Resource Summary Report

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COVID-19 Host Genetics Initiative

RRID:SCR_022272
Type: Tool

Proper Citation

COVID-19 Host Genetics Initiative (RRID:SCR_022272)

Resource Information

URL: https://www.covid19hg.org/

Proper Citation: COVID-19 Host Genetics Initiative (RRID:SCR_022272)

Description: Platform for global network of researchers to investigate role of human genetics in SARS-CoV-2 infection and COVID-19 severity. Provides results of three genome-wide association meta analyses that consist of patients with COVID-19 from studies across countries.

Resource Type: data or information resource, portal, topical portal

Defining Citation: PMID:34237774

Keywords: Investigate role of human genetics in SARS-CoV-2 infection, COVID-19 severity, three genome-wide association meta analyses, patients with COVID-19

Related Condition: Covid-19, COVID-19

Availability: Free, Freely available

Resource Name: COVID-19 Host Genetics Initiative

Resource ID: SCR_022272

Alternate URLs: https://github.com/covid19-hg/

Record Creation Time: 20220511T050132+0000

Record Last Update: 20260905T133012+0000

Ratings and Alerts

No rating or validation information has been found for COVID-19 Host Genetics Initiative.

No alerts have been found for COVID-19 Host Genetics Initiative.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 88 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET .

Cappadona C, et al. (2026) Multi-omics identifies oxidative stress, prothrombotic pathways, and lactoperoxidase variants as key factors in COVID-19 severity. EBioMedicine, 123, 106111.

Lin S, et al. (2026) Causal and shared genetic insights into severe COVID-19 and idiopathic pulmonary fibrosis. iScience, 29(5), 115494.

Tang R, et al. (2026) Mendelian randomization study: investigating the causal impact of Covid-19 on adverse pregnancy outcomes. Virology journal, 23(1).

Testori A, et al. (2026) CMTM8 variants influence BNT162b2 COVID-19 vaccination response by regulating granulocytic/polymorphonuclear myeloid-derived suppressor cell activity. Frontiers in immunology, 17, 1717058.

D'Aversa E, et al. (2026) Integrating Host Genetics and Clinical Setting in Machine Learning Models: Predicting COVID-19 Prognosis for Healthcare Decision-Making (The FeMiNa Study). Diagnostics (Basel, Switzerland), 16(4).

Ran W, et al. (2026) Interferon-stimulated gene GALNT2 restricts respiratory virus infections. Nature microbiology, 11(1), 256.

Ali MS, et al. (2026) A Post-GWAS Analysis of the Shared Genetic Architecture Between COVID-19 and Coronary Artery Disease. International journal of molecular sciences, 27(9).

Wu Z, et al. (2025) Elucidating SARS-CoV-2 neurotropism: a comprehensive Mendelian randomization study on cerebrospinal fluid biomarkers and their relevance to COVID-19 neurological manifestations. Virology journal, 22(1), 123.

Cho B, et al. (2025) PTL-PRS: an R package for transfer learning of polygenic risk scores with pseudovalidation. Bioinformatics (Oxford, England), 41(10).

Song Y, et al. (2025) Does COVID-19 impact the QT interval prolongation? Answers from genetic causal inference. Bioscience reports, 45(1), 1.

Kousathanas A, et al. (2025) Common and rare variant analyses reveal genetic factors underlying idiopathic pulmonary fibrosis and its shared aetiology with severe COVID-19. EBioMedicine, 122, 106048.

Ibargüen-González L, et al. (2025) Host factor PLAC8 is required for pancreas infection by SARS-CoV-2. Communications medicine, 5(1), 34.

Xu X, et al. (2025) Exploring the complex relationship between systemic lupus erythematosus and coronavirus disease 2019: genetic insights and potential protective mechanisms. Journal of global health, 15, 04191.

Xiang R, et al. (2025) Local Genetic Correlations and Pleiotropy Reveal Shared Genetic Architecture Between COVID-19 Phenotypes and Prostate Cancer in European Populations. Journal of Cancer, 16(14), 4245.

Wang H, et al. (2025) Identification of COVID-19 susceptibility genes by Mendelian randomization. Science progress, 108(4), 368504251385959.

Wang C, et al. (2025) Cell type-specific eQTL analysis of COVID-19 based on single-cell transcriptomic data. NAR genomics and bioinformatics, 7(4), lqaf130.

Gao Z, et al. (2024) EpiGePT: a pretrained transformer-based language model for context-specific human epigenomics. Genome biology, 25(1), 310.

Chen J, et al. (2024) Shared Genetic Architecture Between COVID-19 Severity and Alzheimer's Disease Across European and African Ancestries. Research square.

Strausz S, et al. (2024) Genetic Analysis of Obstructive Sleep Apnea and Its Relationship with Severe COVID-19. Annals of the American Thoracic Society, 21(6), 961.

Zhang S, et al. (2024) Exploring COVID-19 causal genes through disease-specific Cis-eQTLs. Virus research, 342, 199341.