

Resource Summary Report

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SAMstrt

RRID:SCR_001780

Type: Tool

Proper Citation

SAMstrt (RRID:SCR_001780)

Resource Information

URL: <https://github.com/shka/R-SAMstrt>

Proper Citation: SAMstrt (RRID:SCR_001780)

Description: Software package that provides the significance analysis of sequencing data with spike-in normalization. The statistical backgrounds and the benefits depend on SAMseq of the samr package.

Abbreviations: SAMstrt

Resource Type: software resource

Defining Citation: [PMID:23995393](#)

Keywords: differential expression, r

Funding: Karolinska Institutet ;
Strategic Research Area Grant for Diabetes

Availability: Free, Available for download, Freely available

Resource Name: SAMstrt

Resource ID: SCR_001780

Alternate IDs: OMICS_01951

License: GNU Lesser General Public License, v3

Record Creation Time: 20220129T080209+0000

Record Last Update: 20260815T182201+0000

Ratings and Alerts

No rating or validation information has been found for SAMstr.

No alerts have been found for SAMstr.

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 [ASWG](#).

Malina T, et al. (2025) Nanodiamonds Interact with Primary Human Macrophages and Dendritic Cells Evoking a Vigorous Interferon Response. *ACS nano*, 19(20), 19057.

Koel M, et al. (2022) Human endometrial cell-type-specific RNA sequencing provides new insights into the embryo-endometrium interplay. *Human reproduction open*, 2022(4), hoac043.

Bieder A, et al. (2020) Dyslexia Candidate Gene and Ciliary Gene Expression Dynamics During Human Neuronal Differentiation. *Molecular neurobiology*, 57(7), 2944.

Einarsdottir E, et al. (2019) A preliminary transcriptome analysis suggests a transitory effect of vitamin D on mitochondrial function in obese young Finnish subjects. *Endocrine connections*, 8(5), 559.

Reichhardt MP, et al. (2019) Complement in Human Pre-implantation Embryos: Attack and Defense. *Frontiers in immunology*, 10, 2234.

Stepanjuk A, et al. (2019) MUC20 expression marks the receptive phase of the human endometrium. *Reproductive biomedicine online*, 39(5), 725.

Tanaka N, et al. (2018) Single-cell RNA-seq analysis reveals the platinum resistance gene COX7B and the surrogate marker CD63. *Cancer medicine*, 7(12), 6193.

Tervaniemi MH, et al. (2018) Intracellular signalling pathways and cytoskeletal functions converge on the psoriasis candidate gene CCHCR1 expressed at P-bodies and centrosomes. *BMC genomics*, 19(1), 432.

Hakonen E, et al. (2018) MANF protects human pancreatic beta cells against stress-induced cell death. *Diabetologia*, 61(10), 2202.

Haapaniemi EM, et al. (2017) Combined immunodeficiency and hypoglycemia associated with mutations in hypoxia upregulated 1. *The Journal of allergy and clinical immunology*, 139(4), 1391.

Yip SH, et al. (2017) Linnorm: improved statistical analysis for single cell RNA-seq expression data. *Nucleic acids research*, 45(22), e179.

Tervaniemi MH, et al. (2016) NOD-like receptor signaling and inflammasome-related pathways are highlighted in psoriatic epidermis. *Scientific reports*, 6, 22745.

Jouhilahti EM, et al. (2016) The human PRD-like homeobox gene LEUTX has a central role in embryo genome activation. *Development (Cambridge, England)*, 143(19), 3459.

Körber I, et al. (2016) Gene-Expression Profiling Suggests Impaired Signaling via the Interferon Pathway in *Cstb*^{-/-} Microglia. *PloS one*, 11(6), e0158195.

Poirion OB, et al. (2016) Single-Cell Transcriptomics Bioinformatics and Computational Challenges. *Frontiers in genetics*, 7, 163.

Madisson E, et al. (2016) Characterization and target genes of nine human PRD-like homeobox domain genes expressed exclusively in early embryos. *Scientific reports*, 6, 28995.

Töhönen V, et al. (2015) Novel PRD-like homeodomain transcription factors and retrotransposon elements in early human development. *Nature communications*, 6, 8207.

Katayama S, et al. (2015) Gene expression analysis of skin grafts and cultured keratinocytes using synthetic RNA normalization reveals insights into differentiation and growth control. *BMC genomics*, 16(1), 476.