Anne E Carpenter

List of Publications by Year
in descending order

152 papers	27,116 citations	14644 66 h-index	8618 146 g-index
190 all docs	190 docs citations	190 times ranked	40778 citing authors

#	Article	IF	Citations
1	CellProfiler: image analysis software for identifying and quantifying cell phenotypes. Genome Biology, 2006, 7, R100.	13.9	4,287
2	A Lentiviral RNAi Library for Human and Mouse Genes Applied to an Arrayed Viral High-Content Screen. Cell, 2006, 124, 1283-1298.	13.5	1,603
3	CellProfiler 3.0: Next-generation image processing for biology. PLoS Biology, 2018, 16, e2005970.	2.6	1,547
4	Opportunities and obstacles for deep learning in biology and medicine. Journal of the Royal Society Interface, 2018, 15, 20170387.	1.5	1,282
5	mTOR Complex 1 Regulates Lipin 1 Localization to Control the SREBP Pathway. Cell, 2011, 146, 408-420.	13.5	1,002
6	Improved structure, function and compatibility for CellProfiler: modular high-throughput image analysis software. Bioinformatics, 2011, 27, 1179-1180.	1.8	948
7	CellProfilerâ„¢: free, versatile software for automated biological image analysis. BioTechniques, 2007, 42, 71-75.	0.8	801
8	Cell Painting, a high-content image-based assay for morphological profiling using multiplexed fluorescent dyes. Nature Protocols, 2016, 11, 1757-1774.	5.5	608
9	CellProfiler 4: improvements in speed, utility and usability. BMC Bioinformatics, 2021, 22, 433.	1.2	592
10	Data-analysis strategies for image-based cell profiling. Nature Methods, 2017, 14, 849-863.	9.0	535
11	CellProfiler Analyst: data exploration and analysis software for complex image-based screens. BMC Bioinformatics, 2008, 9, 482.	1.2	496
12	Long-Range Directional Movement of an Interphase Chromosome Site. Current Biology, 2006, 16, 825-831.	1.8	493
13	Biological imaging software tools. Nature Methods, 2012, 9, 697-710.	9.0	462
14	In germ cells of mouse embryonic ovaries, the decision to enter meiosis precedes premeiotic DNA replication. Nature Genetics, 2006, 38, 1430-1434.	9.4	453
15	Nucleus segmentation across imaging experiments: the 2018 Data Science Bowl. Nature Methods, 2019, 16, 1247-1253.	9.0	433
16	Annotated high-throughput microscopy image sets for validation. Nature Methods, 2012, 9, 637-637.	9.0	416
17	An algorithm-based topographical biomaterials library to instruct cell fate. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 16565-16570.	3.3	355
18	Scoring diverse cellular morphologies in image-based screens with iterative feedback and machine learning. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 1826-1831.	3.3	345

