

Resource Summary Report

Generated by [NIF](#) on Aug 27, 2026

[mCarts](#)

RRID:SCR_010902

Type: Tool

Proper Citation

mCarts (RRID:SCR_010902)

Resource Information

URL: <http://zhanglab.c2b2.columbia.edu/index.php/MCarts>

Proper Citation: mCarts (RRID:SCR_010902)

Description: A hidden Markov model (HMM)-based software to predict clusters RNA motif sites.

Abbreviations: mCarts

Resource Type: software resource

Defining Citation: [PMID:23685613](#)

Availability: Apache License

Resource Name: mCarts

Resource ID: SCR_010902

Alternate IDs: OMICS_00567

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260815T182411+0000

Ratings and Alerts

No rating or validation information has been found for mCarts.

No alerts have been found for mCarts.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Weyn-Vanhentenryck SM, et al. (2018) Precise temporal regulation of alternative splicing during neural development. Nature communications, 9(1), 2189.

Anji A, et al. (2016) Guardian of Genetic Messenger-RNA-Binding Proteins. Biomolecules, 6(1), 4.

Wang T, et al. (2015) Design and bioinformatics analysis of genome-wide CLIP experiments. Nucleic acids research, 43(11), 5263.

Reyes-Herrera PH, et al. (2014) Computational Methods for CLIP-seq Data Processing. Bioinformatics and biology insights, 8, 199.