

Resource Summary Report

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CIRCexplorer2

RRID:SCR_021664

Type: Tool

Proper Citation

CIRCexplorer2 (RRID:SCR_021664)

Resource Information

URL: <https://circexplorer2.readthedocs.io/en/latest/>

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Description: Software package for comprehensive and integrative circular RNA analysis. It is the successor of CIRCexplorer with plenty of new features to facilitate circular RNA identification and characterization. Used to annotate circRNAs, de novo assemble novel circular RNA transcripts and chracterize various of alternative (back-)splicing events of circular RNAs.

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

Defining Citation: [PMID:27365365](#), [PMID:30539552](#)

Keywords: Decipher alternative back splicing, decipher circRNAs splicing pattern, circular RNA analysis, annotate circRNAs

Funding: National Natural Science Foundation of China ;
Ministry of Science and Technology of China

Availability: Free, Available for download, Freely available

Resource Name: CIRCexplorer2

Resource ID: SCR_021664

License: MIT

Record Creation Time: 20220129T080356+0000

Record Last Update: 20260804T043744+0000

Ratings and Alerts

No rating or validation information has been found for CIRCexplorer2.

No alerts have been found for CIRCexplorer2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 40 mentions in open access literature.

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

Gao Y, et al. (2025) Recent advances in investigation of circRNA/lncRNA-miRNA-mRNA networks through RNA sequencing data analysis. Briefings in functional genomics, 24.

Gu B, et al. (2025) Integrated Whole-Transcriptome Analysis to Elucidate the Core Regulatory Network of circRNA Involved in Ovarian Development and Reproductive Capacity Differences in Sheep: circRNA2058-miR-9226-5p-MET Axis. Animals : an open access journal from MDPI, 15(21).

Li M, et al. (2025) Molecular mechanism of nano-vitamin A-mediated regulation of intramuscular fat deposition involving noncoding RNAs in pigs. BMC genomics, 26(1), 716.

Abdelgawad A, et al. (2025) Defining the Parameters for Sorting of RNA Cargo Into Extracellular Vesicles. Journal of extracellular vesicles, 14(7), e70113.

Dong X, et al. (2025) Multi-omics machine learning classifier and blood transcriptomic signature of Parkinson's disease. Research square.

De?irmençay ?, et al. (2025) Integrative Analysis of Dog Serum-Derived CircRNA Expression and Disease Severity, Inflammatory and Cardiac Damage Biomarkers Related to Canine Parvoviral Enteritis. Veterinary medicine and science, 11(3), e70344.

Singh S, et al. (2025) Circular RNA Pde4dip regulates myogenesis by interacting with Zfp143 mRNA: a novel regulatory axis. RNA biology, 22(1), 1.

Wang Y, et al. (2024) Assessment of different enrichment methods revealed the optimal approach to identify bovine circRnas. RNA biology, 21(1), 1.

Singh S, et al. (2024) Global identification of mRNA-interacting circular RNAs by CLIPPR-Seq. Nucleic acids research, 52(6), e29.

Gao Y, et al. (2024) Investigation of the Circular Transcriptome in Alzheimer's Disease Brain. Journal of molecular neuroscience : MN, 74(3), 64.

Wang Q, et al. (2024) An improved transcriptome annotation reveals asymmetric expression and distinct regulation patterns in allotetraploid common carp.

Communications biology, 7(1), 1542.

Petrova M, et al. (2024) BRD2 and BRD3 genes independently evolved RNA structures to control unproductive splicing. NAR genomics and bioinformatics, 6(1), lqad113.

Hu R, et al. (2024) Transcriptional pathobiology and multi-omics predictors for Parkinson's disease. bioRxiv : the preprint server for biology.

Das A, et al. (2023) Identification of potential proteins translated from circular RNA splice variants. European journal of cell biology, 102(1), 151286.

Watts ME, et al. (2023) Circular RNAs arising from synaptic host genes during human neuronal differentiation are modulated by SFPQ RNA-binding protein. BMC biology, 21(1), 127.

Zhao S, et al. (2023) Characterization of cell-type specific circular RNAs associated with colorectal cancer metastasis. NAR cancer, 5(2), zcad021.

Sung HM, et al. (2023) Stress-induced nuclear speckle reorganization is linked to activation of immediate early gene splicing. The Journal of cell biology, 222(12).

Iparraguirre L, et al. (2023) Blood RNA-Seq profiling reveals a set of circular RNAs differentially expressed in frail individuals. Immunity & ageing : I & A, 20(1), 33.

Gao X, et al. (2022) Knockout of circRNAs by base editing back-splice sites of circularized exons. Genome biology, 23(1), 16.

Özdemir S, et al. (2022) Genome-wide profiling of the expression of serum derived exosomal circRNAs in patients with hepatic alveolar echinococcosis. Gene, 814, 146161.