

Resource Summary Report

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ENIGMA

RRID:SCR_013400

Type: Tool

Proper Citation

ENIGMA (RRID:SCR_013400)

Resource Information

URL: <http://bioinformatics.psb.ugent.be/ENIGMA/>

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Description: A software tool to extract gene expression modules from perturbational microarray data, based on the use of combinatorial statistics and graph-based clustering. The modules are further characterized by incorporating other data types, e.g. GO annotation, protein interactions and transcription factor binding information, and by suggesting regulators that might have an effect on the expression of (some of) the genes in the module. Version : ENIGMA 1.1 used GO annotation version : Aug 29th 2007

Resource Type: data analysis software, data processing software, software application, software resource

Defining Citation: [PMID:18402676](#)

Keywords: genome, gene, genetic software, bio.tools

Resource Name: ENIGMA

Resource ID: SCR_013400

Alternate IDs: biotools:enigma, nlx_144365

Alternate URLs: <https://bio.tools/enigma>

Record Creation Time: 20220129T080315+0000

Record Last Update: 20260821T194008+0000

Ratings and Alerts

No rating or validation information has been found for ENIGMA.

No alerts have been found for ENIGMA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 133 mentions in open access literature.

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

Liu S, et al. (2026) Structural covariance network topology in individuals at clinical high risk for psychosis: the ENIGMA-CHR Study. *Molecular psychiatry*, 31(3), 1707.

Lee H, et al. (2026) Visualizing cortical laminar architecture in the living human brain using next-generation ultra-high-gradient diffusion MRI. *Communications biology*, 9(1).

Calomino C, et al. (2026) Subregional thalamic atrophy in Progressive Supranuclear Palsy: A machine learning study. *NeuroImage. Clinical*, 50, 103992.

Palma-Espinosa J, et al. (2025) The balance between integration and segregation drives network dynamics maximizing multistability and metastability. *Scientific reports*, 15(1), 18811.

Thalhammer M, et al. (2025) Heterogeneous, temporally consistent, and plastic brain development after preterm birth. *Nature communications*, 16(1), 8269.

Kochunov P, et al. (2025) Alzheimer's Disease-Like Brain Pattern Biomarker: Capturing Risks and Predicting Disease Onset. *Research square*.

Rößler H, et al. (2025) Transdiagnostic neuroanatomical risk in schizophrenia: integrating regional vulnerability indices with anthropometric and fitness-based markers of cardiometabolic health. *NeuroImage. Clinical*, 48, 103897.

Han LKM, et al. (2025) Lifestyle, Early-life, and Genetic Health Risk Factors Underlying the Brain Age Gap: A Mega-Analysis Across 3,934 Individuals from the ENIGMA MDD Consortium. *bioRxiv : the preprint server for biology*.

Robertson JW, et al. (2025) The Pattern and Stages of Atrophy in Spinocerebellar Ataxia Type 2: Volumetrics from ENIGMA-Ataxia. *Movement disorders : official journal of the Movement Disorder Society*, 40(4), 651.

Du Z, et al. (2025) Connectome-constrained ligand-receptor interaction analysis for understanding brain network communication. *Nature communications*, 16(1), 8179.

Resende GAP, et al. (2024) Comprehensive Two-Dimensional Gas Chromatography-Mass Spectrometry as a Tool for the Untargeted Study of Hop and Their Metabolites. *Metabolites*, 14(4).

Wayment-Steele HK, et al. (2024) The conformational landscape of fold-switcher KaiB is tuned to the circadian rhythm timescale. *Proceedings of the National Academy of Sciences of the United States of America*, 121(45), e2412293121.

Wayment-Steele HK, et al. (2024) The conformational landscape of fold-switcher KaiB is tuned to the circadian rhythm timescale. *bioRxiv : the preprint server for biology*.

Yang K, et al. (2023) Cortical thickness of the inferior parietal lobule as a potential predictor of relapse in men with alcohol dependence. *Research square*.

Sebenius I, et al. (2023) Robust estimation of cortical similarity networks from brain MRI. *Nature neuroscience*, 26(8), 1461.

Kumar K, et al. (2023) Subcortical brain alterations in carriers of genomic copy number variants. *medRxiv : the preprint server for health sciences*.

García-Marín LM, et al. (2023) Shared molecular genetic factors influence subcortical brain morphometry and Parkinson's disease risk. *NPJ Parkinson's disease*, 9(1), 73.

Misawa N, et al. (2023) Fine Particle Adsorption Capacity of Volcanic Soil from Southern Kyushu, Japan. *Nanomaterials (Basel, Switzerland)*, 13(3).

Ou YN, et al. (2023) The genetic architecture of fornix white matter microstructure and their involvement in neuropsychiatric disorders. *Translational psychiatry*, 13(1), 180.

Wingrove J, et al. (2023) Aberrant olfactory network functional connectivity in people with olfactory dysfunction following COVID-19 infection: an exploratory, observational study. *EClinicalMedicine*, 58, 101883.