

Resource Summary Report

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CellProfiler Image Analysis Software

RRID:SCR_007358

Type: Tool

Proper Citation

CellProfiler Image Analysis Software (RRID:SCR_007358)

Resource Information

URL: <http://cellprofiler.org>

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Description: Software tool to enable biologists without training in computer vision or programming to quantitatively measure phenotypes from thousands of images automatically. It counts cells and also measures the size, shape, intensity and texture of every cell (and every labeled subcellular compartment) in every image. It was designed for high throughput screening but can perform automated image analysis for images from time-lapse movies and low-throughput experiments. CellProfiler has an increasing number of algorithms to identify and measure properties of neuronal cell types.

Synonyms: Cell Profiler, CellProfiler - cell image analysis software

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

Defining Citation: [PMID:21349861](#), [PMID:17076895](#), [PMID:19014601](#), [PMID:19188593](#)

Keywords: high-throughput, high content imaging, software, image, cell, phenotype, measurement, subcellular, intensity, size, shape, analysis, algorithm

Funding: NIGMS R01 GM089652;
NIGMS RC2 GM092519;
NHGRI RL1 HG004671

Availability: Free, Available for download, Freely available

Resource Name: CellProfiler Image Analysis Software

Resource ID: SCR_007358

Alternate IDs: SCR_010649, nlx_66812, nif-0000-00280

Alternate URLs: <https://sources.debian.org/src/cellprofiler/>

License: BSD License

Record Creation Time: 20220129T080241+0000

Record Last Update: 20260729T044145+0000

Ratings and Alerts

No rating or validation information has been found for CellProfiler Image Analysis Software.

No alerts have been found for CellProfiler Image Analysis Software.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3265 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Lasse Opsahl EL, et al. (2026) Fibroblast STAT3 Activation Drives Organ-Specific Premetastatic Niche Formation. Cancer research, 86(1), 22.

Pan T, et al. (2026) MEN1 Promotes Ferroptosis by Disrupting CD44 Alternative Splicing to Suppress Lung Cancer. Cancer research, 86(1), 146.

Ma Y, et al. (2026) Exploiting the polypharmacology of alectinib for synergistic RNA splicing disruption with RBM39 degraders. Cell reports, 45(1), 116784.

Molè MA, et al. (2026) Modeling human embryo implantation in vitro. Cell, 189(1), 87.

Autio M, et al. (2025) Spatial Analysis of the Tumor Microenvironment in Diffuse Large B-cell Lymphoma Reveals Clinically Relevant Cell Interactions and Recurrent Cellular Neighborhoods. Cancer immunology research, 13(10), 1674.

Welte T, et al. (2025) Gain-of-Function Chromatin Remodeling Activity of Oncogenic FOXL2C134W Reprograms Glucocorticoid Receptor Occupancy to Drive Granulosa Cell Tumors. Cancer research, 85(5), 875.

Renninger KA, et al. (2025) The rise of CLAVATA: evidence for CLAVATA3 and WOX signaling in the fern gametophyte. The Plant journal : for cell and molecular biology, 121(2), e17207.

Autio M, et al. (2025) Characterization of tumor microenvironment and cell interaction patterns in testicular and diffuse large B-cell lymphomas. Haematologica, 110(6), 1339.

Sisto A, et al. (2025) Autophagy induction by piplartine ameliorates axonal degeneration caused by mutant HSPB1 and HSPB8 in Charcot-Marie-Tooth type 2 neuropathies. *Autophagy*, 21(5), 1116.

Dixon S, et al. (2025) A clinical drug candidate that triggers non-apoptotic cancer cell death. *Research square*.

Chawla Y, et al. (2025) Lactate metabolism in clonal plasma cells and its therapeutic implications in multiple myeloma patients with elevated serum LDH levels. *Cancer & metabolism*, 13(1), 9.

Lovejoy CA, et al. (2025) SRBD1 facilitates chromosome segregation by promoting topoisomerase II γ localization to mitotic chromosomes. *Nature communications*, 16(1), 1675.

Hunt LC, et al. (2025) The ubiquitin-conjugating enzyme UBE2D maintains a youthful proteome and ensures protein quality control during aging by sustaining proteasome activity. *PLoS biology*, 23(1), e3002998.

Ramezani M, et al. (2025) A genome-wide atlas of human cell morphology. *Nature methods*, 22(3), 621.

Kartnig F, et al. (2025) Ex vivo imaging-based high content phenotyping of patients with rheumatoid arthritis. *EBioMedicine*, 111, 105522.

Zhao Y, et al. (2025) VISTA-induced tumor suppression by a four amino acid intracellular motif. *bioRxiv* : the preprint server for biology.

Faust K, et al. (2025) PHARAOH: A collaborative crowdsourcing platform for phenotyping and regional analysis of histology. *Nature communications*, 16(1), 742.

Linthorst NA, et al. (2025) Amelioration of a von Willebrand disease type 2B phenotype in vivo upon treatment with allele-selective siRNAs. *Blood advances*, 9(2), 310.

Leib L, et al. (2025) The proximity-based protein interactome and regulatory logics of the transcription factor p65 NF- κ B/RELA. *EMBO reports*, 26(4), 1144.

Cates K, et al. (2025) Fate erasure logic of gene networks underlying direct neuronal conversion of somatic cells by microRNAs. *Cell reports*, 44(1), 115153.