Resource Summary Report

Generated by NIF on Apr 27, 2025

r3Cseq

RRID:SCR_003198
Type: Tool

Proper Citation

r3Cseq (RRID:SCR_003198)

Resource Information

URL: http://r3cseq.genereg.net/Site/index.html

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Description: An R/Bioconductor package to identify chromosomal interaction regions generated by chromosome conformation capture (3C) coupled to next-generation sequencing (NGS), a technique termed 3C-seq. It performs data analysis for a number of different experimental designs, as it can analyze 3C-seq data with or without a control experiment and it can be used to facilitate data analysis for experiments with multiple replicates. The r3Cseq package provides functions to perform data normalization, statistical analysis for cis/trans interactions and visualization in order to help scientists identify genomic regions that physically interact with the given viewpoints of interest. This tool greatly facilitates hypothesis generation and the interpretation of experimental results.

Abbreviations: r3Cseq

Resource Type: data analysis software, software application, software resource, data processing software

Defining Citation: PMID:23671339

Keywords: next-generation sequencing, genomic, interaction, chromosome conformation capture, chromosome, 3c-seq, r

Funding:

Availability: Acknowledgement requested, GNU General Public License, Version3

Resource Name: r3Cseq

Resource ID: SCR_003198

Alternate IDs: OMICS_01560

Record Creation Time: 20220129T080217+0000

Record Last Update: 20250426T055613+0000

Ratings and Alerts

No rating or validation information has been found for r3Cseq.

No alerts have been found for r3Cseq.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 21 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Zhang Y, et al. (2025) Super-silencer perturbation by EZH2 and REST inhibition leads to large loss of chromatin interactions and reduction in cancer growth. Nature structural & molecular biology, 32(1), 137.

Su D, et al. (2025) Identification of a distal enhancer of Ucp1 essential for thermogenesis and mitochondrial function in brown fat. Communications biology, 8(1), 31.

Li X, et al. (2024) An intronic enhancer of Cebpa regulates adipocyte differentiation and adipose tissue development via long-range loop formation. Cell proliferation, 57(3), e13552.

Guo R, et al. (2024) TEAD2 initiates ground-state pluripotency by mediating chromatin looping. The EMBO journal, 43(10), 1965.

Zhang J, et al. (2024) CTCF mutation at R567 causes developmental disorders via 3D genome rearrangement and abnormal neurodevelopment. Nature communications, 15(1), 5524.

Liu L, et al. (2024) A negatively charged region within carboxy-terminal domain maintains proper CTCF DNA binding. iScience, 27(12), 111452.

Teo WW, et al. (2022) Non-coding RNA LEVER sequestration of PRC2 can mediate long range gene regulation. Communications biology, 5(1), 343.

Downes DJ, et al. (2022) Capture-C: a modular and flexible approach for high-resolution chromosome conformation capture. Nature protocols, 17(2), 445.

Long K, et al. (2022) Exploring high-resolution chromatin interaction changes and functional enhancers of myogenic marker genes during myogenic differentiation. The Journal of biological chemistry, 298(8), 102149.

See YX, et al. (2022) MYC overexpression leads to increased chromatin interactions at super-enhancers and MYC binding sites. Genome research, 32(4), 629.

Tang Y, et al. (2021) Mechanism of REST/NRSF regulation of clustered protocadherin ? genes. Nucleic acids research, 49(8), 4506.

Li LY, et al. (2021) Interplay and cooperation between SREBF1 and master transcription factors regulate lipid metabolism and tumor-promoting pathways in squamous cancer. Nature communications, 12(1), 4362.

Cai Y, et al. (2021) H3K27me3-rich genomic regions can function as silencers to repress gene expression via chromatin interactions. Nature communications, 12(1), 719.

Czimmerer Z, et al. (2018) Dynamic transcriptional control of macrophage miRNA signature via inflammation responsive enhancers revealed using a combination of next generation sequencing-based approaches. Biochimica et biophysica acta. Gene regulatory mechanisms, 1861(1), 14.

Matthews BJ, et al. (2018) Computational prediction of CTCF/cohesin-based intra-TAD loops that insulate chromatin contacts and gene expression in mouse liver. eLife, 7.

Li Y, et al. (2018) Alterations of specific chromatin conformation affect ATRA-induced leukemia cell differentiation. Cell death & disease, 9(2), 200.

Peluso S, et al. (2017) Fibroblast growth factors (FGFs) prime the limb specific Shh enhancer for chromatin changes that balance histone acetylation mediated by E26 transformation-specific (ETS) factors. eLife, 6.

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

Yao L, et al. (2015) Demystifying the secret mission of enhancers: linking distal regulatory elements to target genes. Critical reviews in biochemistry and molecular biology, 50(6), 550.

Verfaillie A, et al. (2015) Decoding the regulatory landscape of melanoma reveals TEADS as regulators of the invasive cell state. Nature communications, 6, 6683.