

Resource Summary Report

Generated by RRID on Sep 10, 2026

Extending Guilt by Association by Degree

RRID:SCR_018427

Type: Tool

Proper Citation

Extending Guilt by Association by Degree (RRID:SCR_018427)

Resource Information

URL: <https://bioconductor.org/packages/EGAD/>

Proper Citation: Extending Guilt by Association by Degree (RRID:SCR_018427)

Description: Software package implements series of highly efficient tools to calculate functional properties of networks based on guilt by association methods. Ultra fast functional analysis of gene networks.

Abbreviations: EGAD

Synonyms: EGAD Bioconductor, Extending guilt by association by degree

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

Keywords: Extending guilt, association by degree, functional properties calculation, guilt network, association method, functional analysis, gene network

Availability: Free, Available for download, Freely available

Resource Name: Extending Guilt by Association by Degree

Resource ID: SCR_018427

License: GPL-2

Record Creation Time: 20220129T080340+0000

Record Last Update: 20260905T132836+0000

Ratings and Alerts

No rating or validation information has been found for Extending Guilt by Association by Degree.

No alerts have been found for Extending Guilt by Association by Degree.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Kouchi Z, et al. (2025) C1-linker region of PARG1 RhoGAP promotes the catalytic recognition fold of RhoA substrate. PloS one, 20(7), e0326924.

Erdman L, et al. (2024) The Hydronephrosis Severity Index guides paediatric antenatal hydronephrosis management based on artificial intelligence applied to ultrasound images alone. Scientific reports, 14(1), 22748.

Hu G, et al. (2021) Homoeologous gene expression and co-expression network analyses and evolutionary inference in allopolyploids. Briefings in bioinformatics, 22(2), 1819.

Liesecke F, et al. (2018) Ranking genome-wide correlation measurements improves microarray and RNA-seq based global and targeted co-expression networks. Scientific reports, 8(1), 10885.

Ficklin SP, et al. (2017) Discovering Condition-Specific Gene Co-Expression Patterns Using Gaussian Mixture Models: A Cancer Case Study. Scientific reports, 7(1), 8617.

O'Meara MJ, et al. (2016) Ligand Similarity Complements Sequence, Physical Interaction, and Co-Expression for Gene Function Prediction. PloS one, 11(7), e0160098.