

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

Basic4Cseq

RRID:SCR_002836

Type: Tool

Proper Citation

Basic4Cseq (RRID:SCR_002836)

Resource Information

URL: <http://www.bioconductor.org/packages/release/bioc/html/Basic4Cseq.html>

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Description: An R/Bioconductor package for basic filtering, analysis and subsequent near-cis visualization of 4C-seq data. Virtual fragment libraries can be created for any BSGenome package, and filter functions for both reads and fragments and basic quality controls are included. Fragment data in the vicinity of the experiment's viewpoint can be visualized as a coverage plot based on a running median approach and a multi-scale contact profile.

Synonyms: Basic4Cseq: an R/Bioconductor package for analyzing 4C-seq data

Resource Type: software resource

Defining Citation: [PMID:25078398](#)

Keywords: software package, unix/linux, mac os x, windows, r, quality control, visualization

Availability: Free, Freely available, Available for download

Resource Name: Basic4Cseq

Resource ID: SCR_002836

Alternate IDs: OMICS_05202

License: GNU Lesser General Public License, v3

Record Creation Time: 20220129T080215+0000

Record Last Update: 20260725T190535+0000

Ratings and Alerts

No rating or validation information has been found for Basic4Cseq.

No alerts have been found for Basic4Cseq.

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](#) .

Wang Z, et al. (2026) Multidimensional mapping of stimulation-responsive regulatory elements and candidate causal variants in T cell activation. Science advances, 12(1), eady2539.

Wang Z, et al. (2023) An autoimmune pleiotropic SNP modulates IRF5 alternative promoter usage through ZBTB3-mediated chromatin looping. Nature communications, 14(1), 1208.

St??pniak K, et al. (2021) Mapping chromatin accessibility and active regulatory elements reveals pathological mechanisms in human gliomas. Nature communications, 12(1), 3621.

Alexander JM, et al. (2019) Live-cell imaging reveals enhancer-dependent Sox2 transcription in the absence of enhancer proximity. eLife, 8.

Fang S, et al. (2019) Tet inactivation disrupts YY1 binding and long-range chromatin interactions during embryonic heart development. Nature communications, 10(1), 4297.

Ooi WF, et al. (2016) Epigenomic profiling of primary gastric adenocarcinoma reveals super-enhancer heterogeneity. Nature communications, 7, 12983.