Resource Summary Report

Generated by NIF on Apr 22, 2025

LOCUSZOOM

RRID:SCR_009257
Type: Tool

Proper Citation

LOCUSZOOM (RRID:SCR_009257)

Resource Information

URL: http://genome.sph.umich.edu/wiki/LocusZoom

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Description: Software application designed to facilitate viewing of local association results together with useful information about a locus, such as the location and orientation of the genes it includes, linkage disequilibrium coefficients and local estimates of recombination rates. It was developed by popular demand, as a result of many questions we have had about How did you make the figures in your talk? or How did you make the figures for your GWAS paper? (entry from Genetic Analysis Software)

Abbreviations: LOCUSZOOM

Resource Type: software resource, software application

Keywords: gene, genetic, genomic

Funding:

Resource Name: LOCUSZOOM

Resource ID: SCR_009257

Alternate IDs: nlx_154436

Record Creation Time: 20220129T080251+0000

Record Last Update: 20250421T053724+0000

Ratings and Alerts

No rating or validation information has been found for LOCUSZOOM.

No alerts have been found for LOCUSZOOM.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 643 mentions in open access literature.

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

Tedja MS, et al. (2025) A genome-wide scan of non-coding RNAs and enhancers for refractive error and myopia. Human genetics, 144(1), 67.

Huang Y, et al. (2025) Genetic factors shaping the plasma lipidome and the relations to cardiometabolic risk in children and adolescents. EBioMedicine, 112, 105537.

Sun Y, et al. (2025) Genome-Wide Association Study Reveals a Causal Relationship Between Allergic Rhinitis and Hazelnut Allergy. Allergy, 80(1), 309.

Wills C, et al. (2025) Relationship between inherited genetic variation and survival from colorectal cancer stratified by tumour location. Scientific reports, 15(1), 2423.

Pan Q, et al. (2025) A genome-wide association study identifies genetic variants associated with hip pain in the UK Biobank cohort (N?=?221,127). Scientific reports, 15(1), 2812.

Halligan NLN, et al. (2025) Variants in the ?-globin locus are associated with pneumonia in African American children. HGG advances, 6(1), 100374.

Zhou X, et al. (2025) Transethnic analysis identifies SORL1 variants and haplotypes protective against Alzheimer's disease. Alzheimer's & dementia : the journal of the Alzheimer's Association, 21(1), e14214.

Fries LE, et al. (2025) Single-Cell RNA-Seq Reveals Adventitial Fibroblast Alterations during Mouse Atherosclerosis. bioRxiv : the preprint server for biology.

Hwang YS, et al. (2025) Identification of Novel Genetic Loci Affecting Age at Onset of Parkinson's Disease: A Genome-wide Association Study. Movement disorders : official journal of the Movement Disorder Society, 40(1), 77.

Pan J, et al. (2025) Gastroesophageal reflux disease increases predisposition to severe COVID-19: Insights from integrated Mendelian randomization and genetic analysis. Annals of human genetics, 89(1), 54.

Valo E, et al. (2025) Genome-wide characterization of 54 urinary metabolites reveals molecular impact of kidney function. Nature communications, 16(1), 325.

Park K, et al. (2024) Genome-wide association study implicates the role of TBXAS1 in the pathogenesis of depressive symptoms among the Korean population. Translational psychiatry, 14(1), 80.

Chen L, et al. (2024) Genetic Susceptibility to Astrovirus Diarrhea in Bangladeshi Infants. Open forum infectious diseases, 11(3), ofae045.

Mackenzie SC, et al. (2024) Genome-wide association reveals a locus in neuregulin 3 associated with gabapentin efficacy in women with chronic pelvic pain. iScience, 27(8), 110370.

Hawkes G, et al. (2024) Whole-genome sequencing in 333,100 individuals reveals rare non-coding single variant and aggregate associations with height. Nature communications, 15(1), 8549.

Yuan M, et al. (2024) Mapping genes for human face shape: Exploration of univariate phenotyping strategies. PLoS computational biology, 20(12), e1012617.

Nishiyama NC, et al. (2024) eQTL in diseased colon tissue identifies novel target genes associated with IBD. bioRxiv : the preprint server for biology.

Liu S, et al. (2024) Genome-wide association study of maternal plasma metabolites during pregnancy. Cell genomics, 4(10), 100657.

Furuta Y, et al. (2024) Common protein-altering variant in GFAP is associated with white matter lesions in the older Japanese population. NPJ genomic medicine, 9(1), 59.

Lee Y, et al. (2024) Genome-wide association study of metabolic dysfunction-associated fatty liver disease in a Korean population. Scientific reports, 14(1), 9753.