</sup> B cells). A unique population of TBET<sup>+</sup>EOMES<sup>+</sup> CD4<sup>+</sup> T cells was associated with individuals with COVID-19 who experienced moderate, rather than severe or lethal, disease. Disease severity correlated with blood creatinine and urea nitrogen levels. Proteomics revealed a major impact of age on the disease-associated plasma signatures and highlighted the divergent contribution of hepatocyte and muscle secretomes to COVID-19 plasma proteins. Aging plasma was enriched in matrisome proteins and heart/aorta smooth muscle cell-specific proteins. These findings reveal age-specific and disease-specific changes associated with COVID-19, and potential soluble mediators of the physiological impact of COVID-19.

Chirinos, J. A., et al. (2020). "Clinical and Proteomic Correlates of Plasma ACE2 (Angiotensin-Converting Enzyme 2) in Human Heart Failure." *Hypertension* 76(5): 1526-1536. <https://doi.org/10.1161/hypertensionaha.120.15829>

ACE2 (angiotensin-converting enzyme 2) is a key component of the renin-angiotensin-aldosterone system. Yet, little is known about the clinical and biologic correlates of circulating ACE2 levels in humans. We assessed the clinical and proteomic correlates of plasma (soluble) ACE2 protein levels in human heart failure. We measured plasma ACE2 using a modified aptamer assay among PHFS (Penn Heart Failure Study) participants (n=2248). We performed an association study of ACE2 against approximately 5000 other plasma proteins measured with the SomaScan platform. Plasma ACE2 was not associated with ACE inhibitor and angiotensin-receptor blocker use. Plasma ACE2 was associated with older age, male sex, diabetes mellitus, a lower estimated glomerular filtration rate, worse New York Heart Association class, a history of coronary artery bypass surgery, and higher pro-BNP (pro-B-type natriuretic peptide) levels. Plasma ACE2 exhibited associations with 1011 other plasma proteins. In pathway overrepresentation analyses, top canonical pathways associated with plasma ACE2 included clathrin-mediated endocytosis signaling, actin cytoskeleton signaling, mechanisms of viral exit from host cells, EIF2 (eukaryotic initiation factor 2) signaling, and the protein ubiquitination pathway. In conclusion, in humans with heart failure,

plasma ACE2 is associated with various clinical factors known to be associated with severe coronavirus disease 2019 (COVID-19), including older age, male sex, and diabetes mellitus, but is not associated with ACE inhibitor and angiotensin-receptor blocker use. Plasma ACE2 protein levels are prominently associated with multiple cellular pathways involved in cellular endocytosis, exocytosis, and intracellular protein trafficking. Whether these have a causal relationship with ACE2 or are relevant to novel coronavirus-2 infection remains to be assessed in future studies.

Demidowich, A. P., et al. (2020). "Colchicine's effects on metabolic and inflammatory molecules in adults with obesity and metabolic syndrome: results from a pilot randomized controlled trial." *Int J Obes (Lond)* **44**(8): 1793-1799. <https://doi.org/10.1038/s41366-020-0598-3>

**OBJECTIVE:** Recent clinical trials have demonstrated that colchicine may have metabolic and cardiovascular benefits in at-risk patients; however, the mechanisms through which colchicine may improve outcomes are still unclear. We sought to examine colchicine's effects on circulating inflammatory and metabolic molecules in adults with obesity and metabolic syndrome (MetS).

**METHODS:** Blood samples were collected pre- and post-intervention during a double-blind randomized controlled trial in which 40 adults with obesity and MetS were randomized to colchicine 0.6 mg or placebo twice-daily for 3 months. Serum samples were analyzed for 1305 circulating factors using the SomaScan Platform. The Benjamini-Hochberg procedure was used to adjust the false discovery rate (FDR) for multiple testing. **RESULTS:** At baseline, age (48.0 +/- 13.8 vs. 44.7 +/- 10.3 years) and BMI (39.8 +/- 6.4 vs. 41.8 +/- 8.2 kg/m<sup>2</sup>) were not different between groups. After controlling for the FDR, 34 molecules were significantly changed by colchicine. Colchicine decreased concentrations of multiple inflammatory molecules, including C-reactive protein, interleukin 6, and resistin, in addition to vascular-related proteins (e.g., oxidized low-density lipoprotein receptor, phosphodiesterase 5A). Conversely, relative to placebo, colchicine significantly increased concentrations of eight molecules including secreted factors associated with metabolism and anti-thrombosis.