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19	Systematic genome-wide screens of gene function. Nature Reviews Genetics, 2004, 5, 11-22.	7.7	302
20	The bromodomain protein Brd4 insulates chromatin from DNA damage signalling. Nature, 2013, 498, 246-250.	13.7	278
21	Label-free cell cycle analysis for high-throughput imaging flow cytometry. Nature Communications, 2016, 7, 10256.	5.8	237
22	Identification of Host-Targeted Small Molecules That Restrict Intracellular Mycobacterium tuberculosis Growth. PLoS Pathogens, 2014, 10, e1003946.	2.1	234
23	Identification of small molecules for human hepatocyte expansion and iPS differentiation. Nature Chemical Biology, 2013, 9, 514-520.	3.9	230
24	Visualization of image data from cells to organisms. Nature Methods, 2010, 7, S26-S41.	9.0	226
25	Multiplex Cytological Profiling Assay to Measure Diverse Cellular States. PLoS ONE, 2013, 8, e80999.	1.1	224
26	Abnormalities in Mitochondrial Structure in Cells from Patients with Bipolar Disorder. American Journal of Pathology, 2010, 177, 575-585.	1.9	216
27	Cell microarrays and RNA interference chip away at gene function. Nature Genetics, 2005, 37, S25-S30.	9.4	211
28	Reconstructing cell cycle and disease progression using deep learning. Nature Communications, 2017, 8, 463.	5.8	210
29	Evaluation of Deep Learning Strategies for Nucleus Segmentation in Fluorescence Images. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2019, 95, 952-965.	1.1	205
30	The Spemann organizer gene, Goosecoid, promotes tumor metastasis. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 18969-18974.	3.3	201
31	A Microscale Human Liver Platform that Supports the Hepatic Stages of Plasmodium falciparum and vivax. Cell Host and Microbe, 2013, 14, 104-115.	5.1	195
32	Image-based profiling for drug discovery: due for a machine-learning upgrade?. Nature Reviews Drug Discovery, 2021, 20, 145-159.	21.5	194
33	High-Throughput Screen for Novel Antimicrobials using a Whole Animal Infection Model. ACS Chemical Biology, 2009, 4, 527-533.	1.6	191
34	Toward performance-diverse small-molecule libraries for cell-based phenotypic screening using multiplexed high-dimensional profiling. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 10911-10916.	3.3	191
35	BRCA1-induced large-scale chromatin unfolding and allele-specific effects of cancer-predisposing mutations. Journal of Cell Biology, 2001, 155, 911-922.	2.3	181
36	Human tumors instigate granulin-expressing hematopoietic cells that promote malignancy by activating stromal fibroblasts in mice. Journal of Clinical Investigation, 2011, 121, 784-799.	3.9	177

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37	Repurposing High-Throughput Image Assays Enables Biological Activity Prediction for Drug Discovery. Cell Chemical Biology, 2018, 25, 611-618.e3.	2.5	176
38	Comparison of Methods for Image-Based Profiling of Cellular Morphological Responses to Small-Molecule Treatment. Journal of Biomolecular Screening, 2013, 18, 1321-1329.	2.6	166
39	Increasing the Content of High-Content Screening: An Overview. Journal of Biomolecular Screening, 2014, 19, 640-650.	2.6	166
40	In Vivo HP1 Targeting Causes Large-Scale Chromatin Condensation and Enhanced Histone Lysine Methylation. Molecular and Cellular Biology, 2005, 25, 4552-4564.	1.1	165
41	Imagining the future of bioimage analysis. Nature Biotechnology, 2016, 34, 1250-1255.	9.4	162
42	An image analysis toolbox for high-throughput C. elegans assays. Nature Methods, 2012, 9, 714-716.	9.0	154
43	Genetic Architecture of Hsp90-Dependent Drug Resistance. Eukaryotic Cell, 2006, 5, 2184-2188.	3.4	149
44	Image-based chemical screening. Nature Chemical Biology, 2007, 3, 461-465.	3.9	142
45	Ligand-Mediated Assembly and Real-Time Cellular Dynamics of Estrogen Receptor Î±-Coactivator Complexes in Living Cells. Molecular and Cellular Biology, 2001, 21, 4404-4412.	1.1	141
46	RNAi living-cell microarrays for loss-of-function screens in Drosophila melanogaster cells. Nature Methods, 2004, 1, 127-132.	9.0	136
47	Identification of Regulators of Polyploidization Presents Therapeutic Targets for Treatment of AMKL. Cell, 2012, 150, 575-589.	13.5	136
48	Applications in image-based profiling of perturbations. Current Opinion in Biotechnology, 2016, 39, 134-142.	3.3	133
49	Diagnostic Potential of Imaging Flow Cytometry. Trends in Biotechnology, 2018, 36, 649-652.	4.9	130
50	Systematic morphological profiling of human gene and allele function via Cell Painting. ELife, 2017, 6, .	2.8	129
51	Increased expression of the immune modulatory molecule PD-L1 (CD274) in anaplastic meningioma. Oncotarget, 2015, 6, 4704-4716.	0.8	127
52	Dynamic proteomics in individual human cells uncovers widespread cell-cycle dependence of nuclear proteins. Nature Methods, 2006, 3, 525-531.	9.0	125
53	Large-scale chromatin structure and function. Current Opinion in Cell Biology, 1999, 11, 307-311.	2.6	121
54	Microarrays of lentiviruses for gene function screens in immortalized and primary cells. Nature Methods, 2006, 3, 117-122.	9.0	121

