

Resource Summary Report

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DeepCell

RRID:SCR_022197

Type: Tool

Proper Citation

DeepCell (RRID:SCR_022197)

Resource Information

URL: <https://vanvalen.github.io/about/>

Proper Citation: DeepCell (RRID:SCR_022197)

Description: Software for segmenting individual cells in microscopy images using deep learning. Cell segmentation software.

Synonyms: Deepcell

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

Defining Citation: [DOI:10.1371/journal.pcbi.1005177](https://doi.org/10.1371/journal.pcbi.1005177)

Keywords: segmenting individual cells, microscopy image, cell segmentation

Funding: Paul Allen Family Foundation ;
NIGMS F32 GM119319;
NIGMS P50 GM107615;
NLM DP1 LM01150

Availability: Free, Available for download, Freely available

Resource Name: DeepCell

Resource ID: SCR_022197

Record Creation Time: 20220427T191217+0000

Record Last Update: 20260817T040658+0000

Ratings and Alerts

No rating or validation information has been found for DeepCell.

No alerts have been found for DeepCell.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Lin Y, et al. (2026) TiRank prioritizes phenotypic niches in tumor microenvironment for clinical biomarker discovery. *Genome medicine*, 18(1), 23.

Ayub S, et al. (2026) Multi-view deep learning of highly multiplexed imaging data improves association of cell states with clinical outcomes. *Bioinformatics advances*, 6(1), vbag010.

Forjaz A, et al. (2026) Deep Learning Enabled 3D Multi-Omic Analysis Reveals Molecular Signatures of Heterogeneous Response to Chemotherapy in Pancreatic Cancer. *bioRxiv* : the preprint server for biology.

Lee Y, et al. (2025) Segmentation aware probabilistic phenotyping of single-cell spatial protein expression data. *Nature communications*, 16(1), 389.

Chung DC, et al. (2025) CD103+CD56+ ILCs Are Associated with an Altered CD8+ T-cell Profile within the Tumor Microenvironment. *Cancer immunology research*, 13(4), 527.

Shi C, et al. (2025) CellBinDB: a large-scale multimodal annotated dataset for cell segmentation with benchmarking of universal models. *GigaScience*, 14.

Yoffe L, et al. (2025) Acquisition of discrete immune suppressive barriers contributes to the initiation and progression of preinvasive to invasive human lung cancer. *bioRxiv* : the preprint server for biology.

Christenson ES, et al. (2025) Nivolumab and Relatlimab for the Treatment of Patients with Unresectable or Metastatic Mismatch Repair-Proficient Colorectal Cancer. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(15), 3182.

Lacinski RA, et al. (2024) Spatial multiplexed immunofluorescence analysis reveals coordinated cellular networks associated with overall survival in metastatic osteosarcoma. *Bone research*, 12(1), 55.

Santamaria-Martinez A, et al. (2024) Development of patient-derived lymphomoids with preserved tumor architecture for lymphoma therapy screening. *Nature communications*, 15(1), 10650.

Ohara K, et al. (2024) The evolution of metastatic upper tract urothelial carcinoma through genomic-transcriptomic and single-cell protein markers analysis. *Nature communications*, 15(1), 2009.

Heussner RT, et al. (2023) Quantitative image analysis pipeline for detecting circulating hybrid cells in immunofluorescence images with human-level accuracy. *bioRxiv* : the preprint server for biology.

Weeratunga P, et al. (2023) Single cell spatial analysis reveals inflammatory foci of immature neutrophil and CD8 T cells in COVID-19 lungs. *Nature communications*, 14(1), 7216.

Wen C, et al. (2021) 3DeeCellTracker, a deep learning-based pipeline for segmenting and tracking cells in 3D time lapse images. *eLife*, 10.