

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: topical portal, data or information resource, 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: 20260804T043750+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 48 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

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

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

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.

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

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.

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

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

Martelloni G, et al. (2024) Host genetics and COVID-19 severity: increasing the accuracy of latest severity scores by Boolean quantum features. *Frontiers in genetics*, 15, 1362469.

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.

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

Fam BSO, et al. (2024) Human genetic determinants of COVID-19 in Brazil: challenges and future plans. *Genetics and molecular biology*, 46(3 Suppl 1), e20230128.

Wang Y, et al. (2024) The risk of common hypoglycemic and antihypertensive medications and COVID-19: A 2-sample Mendelian randomization study. *Medicine*, 103(6), e36423.

Ma Y, et al. (2024) Integration of human organoids single-cell transcriptomic profiles and human genetics repurposes critical cell type-specific drug targets for severe COVID-19. *Cell proliferation*, 57(3), e13558.

Jose S, et al. (2024) The ethics of using COVID-19 host genomic information for clinical and public health decision-making: A survey of US health professionals. *HGG advances*, 5(1), 100255.

Song L, et al. (2024) Investigating causal associations between pneumonia and lung cancer using a bidirectional mendelian randomization framework. *BMC cancer*, 24(1), 721.

Chen Y, et al. (2024) Investigating the shared genetic architecture between COVID-19 and obesity: a large-scale genome wide cross-trait analysis. *Frontiers in endocrinology*, 15, 1325939.

Li G, et al. (2024) Genetic susceptibility association between viral infection and colorectal cancer risk: a two-sample Mendelian randomization analysis. *Infectious agents and cancer*, 19(1), 37.

Pietzner M, et al. (2024) Complex patterns of multimorbidity associated with severe COVID-19 and long COVID. *Communications medicine*, 4(1), 94.

Rohn H, et al. (2024) Influence of HLA-G 3' Untranslated Region Haplotypes and SNP +3422 Gene Variants as Host Genetic Factors on the Outcomes of SARS-CoV-2 Infection During Acute and Post-Acute Phases in a German Cohort. *HLA*, 104(6), e15799.