

Resource Summary Report

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CellOrganizer

RRID:SCR_014828

Type: Tool

Proper Citation

CellOrganizer (RRID:SCR_014828)

Resource Information

URL: <http://cellorganizer.org>

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Description: Image analysis software that learns modular models of things such as cell shape, nuclear shape, vesicular organelle distribution and microtubule distribution directly from 2D or 3D images and can produce specific instances of cell geometries without the need to create them by hand or to segment microscope images. These geometries can be combined with biochemical models to perform spatially realistic cell simulations if used in conjunction with MCell.

Synonyms: Cell Organizer

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

Keywords: image analysis, source code, model, modular model, cell shape, organelle, microtubule, distribution, 2d, 3d, cell geometry

Funding: Alexander von Humboldt Foundation ;
Freiburg Institute for Advanced Studies ;
NIGMS GM075205;
NIGMS GM090033;
NIGMS GM103712;
NSF MCB1121919;
NSF MCB1121793

Availability: Available for download

Resource Name: CellOrganizer

Resource ID: SCR_014828

Record Creation Time: 20220129T080322+0000

Record Last Update: 20260905T132751+0000

Ratings and Alerts

No rating or validation information has been found for CellOrganizer.

No alerts have been found for CellOrganizer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Sun H, et al. (2022) Improving and evaluating deep learning models of cellular organization. *Bioinformatics (Oxford, England)*, 38(23), 5299.

Li Y, et al. (2021) A LAT-Based Signaling Complex in the Immunological Synapse as Determined with Live Cell Imaging Is Less Stable in T Cells with Regulatory Capability. *Cells*, 10(2).

Ruan X, et al. (2020) Image-derived models of cell organization changes during differentiation and drug treatments. *Molecular biology of the cell*, 31(7), 655.

Ruan X, et al. (2019) Evaluation of methods for generative modeling of cell and nuclear shape. *Bioinformatics (Oxford, England)*, 35(14), 2475.

Donovan RM, et al. (2016) Unbiased Rare Event Sampling in Spatial Stochastic Systems Biology Models Using a Weighted Ensemble of Trajectories. *PLoS computational biology*, 12(2), e1004611.

Johnson GR, et al. (2015) Automated Learning of Subcellular Variation among Punctate Protein Patterns and a Generative Model of Their Relation to Microtubules. *PLoS computational biology*, 11(12), e1004614.