**CONCLUSIONS:** In adults with obesity, colchicine significantly affected concentrations of proteins involved in the innate immune system, endothelial function and atherosclerosis, uncovering new mechanisms behind its cardiometabolic effects. Further research is warranted to investigate whether colchicine's IL-6 suppressive effects may be beneficial in COVID-19.

Filbin, M. R., et al. (2021). "Longitudinal proteomic analysis of severe COVID-19 reveals survival-associated signatures, tissue-specific cell death, and cell-cell interactions." *Cell Rep Med* **2**(5): 100287. <https://doi.org/10.1016/j.xcrm.2021.100287>

Mechanisms underlying severe coronavirus disease 2019 (COVID-19) disease remain poorly understood. We analyze several thousand plasma proteins longitudinally in 306 COVID-19 patients and 78 symptomatic controls, uncovering immune and non-immune proteins linked to COVID-19. Deconvolution of our plasma proteome data using published scRNA-seq datasets reveals contributions from circulating immune and tissue cells. Sixteen percent of patients display reduced inflammation yet comparably poor outcomes. Comparison of patients who died to severely ill survivors identifies dynamic immune-cell-derived and tissue-associated proteins associated with survival, including exocrine pancreatic proteases. Using derived tissue-specific and cell-type-specific intracellular death signatures, cellular angiotensin-converting enzyme 2 (ACE2) expression, and our data, we infer whether organ damage resulted from direct or indirect effects of infection. We propose a model in which interactions among myeloid, epithelial, and T cells drive tissue damage. These datasets provide important insights and a rich resource for analysis of mechanisms of severe COVID-19 disease.

Galbraith, M. D., et al. (2021). "Seroconversion stages COVID19 into distinct pathophysiological states." *Elife* **10**. <https://doi.org/10.7554/elife.65508>

COVID19 is a heterogeneous medical condition involving diverse underlying pathophysiological processes including hyperinflammation, endothelial damage, thrombotic microangiopathy, and end-organ damage. Limited knowledge about the molecular mechanisms driving these processes and lack of staging biomarkers hamper the ability to stratify patients for targeted therapeutics. We report here the results of a cross-sectional multi-omics analysis of hospitalized COVID19 patients revealing that seroconversion status associates with distinct underlying pathophysiological states. Low antibody titers associate with hyperactive T cells and NK cells, high levels of IFN alpha, gamma and lambda ligands, markers of systemic complement activation, and depletion of lymphocytes, neutrophils, and platelets. Upon seroconversion, all of these processes are attenuated, observing instead increases in B cell subsets, emergency hematopoiesis, increased D-dimer, and hypoalbuminemia. We propose that seroconversion status could potentially be used as a biosignature to stratify patients for therapeutic intervention and to inform analysis of clinical trial results in heterogeneous patient populations.

Gaziano, L., et al. (2021). "Actionable druggable genome-wide Mendelian randomization identifies repurposing opportunities for COVID-19." *Nat Med* **27**(4): 668-676. <https://doi.org/10.1038/s41591-021-01310-z>

