

Resource Summary Report

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OLIN

RRID:SCR_001304

Type: Tool

Proper Citation

OLIN (RRID:SCR_001304)

Resource Information

URL: <https://www.bioconductor.org/packages/release/bioc/html/OLIN.html>

Proper Citation: OLIN (RRID:SCR_001304)

Description: Software functions for normalization of two-color microarrays by optimised local regression and for detection of artifacts in microarray data.

Abbreviations: OLIN

Synonyms: Optimised Local Intensity-dependent Normalisation

Resource Type: software resource

Defining Citation: [PMID:15585527](#)

Keywords: r, normalization, visualization, quality control, two-channel, microarray, preprocessing, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: OLIN

Resource ID: SCR_001304

Alternate IDs: biotools:olin, OMICS_02029

Alternate URLs: <http://itb.biologie.hu-berlin.de/~futschik/software/R/OLIN/index.html>

License: GNU General Public License, v2

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260801T190137+0000

Ratings and Alerts

No rating or validation information has been found for OLIN.

No alerts have been found for OLIN.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 18 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Lisik D, et al. (2025) All-cause and cause-specific mortality in respiratory symptom clusters: a population-based multicohort study. *Respiratory research*, 26(1), 150.

Diaz LR, et al. (2024) Ribogenesis boosts controlled by HEATR1-MYC interplay promote transition into brain tumour growth. *EMBO reports*, 25(1), 168.

Meng F, et al. (2023) Hsa_circ_0021727 (circ-CD44) promotes ESCC progression by targeting miR-23b-5p to activate the TAB1/NF- κ B pathway. *Cell death & disease*, 14(1), 9.

Schyllert C, et al. (2020) Low socioeconomic status relates to asthma and wheeze, especially in women. *ERJ open research*, 6(3).

Tanash H, et al. (2020) Decreased Risk of Ischemic Heart Disease in Individuals with Severe Alpha 1-Antitrypsin Deficiency (PiZZ) in Comparison with the General Population. *International journal of chronic obstructive pulmonary disease*, 15, 1245.

Chen H, et al. (2017) Intrinsic functional connectivity variance and state-specific under-connectivity in autism. *Human brain mapping*, 38(11), 5740.

Tibiletti T, et al. (2016) Deletion of the gene family of small chlorophyll-binding proteins (ScpABCDE) offsets C/N homeostasis in *Synechocystis* PCC 6803. *Biochimica et biophysica acta*, 1857(4), 396.

Cash AC, et al. (2012) Fine scale analysis of gene expression in *Drosophila melanogaster* gonads reveals Programmed cell death 4 promotes the differentiation of female germline stem cells. *BMC developmental biology*, 12, 4.

Hardy KM, et al. (2011) FGF signalling through RAS/MAPK and PI3K pathways regulates cell movement and gene expression in the chicken primitive streak without affecting E-cadherin expression. *BMC developmental biology*, 11, 20.

Blanco E, et al. (2010) Gene expression following induction of regeneration in *Drosophila* wing imaginal discs. Expression profile of regenerating wing discs. *BMC developmental biology*, 10, 94.

Burns C, et al. (2010) Analysis of the Basidiomycete *Coprinopsis cinerea* reveals conservation of the core meiotic expression program over half a billion years of evolution. *PLoS genetics*, 6(9), e1001135.

Costello JC, et al. (2009) Gene networks in *Drosophila melanogaster*: integrating experimental data to predict gene function. *Genome biology*, 10(9), R97.

Konieczka JH, et al. (2009) BioNetBuilder2.0: bringing systems biology to chicken and other model organisms. *BMC genomics*, 10 Suppl 2(Suppl 2), S6.

Blanco E, et al. (2008) Conserved chromosomal clustering of genes governed by chromatin regulators in *Drosophila*. *Genome biology*, 9(9), R134.

Eads BD, et al. (2007) Profiling sex-biased gene expression during parthenogenetic reproduction in *Daphnia pulex*. *BMC genomics*, 8, 464.

Esteves GH, et al. (2007) New insights about host response to smallpox using microarray data. *BMC systems biology*, 1, 38.

Beltran S, et al. (2007) Functional dissection of the *ash2* and *ash1* transcriptomes provides insights into the transcriptional basis of wing phenotypes and reveals conserved protein interactions. *Genome biology*, 8(4), R67.

Dabrowski S, et al. (2003) Cloning, expression, and purification of the His6-tagged hyper-thermostable dUTPase from *Pyrococcus woesei* in *Escherichia coli*: application in PCR. *Protein expression and purification*, 31(1), 72.