

Resource Summary Report

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Fcirc

RRID:SCR_018090

Type: Tool

Proper Citation

Fcirc (RRID:SCR_018090)

Resource Information

URL: <https://github.com/WangHYLab/fcirc>

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Description: Software Python pipeline for linear and circular RNAs of known fusions exploration. Pipeline for exploring linear transcripts and circRNAs of known fusions based on RNA-Seq data. Known fusion genes are from multiple databases like COSMIC, ChimerDB, TicDB, FARE-CAFE and FusionCancer or user-added gene-pairs.

Abbreviations: Fcirc

Synonyms: Comprehensive Pipeline for Exploration of Fusion Linear and Circular RNAs

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

Keywords: Fusion gene, linear and circular RNA, fusion exploration, RNAseq data, linear transcript, circRNA, gene, data, pipeline, bio.tools

Funding: National Key Research and Development Program 2017YFC0908500 ;
National Natural Science Foundation of China 31571363 ;
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National Natural Science Foundation of China 81573023

Availability: Free, Available for download, Freely available

Resource Name: Fcirc

Resource ID: SCR_018090

Alternate IDs: biotools:Fcirc

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

License: MIT

Record Creation Time: 20220129T080338+0000

Record Last Update: 20260829T182604+0000

Ratings and Alerts

No rating or validation information has been found for Fcirc.

No alerts have been found for Fcirc.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

Araya P, et al. (2025) Interferon signaling modulates Down syndrome-associated Alzheimer's disease pathology in a mouse model. iScience, 28(8), 113130.

Cai Z, et al. (2020) Fcirc: A comprehensive pipeline for the exploration of fusion linear and circular RNAs. GigaScience, 9(6).