Drug repurposing provides a rapid approach to meet the urgent need for therapeutics to address COVID-19. To identify therapeutic targets relevant to COVID-19, we conducted Mendelian randomization analyses, deriving genetic instruments based on transcriptomic and proteomic data for 1,263 actionable proteins that are targeted by approved drugs or in clinical phase of drug development. Using summary statistics from the Host Genetics Initiative and the Million Veteran Program, we studied 7,554 patients hospitalized with COVID-19 and >1 million controls. We found significant Mendelian randomization results for three proteins (ACE2,  $P = 1.6 \times 10^{-6}$ ); IFNAR2,  $P = 9.8 \times 10^{-11}$ ) and IL-10RB,  $P = 2.3 \times 10^{-14}$ ) using cis-expression quantitative trait loci genetic instruments that also had strong evidence for colocalization with COVID-19 hospitalization. To disentangle the shared expression quantitative trait loci signal for IL10RB and IFNAR2, we conducted phenome-wide association scans and pathway enrichment analysis, which suggested that IFNAR2 is more likely to play a role in COVID-19 hospitalization. Our findings prioritize trials of drugs targeting IFNAR2 and ACE2 for early management of COVID-19.

Hernandez Cordero, A. I., et al. (2021). "Multi-omics highlights ABO plasma protein as a causal risk factor for COVID-19." *Hum Genet* **140**(6): 969-979. <https://doi.org/10.1007/s00439-021-02264-5>

SARS-CoV-2 is responsible for the coronavirus disease 2019 (COVID-19) and the current health crisis. Despite intensive research efforts, the genes and pathways that contribute to COVID-19 remain poorly understood. We, therefore, used an integrative genomics (IG) approach to identify candidate genes responsible for COVID-19 and its severity. We used Bayesian colocalization (COLOC) and summary-based Mendelian randomization to combine gene expression quantitative trait loci (eQTLs) from the Lung eQTL ( $n = 1,038$ ) and eQTLGen ( $n = 31,784$ ) studies with published COVID-19 genome-wide association study (GWAS) data from the COVID-19 Host Genetics Initiative. Additionally, we used COLOC to integrate plasma protein quantitative trait loci (pQTL) from the INTERVAL study ( $n = 3,301$ ) with COVID-19 loci. Finally, we determined any causal associations between plasma proteins and COVID-19 using multi-variable two-sample Mendelian randomization (MR). The expression of 18 genes in lung and/or blood colocalized with COVID-19 loci. Of these, 12 genes were in suggestive loci (PGWAS  $< 5 \times 10^{-05}$ ). LZTFL1, SLC6A20, ABO, IL10RB and IFNAR2 and OAS1 had been previously associated with a heightened risk of COVID-19 (PGWAS  $< 5 \times 10^{-08}$ ). We identified a causal association between OAS1 and COVID-19 GWAS. Plasma ABO protein, which is associated with blood type in humans, demonstrated a significant causal relationship with COVID-19 in the MR analysis; increased plasma levels were associated with an increased risk of COVID-19 and, in particular, severe COVID-19. In summary, our study identified genes

associated with COVID-19 that may be prioritized for future investigations. Importantly, this is the first study to demonstrate a causal association between plasma ABO protein and COVID-19.

Mills, R. J., et al. (2021). "BET inhibition blocks inflammation-induced cardiac dysfunction and SARS-CoV-2 infection." *Cell* **184**(8): 2167-2182 e2122. <https://doi.org/10.1016/j.cell.2021.03.026>

Cardiac injury and dysfunction occur in COVID-19 patients and increase the risk of mortality. Causes are ill defined but could be through direct cardiac infection and/or inflammation-induced dysfunction. To identify mechanisms and cardio-protective drugs, we use a state-of-the-art pipeline combining human cardiac organoids with phosphoproteomics and single nuclei RNA sequencing. We identify an inflammatory "cytokine-storm", a cocktail of interferon gamma, interleukin 1beta, and poly(I:C), induced diastolic dysfunction. Bromodomain-containing protein 4 is activated along with a viral response that is consistent in both human cardiac organoids (hCOs) and hearts of SARS-CoV-2-infected K18-hACE2 mice. Bromodomain and extraterminal family inhibitors (BETi) recover dysfunction in hCOs and completely prevent cardiac dysfunction and death in a mouse cytokine-storm model. Additionally, BETi decreases transcription of genes in the viral response, decreases ACE2 expression, and reduces SARS-CoV-2 infection of cardiomyocytes. Together, BETi, including the Food and Drug Administration (FDA) breakthrough designated drug, apabetalone, are promising candidates to prevent COVID-19 mediated cardiac damage.

