

Resource Summary Report

Generated by [nidm-terms](#) on Jul 29, 2026

CQN

RRID:SCR_001786

Type: Tool

Proper Citation

CQN (RRID:SCR_001786)

Resource Information

URL: <http://www.bioconductor.org/packages/2.13/bioc/html/cqn.html>

Proper Citation: CQN (RRID:SCR_001786)

Description: A normalization tool for RNA-Seq data, implementing the conditional quantile normalization method.

Abbreviations: CQN

Synonyms: Conditional Quantile Normalization

Resource Type: software resource

Defining Citation: [PMID:22285995](#)

Keywords: rna-seq, differential expression, preprocessing, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: CQN

Resource ID: SCR_001786

Alternate IDs: OMICS_01949, biotools:cqn

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

License: Artistic License, v3

Record Creation Time: 20220129T080209+0000

Record Last Update: 20260725T190509+0000

Ratings and Alerts

No rating or validation information has been found for CQN.

No alerts have been found for CQN.

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 [nidm-terms](#) .

Hosseinzadeh L, et al. (2024) The androgen receptor interacts with GATA3 to transcriptionally regulate a luminal epithelial cell phenotype in breast cancer. *Genome biology*, 25(1), 44.

Park MH, et al. (2019) CCN1 interlinks integrin and hippo pathway to autoregulate tip cell activity. *eLife*, 8.

Grand Moursel L, et al. (2018) Brain Transcriptomic Analysis of Hereditary Cerebral Hemorrhage With Amyloidosis-Dutch Type. *Frontiers in aging neuroscience*, 10, 102.

de la Torre-Ubieta L, et al. (2018) The Dynamic Landscape of Open Chromatin during Human Cortical Neurogenesis. *Cell*, 172(1-2), 289.

Hsu SC, et al. (2017) The BET Protein BRD2 Cooperates with CTCF to Enforce Transcriptional and Architectural Boundaries. *Molecular cell*, 66(1), 102.

Amabile A, et al. (2016) Inheritable Silencing of Endogenous Genes by Hit-and-Run Targeted Epigenetic Editing. *Cell*, 167(1), 219.