

Resource Summary Report

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CoSMoS_Analysis

RRID:SCR_016896

Type: Tool

Proper Citation

CoSMoS_Analysis (RRID:SCR_016896)

Resource Information

URL: https://github.com/gelles-brandeis/CoSMoS_Analysis

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Description: Software tools for analyzing co-localization single-molecule spectroscopy image data.

Abbreviations: CoSMoS Analysis

Synonyms: co-localization single-molecule spectroscopy, Co-localization Single-Molecule Spectroscopy Analysis, co-localization single molecule spectroscopy, CoSMoS

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

Keywords: co-localization, single, molecule, spectroscopy, image, data, analysis

Funding: NIGMS ;
NIH

Availability: Free, Available for download, Freely available

Resource Name: CoSMoS_Analysis

Resource ID: SCR_016896

License: GNU General Public License (GPL), version 3

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260729T044425+0000

Ratings and Alerts

No rating or validation information has been found for CoSMoS_Analysis.

No alerts have been found for CoSMoS_Analysis.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 17 mentions in open access literature.

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

Fu X, et al. (2025) Dynamics and evolutionary conservation of B complex protein recruitment during spliceosome activation. *Nucleic acids research*, 53(4).

Azam TP, et al. (2025) Mechanism of client loading from BiP to Grp94 and its disruption by select inhibitors. *Nature communications*, 16(1), 3575.

Fu X, et al. (2024) Dynamics and Evolutionary Conservation of B Complex Protein Recruitment During Spliceosome Activation. *bioRxiv : the preprint server for biology*.

Amasino AL, et al. (2023) Regulation of replication origin licensing by ORC phosphorylation reveals a two-step mechanism for Mcm2-7 ring closing. *Proceedings of the National Academy of Sciences of the United States of America*, 120(29), e2221484120.

Amasino A, et al. (2023) Regulation of replication origin licensing by ORC phosphorylation reveals a two-step mechanism for Mcm2-7 ring closing. *bioRxiv : the preprint server for biology*.

Asada R, et al. (2023) Single-molecule quantitation of RNA-binding protein occupancy and stoichiometry defines a role for Yra1 (Aly/REF) in nuclear mRNP organization. *Cell reports*, 42(11), 113415.

Hansen SR, et al. (2022) Multi-step recognition of potential 5' splice sites by the *Saccharomyces cerevisiae* U1 snRNP. *eLife*, 11.

Fu X, et al. (2022) Identification of transient intermediates during spliceosome activation by single molecule fluorescence microscopy. *Proceedings of the National Academy of Sciences of the United States of America*, 119(48), e2206815119.

Baek I, et al. (2021) Single-molecule studies reveal branched pathways for activator-dependent assembly of RNA polymerase II pre-initiation complexes. *Molecular cell*, 81(17), 3576.

Gupta S, et al. (2021) A helicase-tethered ORC flip enables bidirectional helicase loading. *eLife*, 10.

Jin Y, et al. (2021) The ER Chaperones BiP and Grp94 Regulate the Formation of Insulin-Like Growth Factor 2 (IGF2) Oligomers. *Journal of molecular biology*, 433(13), 166963.

Harden TT, et al. (2020) Alternative transcription cycle for bacterial RNA polymerase. *Nature communications*, 11(1), 448.

Rodgers ML, et al. (2019) Transcription Increases the Cooperativity of Ribonucleoprotein Assembly. *Cell*, 179(6), 1370.

Stumper SK, et al. (2019) Delayed inhibition mechanism for secondary channel factor regulation of ribosomal RNA transcription. *eLife*, 8.

Kaur H, et al. (2019) Analysis of spliceosome dynamics by maximum likelihood fitting of dwell time distributions. *Methods (San Diego, Calif.)*, 153, 13.

Champasa K, et al. (2019) A conserved Mcm4 motif is required for Mcm2-7 double-hexamer formation and origin DNA unwinding. *eLife*, 8.

Chadda R, et al. (2016) Measuring Membrane Protein Dimerization Equilibrium in Lipid Bilayers by Single-Molecule Fluorescence Microscopy. *Methods in enzymology*, 581, 53.