Moin, A. S. M., et al. (2021). "Soluble Neuropilin-1 Response to Hypoglycemia in Type 2 Diabetes: Increased Risk or Protection in SARS-CoV-2 Infection?" *Front Endocrinol (Lausanne)* **12**: 665134. <https://doi.org/10.3389/fendo.2021.665134>

**Introduction:** Neuropilin-1(NRP1) is a cofactor that enhances SARS-CoV-2 coronavirus cell infectivity when co-expressed with angiotensin-converting enzyme 2(ACE2). The Renin-Angiotensin System (RAS) is activated in type 2 diabetes (T2D); therefore, the aim of this study was to determine if hypoglycaemia-induced stress in T2D would potentiate serum NRP1(sNRP1) levels, reflecting an increased risk for SARS-CoV-2 infection.

**Methods:** A case-control study of aged-matched T2D (n = 23) and control (n = 23) subjects who underwent a hyperinsulinemic clamp over 1-hour to hypoglycemia(<40mg/dl) with subsequent timecourse of 4-hours and 24-hours. Slow Off-rate Modified Aptamer (SOMA)-scan plasma protein measurement determined RAS-related proteins: renin (REN), angiotensinogen (AGT), ACE2, soluble NRP1(sNRP1), NRP1 ligands (Vascular endothelial growth factor, VEGF and Class 3 Semaphorins, SEM3A) and NRP1 proteolytic enzyme (A Disintegrin and Metalloproteinase 9, ADAM9).

**Results:** Baseline RAS overactivity was present with REN elevated and AGT decreased in T2D (p<0.05); ACE2 was unchanged. Baseline sNRP1, VEGF and ADAM9 did not differ between T2D and controls and remained unchanged in response to hypoglycaemia. However, 4-hours post-hypoglycemia, sNRP1, VEGF and ADAM9 were elevated in T2D(p<0.05). SEMA3A was not different at baseline; at hypoglycemia, SEMA3A decreased in controls only. Post-hypoglycemia, SEMA3A levels were higher in T2D versus controls. sNRP1 did not correlate with ACE2, REN or AGT. T2D subjects stratified according to ACE inhibitor (ACEi) therapies showed no difference in sNRP1 levels at either glucose normalization or hypoglycaemia.

**Conclusion:** Hypoglycemia potentiated both plasma sNRP1 level elevation and its ligands VEGF and SEMA3A, likely through an ADAM9-mediated mechanism that was not associated with RAS overactivity or ACEi therapy; however, whether this is protective or promotes increased risk for SARS-CoV-2 infection in T2D is unclear.

Moin, A. S. M., et al. (2021). "Type 2 Diabetes Coagulopathy Proteins May Conflict With Biomarkers Reflective of COVID-19 Severity." *Front Endocrinol (Lausanne)* **12**: 658304. <https://doi.org/10.3389/fendo.2021.658304>

**Objective:** Detailed proteomic analysis in a cohort of patients with differing severity of COVID-19 disease identified biomarkers within the complement and coagulation cascades as biomarkers for disease severity has been reported; however, it is unclear if these proteins differ sufficiently from other conditions to be considered as biomarkers.

**Methods:** A prospective, parallel study in T2D (n = 23) and controls (n = 23). A hyperinsulinemic clamp was performed and normoglycemia induced in T2D [4.5 +/- 0.07 mmol/L (81 +/- 1.2 mg/dl)] for 1-h, following which blood glucose was decreased to  $\leq 2.0$  mmol/L (36 mg/dl). Proteomic analysis for the complement and coagulation cascades were measured using Slow Off-rate Modified Aptamer (SOMA)-scan.

