

# Resource Summary Report

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## PANOGA

RRID:SCR\_006242

Type: Tool

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### Proper Citation

PANOGA (RRID:SCR\_006242)

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### Resource Information

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

**Proper Citation:** PANOGA (RRID:SCR\_006242)

**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:** analysis service resource, service resource, data analysis service, production 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:** 20260728T043230+0000

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## Ratings and Alerts

No rating or validation information has been found for PANOGA.

No alerts have been found for PANOGA.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 7 mentions in open access literature.

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

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.