

Resource Summary Report

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PANOGA

RRID:SCR_006242

Type: Tool

Proper Citation

PANOGA (RRID:SCR_006242)

Resource Information

URL: <http://panoga.sabanciuniv.edu/>

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Description: A web server to devise functionally important pathways through the identification of single nucleotide polymorphism (SNP)-targeted genes within these pathways. The strength of the methodology stems from its multidimensional perspective, where evidence from the following five resources is combined: (i) genetic association information obtained through GWAS, (ii) SNP functional information, (iii) protein-protein interaction network, (iv) linkage disequilibrium and (v) biochemical pathways.

Abbreviations: PANOGA

Synonyms: Pathway and Network-Oriented GWAS Analysis, Pathway and Network Oriented GWAS (Genome-Wide Association Study) Analysis, Pathway and Network Oriented GWAS Analysis

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

Defining Citation: [PMID:24413675](#)

Keywords: single nucleotide polymorphism, genome-wide association study, pathway, function, gene, genetic association, protein-protein interaction network, linkage disequilibrium, protein-protein interaction

Availability: Free, Public, Free for academic use, (source code upon request)

Resource Name: PANOGA

Resource ID: SCR_006242

Alternate IDs: OMICS_02238

Record Creation Time: 20220129T080235+0000

Record Last Update: 20260801T190931+0000

Ratings and Alerts

No rating or validation information has been found for PANOGA.

No alerts have been found for PANOGA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Everest E, et al. (2021) Investigation of multiple sclerosis-related pathways through the integration of genomic and proteomic data. PeerJ, 9, e11922.

Ozdemir O, et al. (2019) Identification of epilepsy related pathways using genome-wide DNA methylation measures: A trio-based approach. PloS one, 14(2), e0211917.

Demiray SB, et al. (2019) Differential gene expression analysis of human cumulus cells. Clinical and experimental reproductive medicine, 46(2), 76.

Kandemir B, et al. (2017) In silico analyses and global transcriptional profiling reveal novel putative targets for Pea3 transcription factor related to its function in neurons. PloS one, 12(2), e0170585.

Ozer B, et al. (2015) A novel analysis strategy for integrating methylation and expression data reveals core pathways for thyroid cancer aetiology. BMC genomics, 16 Suppl 12(Suppl 12), S7.

Ozden S, et al. (2015) Assessment of global and gene-specific DNA methylation in rat liver and kidney in response to non-genotoxic carcinogen exposure. Toxicology and applied pharmacology, 289(2), 203.

Bakir-Gungor B, et al. (2013) Identifying SNP targeted pathways in partial epilepsies with genome-wide association study data. Epilepsy research, 105(1-2), 92.