**Results:** Thirty-four proteins were measured. At baseline, 4 of 18 were found to differ in T2D versus controls for platelet degranulation [Neutrophil-activating peptide-2 (p = 0.014), Thrombospondin-1 (p = 0.012), Platelet factor-4 (p = 0.007), and Kininogen-1 (p = 0.05)], whilst 3 of 16 proteins differed for complement and coagulation cascades [Coagulation factor IX (p < 0.05), Kininogen-1 (p = 0.05), and Heparin cofactor-2 (p = 0.007)]; STRING analysis demonstrated the close relationship of these proteins to one another. Induced euglycemia in T2D showed no protein changes versus baseline. At hypoglycemia, however, four proteins changed in controls from baseline [Thrombospondin-1 (p < 0.014), platelet factor-4 (p < 0.01), Platelet basic protein (p < 0.008), and Vitamin K-dependent protein-C (p < 0.00003)], and one protein changed in T2D [Vitamin K-dependent protein-C, (p < 0.0002)].

**Conclusion:** Seven of 34 proteins suggested to be biomarkers of COVID-19 severity within the platelet degranulation and complement and coagulation cascades differed in T2D versus controls, with further changes occurring at hypoglycemia, suggesting that validation of these biomarkers is critical. It is unclear if these protein changes in T2D may predict worse COVID-19 disease for these patients.

Moin, A. S. M., et al. (2020). "Letter to the Editor: Pro-fibrotic M2 macrophage markers may increase the risk for COVID19 in type 2 diabetes with obesity." *Metabolism* **112**: 154374.  
<https://doi.org/10.1016/j.metabol.2020.154374>

Moin, A. S. M., et al. (2021). "Vitamin D Association With Macrophage-Derived Cytokines in Polycystic Ovary Syndrome: An Enhanced Risk of COVID-19 Infection?" *Front Endocrinol (Lausanne)* **12**: 638621. <https://doi.org/10.3389/fendo.2021.638621>

**Background:** Women with polycystic ovary syndrome (PCOS) often have vitamin D deficiency, a known risk factor for severe COVID-19 disease. Alveolar macrophage-derived cytokines contribute to the inflammation underlying pulmonary disease in COVID-19. We sought to determine if basal macrophage activation, as a risk factor for COVID-19 infection, was present in PCOS and, if so, was further enhanced by vitamin D deficiency.

**Methods:** A cross-sectional study in 99 PCOS and 68 control women who presented sequentially. Plasma levels of a macrophage-derived cytokine panel were determined by Slow Off-rate Modified Aptamer (SOMA)-scan plasma protein measurement. Vitamin D was measured by tandem mass spectroscopy.

**Results:** Vitamin D was lower in PCOS women (p<0.0001) and correlated negatively with body mass index (BMI) in PCOS (r=0.28, p=0.0046). Basal macrophage activation markers CXCL5, CD163 and MMP9 were elevated, whilst protective CD200 was decreased (p<0.05); changes in these variables were related to, and fully accounted for, by BMI. PCOS and control women were then stratified according to vitamin D concentration. Vitamin D deficiency was associated with decreased CD80 and IFN-gamma in PCOS and IL-12 in both groups (p<0.05). These factors, important in initiating and maintaining the immune response, were again accounted for by BMI.

**Conclusion:** Basal macrophage activation was higher in PCOS with macrophage changes related with increased infection risk associating with vitamin D; all changes were BMI dependent, suggesting that obese PCOS with vitamin D deficiency may be at greater risk of more severe COVID-19 infection, but that it is obesity-related rather than an independent PCOS factor.

