

Resource Summary Report

Generated by SPARC SAWG on Aug 9, 2026

vsn

RRID:SCR_001459

Type: Tool

Proper Citation

vsn (RRID:SCR_001459)

Resource Information

URL: <http://www.bioconductor.org/packages/release/bioc/html/vsn.html>

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Description: Software package that implements a method for normalizing microarray intensities, both between colours within array, and between arrays. The method uses a robust variant of the maximum-likelihood estimator for the stochastic model of microarray data described in the references. The model incorporates data calibration (a.k.a. normalization), a model for the dependence of the variance on the mean intensity, and a variance stabilizing data transformation. Differences between transformed intensities are analogous to normalized log-ratios. However, in contrast to the latter, their variance is independent of the mean, and they are usually more sensitive and specific in detecting differential transcription.

Abbreviations: vsn

Synonyms: vsn - Variance stabilization and calibration for microarray data

Resource Type: software resource

Keywords: microarray, preprocessing, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: vsn

Resource ID: SCR_001459

Alternate IDs: OMICS_01977, biotools:vsn

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

License: Artistic License, v3

Record Creation Time: 20220129T080207+0000

Record Last Update: 20260808T185727+0000

Ratings and Alerts

No rating or validation information has been found for vsn.

No alerts have been found for vsn.

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 [SPARC SAWG](#) .

Hellkamp M, et al. (2026) Targeting metabolic dependencies to reverse chemoradiotherapy resistance in colorectal cancer. Journal of experimental & clinical cancer research : CR, 45(1).

Bökenkamp JE, et al. (2025) Proteogenomic analysis reveals adaptive strategies for alleviating the consequences of aneuploidy in cancer. The EMBO journal, 44(6), 1829.

Schmidt L, et al. (2025) Protocol for generating protein profiles and distance-based network analysis of murine tissue slices. STAR protocols, 6(1), 103578.

Johansson E, et al. (2024) HIV-2 mediated effects on target and bystander cells induce plasma proteome remodeling. iScience, 27(4), 109344.

de Goede OM, et al. (2021) Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. Cell, 184(10), 2633.

Busch JD, et al. (2019) MitoRibo-Tag Mice Provide a Tool for In Vivo Studies of Mitoribosome Composition. Cell reports, 29(6), 1728.