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55	CellProfiler Analyst: interactive data exploration, analysis and classification of large biological image sets. Bioinformatics, 2016, 32, 3210-3212.	1.8	119
56	A call for bioimaging software usability. Nature Methods, 2012, 9, 666-670.	9.0	116
57	ZFHX4 Interacts with the NuRD Core Member CHD4 and Regulates the Glioblastoma Tumor-Initiating Cell State. Cell Reports, 2014, 6, 313-324.	2.9	106
58	Niche-based screening identifies small-molecule inhibitors of leukemia stem cells. Nature Chemical Biology, 2013, 9, 840-848.	3.9	103
59	A dataset of images and morphological profiles of 30 000 small-molecule treatments using the Cell Painting assay. GigaScience, 2017, 6, 1-5.	3.3	102
60	Applying Faster R-CNN for Object Detection on Malaria Images. , 2017, 2017, 808-813.		96
61	Alteration of Large-Scale Chromatin Structure by Estrogen Receptor. Molecular and Cellular Biology, 2002, 22, 3437-3449.	1.1	94
62	Systematic, multiparametric analysis of Mycobacterium tuberculosis intracellular infection offers insight into coordinated virulence. PLoS Pathogens, 2017, 13, e1006363.	2.1	94
63	Workflow and Metrics for Image Quality Control in Large-Scale High-Content Screens. Journal of Biomolecular Screening, 2012, 17, 266-274.	2.6	92
64	Introduction to the Quantitative Analysis of Two-Dimensional Fluorescence Microscopy Images for Cell-Based Screening. PLoS Computational Biology, 2009, 5, e1000603.	1.5	91
65	Using CellProfiler for Automatic Identification and Measurement of Biological Objects in Images. Current Protocols in Molecular Biology, 2015, 109, 14.17.1-14.17.13.	2.9	84
66	Pipeline for illumination correction of images for highâ€throughput microscopy. Journal of Microscopy, 2014, 256, 231-236.	0.8	83
67	An open-source solution for advanced imaging flow cytometry data analysis using machine learning. Methods, 2017, 112, 201-210.	1.9	82
68	Predicting cell health phenotypes using image-based morphology profiling. Molecular Biology of the Cell, 2021, 32, 995-1005.	0.9	71
69	Using CellProfiler for Automatic Identification and Measurement of Biological Objects in Images. Current Protocols in Molecular Biology, 2008, 82, Unit 14.17.	2.9	67
70	Discovery of New Anti-Schistosomal Hits by Integration of QSAR-Based Virtual Screening and High Content Screening. Journal of Medicinal Chemistry, 2016, 59, 7075-7088.	2.9	67
71	Distinctive Actions of Membrane-Targeted Versus Nuclear Localized Estrogen Receptors in Breast Cancer Cells. Molecular Endocrinology, 2005, 19, 1606-1617.	3.7	66
72	Mining for osteogenic surface topographies: In silico design to inÂvivo osseo-integration. Biomaterials, 2017, 137, 49-60.	5.7	66