Montgomery, R.R., Steen, H. (2021) Using 'big data' to disentangle aging and COVID-19. *Nat Aging* **1**: 496–497. <https://doi.org/10.1038/s43587-021-00078-8>

Pietzner, M., et al. (2020). "Genetic architecture of host proteins involved in SARS-CoV-2 infection." *Nat Commun* **11**(1): 6397. <https://doi.org/10.1038/s41467-020-19996-z>

Understanding the genetic architecture of host proteins interacting with SARS-CoV-2 or mediating the maladaptive host response to COVID-19 can help to identify new or repurpose existing drugs targeting those proteins. We present a genetic discovery study of 179 such host proteins among 10,708 individuals using an aptamer-based technique. We identify 220 host DNA sequence variants acting in cis (MAF 0.01-49.9%) and explaining 0.3-70.9% of the variance of 97 of these proteins, including 45 with no previously known protein quantitative trait loci (pQTL) and 38 encoding current drug targets. Systematic characterization of pQTLs across the phenome identified protein-drug-disease links and evidence that putative viral interaction partners such as MARK3 affect immune response. Our results accelerate the evaluation and prioritization of new drug development programmes and repurposing of trials to prevent, treat or reduce adverse outcomes. Rapid sharing and detailed interrogation of results is facilitated through an interactive webserver ( <https://omicscience.org/apps/covidpgwas/> ).

Ramaswamy, A., et al. (2021). "Immune dysregulation and autoreactivity correlate with disease severity in SARS-CoV-2-associated multisystem inflammatory syndrome in children." *Immunity* **54**(5): 1083-1095 e1087. <https://doi.org/10.1016/j.immuni.2021.04.003>

Multisystem inflammatory syndrome in children (MIS-C) is a life-threatening post-infectious complication occurring unpredictably weeks after mild or asymptomatic SARS-CoV-2 infection. We profiled MIS-C, adult COVID-19, and healthy pediatric and adult individuals using single-cell RNA sequencing, flow cytometry, antigen receptor repertoire analysis, and unbiased serum proteomics, which collectively identified a signature in MIS-C patients that correlated with disease severity. Despite having no evidence of active infection, MIS-C patients had elevated S100A-family alarmins and decreased antigen presentation signatures, indicative of myeloid dysfunction. MIS-C patients showed elevated expression of cytotoxicity genes in NK and CD8(+) T cells and expansion of specific IgG-expressing plasmablasts. Clinically severe MIS-C patients displayed skewed memory T cell TCR repertoires and autoimmunity characterized by endothelium-reactive IgG. The alarmin, cytotoxicity, TCR repertoire, and plasmablast signatures we defined have potential for application in the clinic to better diagnose and potentially predict disease severity early in the course of MIS-C.

Richardson, T. G., et al. (2021). "Evaluating the effects of cardiometabolic exposures on circulating proteins which may contribute to severe SARS-CoV-2." *EBioMedicine* **64**: 103228. <https://doi.org/10.1016/j.ebiom.2021.103228>

**BACKGROUND:** Developing insight into the pathogenesis of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is of critical importance to overcome the global pandemic caused by coronavirus disease 2019 (covid-19). In this study, we have applied Mendelian randomization (MR) to systematically evaluate the effect of 10 cardiometabolic risk factors and genetic liability to lifetime smoking on 97 circulating host proteins postulated to either interact or contribute to the maladaptive host response of SARS-CoV-2.

**METHODS:** We applied the inverse variance weighted (IVW) approach and several robust MR methods in a two-sample setting to systemically estimate the genetically predicted effect of each risk factor in turn on levels of each circulating protein. Multivariable MR was conducted to simultaneously evaluate the effects of multiple risk factors on the same protein. We also applied MR using cis-regulatory variants at the genomic location responsible for encoding these proteins to estimate whether their circulating levels may influence severe SARS-CoV-2.

