Resource Summary Report

Generated by RRID on Aug 10, 2026

ImmunoBase

RRID:SCR_014642
Type: Tool

Proper Citation

ImmunoBase (RRID:SCR_014642)

Resource Information

URL: https://www.immunobase.org/about/

Proper Citation: ImmunoBase (RRID:SCR_014642)

Description: Web based resource focused on the genetics and genomics of immunologically related human diseases. Their mission is to provide a curated and integrated set of datasets and tools to support and promote research in this area. The current focus of the site is to integrate and curate summary case/control association statistics from the consortium of 12 diseases originally targeted by the ImmunoChip consortium.

Resource Type: database, data or information resource

Keywords: immunology, database, web based, genetics, genomics, immunologically related human diseases, gwas, FASEB list

Funding: Juvenile Diabetes Research Foundation Wellcome Trust Diabetes and Inflammation Laboratory

Resource Name: ImmunoBase

Resource ID: SCR_014642

Record Creation Time: 20220129T080321+0000

Record Last Update: 20260808T190436+0000

Ratings and Alerts

No rating or validation information has been found for ImmunoBase.

No alerts have been found for ImmunoBase.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 45 mentions in open access literature.

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

Greenwood E, et al. (2025) Haplotype rather than single causal variants effects contribute to regulatory gene expression associations in human myeloid cells. bioRxiv : the preprint server for biology.

Kim EE, et al. (2024) PASTRY: achieving balanced power for detecting risk and protective minor alleles in meta-analysis of association studies with overlapping subjects. BMC bioinformatics, 25(1), 24.

Iakovliev A, et al. (2023) Genome-wide aggregated trans-effects on risk of type 1 diabetes: A test of the "omnigenic" sparse effector hypothesis of complex trait genetics. American journal of human genetics, 110(6), 913.

Newman JRB, et al. (2023) Shifts in isoform usage underlie transcriptional differences in regulatory T cells in type 1 diabetes. Communications biology, 6(1), 988.

Alvelos MI, et al. (2021) The RNA-binding profile of the splicing factor SRSF6 in immortalized human pancreatic ?-cells. Life science alliance, 4(3).

Võsa U, et al. (2021) Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. Nature genetics, 53(9), 1300.

Thaventhiran JED, et al. (2020) Whole-genome sequencing of a sporadic primary immunodeficiency cohort. Nature, 583(7814), 90.

Chen XF, et al. (2020) Multiomics dissection of molecular regulatory mechanisms underlying autoimmune-associated noncoding SNPs. JCI insight, 5(17).

González-Serna D, et al. (2020) A cross-disease meta-GWAS identifies four new susceptibility loci shared between systemic sclerosis and Crohn's disease. Scientific reports, 10(1), 1862.

Wheeler HE, et al. (2019) Imputed gene associations identify replicable trans-acting genes enriched in transcription pathways and complex traits. Genetic epidemiology, 43(6), 596.

Hoefsmit EP, et al. (2019) Susceptible loci associated with autoimmune disease as potential biomarkers for checkpoint inhibitor-induced immune-related adverse events. ESMO open, 4(4), e000472.

Pouget JG, et al. (2019) Cross-disorder analysis of schizophrenia and 19 immune-mediated diseases identifies shared genetic risk. Human molecular genetics, 28(20), 3498.

Nath AP, et al. (2019) Multivariate Genome-wide Association Analysis of a Cytokine Network Reveals Variants with Widespread Immune, Haematological, and Cardiometabolic Pleiotropy. American journal of human genetics, 105(6), 1076.

Gao P, et al. (2019) Risk variants disrupting enhancers of TH1 and TREG cells in type 1 diabetes. Proceedings of the National Academy of Sciences of the United States of America, 116(15), 7581.

de Almeida RC, et al. (2018) Integrative Analysis Identifies Genetic Variants Associated With Autoimmune Diseases Affecting Putative MicroRNA Binding Sites. Frontiers in genetics, 9, 139.

Márquez A, et al. (2018) Meta-analysis of Immunochip data of four autoimmune diseases reveals novel single-disease and cross-phenotype associations. Genome medicine, 10(1), 97.

Bonifacio E, et al. (2018) Genetic scores to stratify risk of developing multiple islet autoantibodies and type 1 diabetes: A prospective study in children. PLoS medicine, 15(4), e1002548.

Zhernakova DV, et al. (2018) Individual variations in cardiovascular-disease-related protein levels are driven by genetics and gut microbiome. Nature genetics, 50(11), 1524.

Wohlers I, et al. (2018) Evidence for a potential role of miR-1908-5p and miR-3614-5p in autoimmune disease risk using integrative bioinformatics. Journal of autoimmunity, 94, 83.

Odhams CA, et al. (2017) Profiling RNA-Seq at multiple resolutions markedly increases the number of causal eQTLs in autoimmune disease. PLoS genetics, 13(10), e1007071.