Resource Summary Report

Generated by RRID on Aug 2, 2026

GWASrap

RRID:SCR_013144
Type: Tool

Proper Citation

GWASrap (RRID:SCR_013144)

Resource Information

URL: http://jjwanglab.org/gwasrap

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Description: GWASrap is a comprehensive web-based bioinformatics tool to systematically support variant representation, annotation and prioritization for data generated from genome-wide association studies (GWAS) and Next Generation Sequencing (NGS). Our web-based framework utilizes state-of-the-art web technologies to maximize user interaction and visualization of the results. For a given SNP dataset with its P-values, GWASrap will first provide a Circos-style plot to visualize any genetic variants at either the genome or chromosome level. The tool then combines different genomic features (SNP/CNV density, disease susceptibility loci, etc.) with comprehensive annotations that give the researcher an intuitive view of the functional significance of the different genomic regions. The detailed statistics of the underlying study are also displayed on the web page, including variant distribution in different functional categories, classic Manhattan plot and QQ plot. Users can perform interactive operations in the Manhattan panel, such as zooming in and out to search regions or markers of interest. The system can also display a comprehensive range of relevant information from variant genetic attributes to nearby genomic elements, such as enhancers or non-coding RNAs. Furthermore, researchers can obtain extensive functional predictions for various features including transcription factor-binding sites, miRNA and miRNA target sites, and their predicted changes caused by the genetic variants. Our system can re-prioritize genetic variants by combining the original statistical value and variant prioritization score based on a simple additive effect equation. Researchers can also re-evaluate the significance of a trait/disease-associated SNP (TAS) using the dynamic linkage disequilibrium (LD) panel or the tree-like network panel. The GWASrap supports input variants in different formats, not only common variants with a dbSNP rs ID but also rare variants from NGS data, which are represented by chromosome and locations. GWASrap provides a range of web services for data retrieving about the annotation information and effect prediction of each variant in dbSNP using the SOAP interface. The WSDL for each service is available in the API tab. Each service returns JSON string including all related information with key/value. GWASrap provides running results about some current published GWAS as well as a

category view for each hot disease / trait. The dataset is brought from published database GWAS or curated from literature.

Abbreviations: GWASrap

Synonyms: GWASrap - SNPs Representing Annotating and Prioritizing Tool for Genome Wide Association Study

Resource Type: data analysis service, data or information resource, data access protocol, service resource, data set, production service resource, software resource, analysis service resource, web service

Defining Citation: PMID:22801476

Keywords: genome wide association study, annotation, next generation sequencing, genetic variant, prioritize, visualize, genome, chromosome, functional prediction, transcription factor-binding site, mirna, mirna target site, prediction, target site, transcription factor, binding site, statistics, trait/disease-associated snp, single nucleotide polymorphism, trait, disease, representation, linkage disequilibrium

Related Condition: Bipolar Disorder, Alzheimer's disease, Depression, Parkinson Disease, Diabetes Mellitus, Amyotrophic Lateral Sclerosis, Rheumatoid Arthritis, HIV-1 Disease, Human immunodeficiency virus, Hematopoietic System Disease, Prostate Cancer, Coronary Artery Disease, Schizophrenia, Arteriopathy, Multiple Sclerosis, Crohn""s Disease, Hypertension, Breast Cancer

Resource Name: GWASrap

Resource ID: SCR_013144

Alternate IDs: nlx_151497

Record Creation Time: 20220129T080314+0000

Record Last Update: 20260801T190735+0000

Ratings and Alerts

No rating or validation information has been found for GWASrap.

No alerts have been found for GWASrap.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Montgomery GW, et al. (2014) The future for genetic studies in reproduction. Molecular human reproduction, 20(1), 1.

Vinayagamoorthy N, et al. (2014) New variants including ARG1 polymorphisms associated with C-reactive protein levels identified by genome-wide association and pathway analysis. PloS one, 9(4), e95866.