**FINDINGS:** In total, we identified evidence supporting 105 effects between risk factors and circulating proteins which were robust to multiple testing corrections and sensitivity analyses. For example, body mass index provided evidence of an effect on 23 circulating proteins with a variety of functions, such as inflammatory markers c-reactive protein (IVW Beta=0.34 per standard deviation change, 95% CI=0.26 to 0.41,  $P = 2.19 \times 10^{-16}$ ) and interleukin-1 receptor antagonist (IVW Beta=0.23, 95% CI=0.17 to 0.30,  $P = 9.04 \times 10^{-12}$ ). Further analyses using multivariable MR provided evidence that the effect of BMI on lowering immunoglobulin G, an antibody class involved in protection from infection, is substantially mediated by raised triglycerides levels (IVW Beta=-0.18, 95% CI=-0.25 to -0.12,  $P = 2.32 \times 10^{-08}$ , proportion mediated=44.1%). The strongest evidence that any of the circulating proteins highlighted by our initial analysis influence severe SARS-CoV-2 was identified for soluble glycoprotein 130 (odds ratio=1.81, 95% CI=1.25 to 2.62,  $P = 0.002$ ), a signal transducer for interleukin-6 type cytokines which are involved in inflammatory response. However, based on current case samples for severe SARS-CoV-2 we were unable to replicate findings in independent samples.

**INTERPRETATION:** Our findings highlight several key proteins which are influenced by established exposures for disease. Future research to determine whether these circulating proteins mediate environmental effects onto risk of SARS-CoV-2 infection or covid-19 progression are warranted to help elucidate therapeutic strategies for severe covid-19 disease.

Sullivan, K. D., et al. (2021). "The COVIDome Explorer researcher portal." *Cell Rep* **36**(7): 109527. <https://doi.org/10.1016/j.celrep.2021.109527>

COVID-19 pathology involves dysregulation of diverse molecular, cellular, and physiological processes. To expedite integrated and collaborative COVID-19 research, we completed multi-omics analysis of hospitalized COVID-19 patients, including matched analysis of the whole-blood transcriptome, plasma proteomics with two complementary platforms, cytokine profiling, plasma and red blood cell metabolomics, deep immune cell phenotyping by mass cytometry, and clinical data annotation. We refer to this multidimensional dataset as the COVIDome. We then created the COVIDome Explorer, an online researcher portal where the data can be analyzed and visualized in real time. We illustrate herein the use of the COVIDome dataset through a multi-omics analysis of biosignatures associated with C-reactive protein (CRP), an established marker of poor prognosis in COVID-19, revealing associations between CRP levels and damage-associated molecular patterns, depletion of protective serpins, and mitochondrial metabolism dysregulation. We expect that the COVIDome Explorer will rapidly accelerate data sharing, hypothesis testing, and discoveries worldwide.

Zhou, S., et al. (2021). "A Neanderthal OAS1 isoform protects individuals of European ancestry against COVID-19 susceptibility and severity." *Nat Med* **27**(4): 659-667. <https://doi.org/10.1038/s41591-021-01281-1>

To identify circulating proteins influencing Coronavirus Disease 2019 (COVID-19) susceptibility and severity, we undertook a two-sample Mendelian randomization (MR) study, rapidly scanning hundreds of circulating proteins while reducing bias due to reverse causation and confounding. In up to 14,134 cases and 1.2 million controls, we found that an s.d. increase in OAS1 levels was associated with reduced COVID-19 death or ventilation (odds ratio (OR) = 0.54,  $P = 7 \times 10^{-8}$ ), hospitalization (OR = 0.61,  $P = 8 \times 10^{-8}$ ) and susceptibility (OR = 0.78,  $P = 8 \times 10^{-6}$ ). Measuring OAS1 levels in 504 individuals, we found that higher plasma OAS1 levels in a non-infectious state were associated with reduced COVID-19 susceptibility and severity. Further analyses suggested that a Neanderthal isoform of OAS1 in individuals of European ancestry affords this protection. Thus, evidence from MR and a case-control study support a protective role for OAS1 in COVID-19 adverse outcomes. Available pharmacological agents that increase OAS1 levels could be prioritized for drug development.



## **Preprints**

Roh J, et al. Plasma Proteomics of COVID-19 Associated Cardiovascular Complications: Implications for Pathophysiology and Therapeutics.

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