

Resource Summary Report

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RankAggreg

RRID:SCR_002225

Type: Tool

Proper Citation

RankAggreg (RRID:SCR_002225)

Resource Information

URL: <http://cran.r-project.org/web/packages/RankAggreg/>

Proper Citation: RankAggreg (RRID:SCR_002225)

Description: Software package that performs aggregation of ordered lists based on the ranks using several different algorithms: Borda count, Cross-Entropy Monte Carlo algorithm, Genetic algorithm, and a brute force algorithm.

Synonyms: RankAggreg: Weighted rank aggregation

Resource Type: software resource

Defining Citation: [PMID:19228411](#)

Keywords: standalone software, mac os x, unix/linux, windows, r

Availability: GNU Lesser General Public License, v2, v2.1, v3

Resource Name: RankAggreg

Resource ID: SCR_002225

Alternate IDs: OMICS_03526

Record Creation Time: 20220129T080212+0000

Record Last Update: 20260815T182210+0000

Ratings and Alerts

No rating or validation information has been found for RankAggreg.

No alerts have been found for RankAggreg.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 48 mentions in open access literature.

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

Kianpoor S, et al. (2025) Unlocking the genetic code: a comprehensive Genome-Wide association study and gene set enrichment analysis of cell-mediated immunity in chickens. *BMC genomics*, 26(1), 337.

Kianpoor S, et al. (2025) Mixture of common and uncommon pathways and genes regulating primary and secondary immunoglobulin M responses in chickens. *Poultry science*, 104(9), 105400.

Clark MK, et al. (2025) Selection of stable reference genes for accurate reverse-transcription quantitative PCR in cotton-herbivore studies using virus-induced gene silencing. *Scientific reports*, 15(1), 24482.

Lee HJ, et al. (2024) Dataset for selection of stable reference genes for accurate quantitative gene expression analysis in silvertip tetra (*Hasemania nana*): Implications for sex differentiation and determination. *Data in brief*, 53, 110221.

Jiang G, et al. (2024) A comprehensive workflow for optimizing RNA-seq data analysis. *BMC genomics*, 25(1), 631.

Melograna F, et al. (2024) Individual-network based predictions of microbial interaction signatures for response to biological therapies in IBD patients. *Frontiers in molecular biosciences*, 11, 1490533.

Wang RM, et al. (2023) Immunomodulatory contribution of mast cells to the regenerative biomaterial microenvironment. *NPJ Regenerative medicine*, 8(1), 53.

Chatelain P, et al. (2022) Reliable reference genes and abiotic stress marker genes in *Klebsormidium nitens*. *Scientific reports*, 12(1), 18988.

Zhao Y, et al. (2021) High-throughput screening of circRNAs reveals novel mechanisms of tuberous sclerosis complex-related renal angiomyolipoma. *Human genomics*, 15(1), 43.

Heidari M, et al. (2021) Integrated Analysis of lncRNAs, mRNAs, and TFs to Identify Regulatory Networks Underlying MAP Infection in Cattle. *Frontiers in genetics*, 12, 668448.

Chen J, et al. (2021) Genome-wide identification of ubiquitin proteasome subunits as superior reference genes for transcript normalization during receptacle development in strawberry cultivars. *BMC genomics*, 22(1), 88.

Bannister HJ, et al. (2021) Improving the visual communication of environmental model projections. *Scientific reports*, 11(1), 19157.

Hasankhani A, et al. (2021) Integrated Network Analysis to Identify Key Modules and Potential Hub Genes Involved in Bovine Respiratory Disease: A Systems Biology Approach. *Frontiers in genetics*, 12, 753839.

Linardi M, et al. (2021) Identification and selection of optimal reference genes for qPCR-based gene expression analysis in *Fucus distichus* under various abiotic stresses. *PloS one*, 16(4), e0233249.

Sheybani N, et al. (2021) An integrated analysis of mRNAs, lncRNAs, and miRNAs based on weighted gene co-expression network analysis involved in bovine endometritis. *Scientific reports*, 11(1), 18050.

Grassin-Delyle S, et al. (2021) Metabolomics of exhaled breath in critically ill COVID-19 patients: A pilot study. *EBioMedicine*, 63, 103154.

Souza MR, et al. (2020) Transcriptome analysis identifies genes involved with the development of umbilical hernias in pigs. *PloS one*, 15(5), e0232542.

Herath S, et al. (2020) Selection and validation of reference genes for normalisation of gene expression in ischaemic and toxicological studies in kidney disease. *PloS one*, 15(5), e0233109.

Ehsani R, et al. (2020) Robust Distance Measures for kNN Classification of Cancer Data. *Cancer informatics*, 19, 1176935120965542.

Li L, et al. (2020) Selection and Validation of Reference Genes for Normalisation of Gene Expression in *Glehnia littoralis*. *Scientific reports*, 10(1), 7374.