

# Resource Summary Report

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## Gene Relationships Across Implicated Loci

RRID:SCR\_008537

Type: Tool

### Proper Citation

Gene Relationships Across Implicated Loci (RRID:SCR\_008537)

### Resource Information

**URL:** <http://www.broad.mit.edu/mpg/grail/>

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**Description:** A tool to examine relationships between genes in different disease associated loci. Given several genomic regions or SNPs associated with a particular phenotype or disease, GRAIL looks for similarities in the published scientific text among the associated genes. As input, users can upload either (1) SNPs that have emerged from a genome-wide association study or (2) genomic regions that have emerged from a linkage scan or are associated common or rare copy number variants. SNPs should be listed according to their rs#'s and must be listed in HapMap. Genomic Regions are specified by a user-defined identifier, the chromosome that it is located on, and the start and end base-pair positions for the region. Grail can take two sets of inputs - Query regions and Seed regions. Seed regions are definitely associated SNPs or genomic regions, and Query regions are those regions that the user is attempting to evaluate against them. In many applications the two sets are identical. Based on textual relationships between genes, GRAIL assigns a p-value to each region suggesting its degree of functional connectivity, and picks the best candidate gene. GRAIL is developed by Soumya Raychaudhuri in the labs of David Altshuler and Mark Daly at the Center for Human Genetic Research of Massachusetts General Hospital and Harvard Medical School, and the Broad Institute. GRAIL is described in manuscript, currently in preparation.

**Synonyms:** GRAIL

**Resource Type:** analysis service resource, resource, data analysis service, production service resource, service resource

**Defining Citation:** [PMID:19557189](https://pubmed.ncbi.nlm.nih.gov/19557189/)

**Keywords:** software, text mining, genotype, phenotype, snp

**Funding:** NIAMS 1K08AR055688-01A1;  
NIAMS AR007530;  
NHGRI U01HG004171;  
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**Resource Name:** Gene Relationships Across Implicated Loci

**Resource ID:** SCR\_008537

**Alternate IDs:** nif-0000-30627

**Record Creation Time:** 20220129T080248+0000

**Record Last Update:** 20250407T215718+0000

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## Ratings and Alerts

No rating or validation information has been found for Gene Relationships Across Implicated Loci .

No alerts have been found for Gene Relationships Across Implicated Loci .

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Choi J, et al. (2015) Genomic landscape of cutaneous T cell lymphoma. Nature genetics, 47(9), 1011.

Nalls MA, et al. (2011) Multiple loci are associated with white blood cell phenotypes. PLoS genetics, 7(6), e1002113.

Casselbrant ML, et al. (2009) Otitis media: a genome-wide linkage scan with evidence of susceptibility loci within the 17q12 and 10q22.3 regions. BMC medical genetics, 10, 85.

Raychaudhuri S, et al. (2009) Identifying relationships among genomic disease regions: predicting genes at pathogenic SNP associations and rare deletions. PLoS genetics, 5(6), e1000534.