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73	Labelâ€Free Identification of White Blood Cells Using Machine Learning. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2019, 95, 836-842.	1.1	66
74	CellProfiler Analyst 3.0: accessible data exploration and machine learning for image analysis. Bioinformatics, 2021, 37, 3992-3994.	1.8	66
75	Common Effects of Acidic Activators on Large-Scale Chromatin Structure and Transcription. Molecular and Cellular Biology, 2005, 25, 958-968.	1.1	61
76	Objective assessment of stored blood quality by deep learning. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 21381-21390.	3.3	57
77	Small molecules discovered in a pathway screen target the Rho pathway in cytokinesis. Nature Chemical Biology, 2010, 6, 457-463.	3.9	56
78	Regulation of Nuclear Receptor Transcriptional Activity by a Novel DEAD Box RNA Helicase (DP97). Journal of Biological Chemistry, 2003, 278, 4628-4638.	1.6	55
79	High- and low-throughput scoring of fat mass and body fat distribution in C. elegans. Methods, 2014, 68, 492-499.	1.9	54
80	Visualization of Parameter Space for Image Analysis. IEEE Transactions on Visualization and Computer Graphics, 2011, 17, 2402-2411.	2.9	52
81	CP-CHARM: segmentation-free image classification made accessible. BMC Bioinformatics, 2016, 17, 51.	1.2	52
82	A Novel Small Molecule Regulator of Guanine Nucleotide Exchange Activity of the ADP-ribosylation Factor and Golgi Membrane Trafficking. Journal of Biological Chemistry, 2008, 283, 31087-31096.	1.6	51
83	A Chemical Screen Probing the Relationship between Mitochondrial Content and Cell Size. PLoS ONE, 2012, 7, e33755.	1.1	51
84	Open-source deep-learning software for bioimage segmentation. Molecular Biology of the Cell, 2021, 32, 823-829.	0.9	50
85	QSAR-Driven Discovery of Novel Chemical Scaffolds Active against Schistosoma mansoni. Journal of Chemical Information and Modeling, 2016, 56, 1357-1372.	2.5	47
86	Quality Control for High-Throughput Imaging Experiments Using Machine Learning in Cellprofiler. Methods in Molecular Biology, 2018, 1683, 89-112.	0.4	46
87	Leveraging machine vision in cell-based diagnostics to do more with less. Nature Materials, 2019, 18, 414-418.	13.3	44
88	Keras R-CNN: library for cell detection in biological images using deep neural networks. BMC Bioinformatics, 2020, 21, 300.	1.2	44
89	Pharmacological HIF2Î± inhibition improves VHL diseaseâ€“associated phenotypes in zebrafish model. Journal of Clinical Investigation, 2015, 125, 1987-1997.	3.9	43
90	High Content Image Analysis Identifies Novel Regulators of Synaptogenesis in a High-Throughput RNAi Screen of Primary Neurons. PLoS ONE, 2014, 9, e91744.	1.1	42

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91	CellProfiler Tracer: exploring and validating high-throughput, time-lapse microscopy image data. BMC Bioinformatics, 2015, 16, 368.	1.2	38
92	Labelâ€Free Leukemia Monitoring by Computer Vision. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2020, 97, 407-414.	1.1	38
93	Genome-scale RNAi on living-cell microarrays identifies novel regulators of Drosophila melanogaster TORC1â€“S6K pathway signaling. Genome Research, 2011, 21, 433-446.	2.4	36
94	Quantifying co-cultured cell phenotypes in high-throughput using pixel-based classification. Methods, 2016, 96, 6-11.	1.9	32
95	BIN1 protein isoforms are differentially expressed in astrocytes, neurons, and microglia: neuronal and astrocyte BIN1 are implicated in tau pathology. Molecular Neurodegeneration, 2020, 15, 44.	4.4	32
96	A High-Content Screen Identifies TPP1 and Aurora B as Regulators of Axonal Mitochondrial Transport. Cell Reports, 2019, 28, 3224-3237.e5.	2.9	31
97	Morphological Profiles of RNAi-Induced Gene Knockdown Are Highly Reproducible but Dominated by Seed Effects. PLoS ONE, 2015, 10, e0131370.	1.1	31
98	Capturing single-cell heterogeneity via data fusion improves image-based profiling. Nature Communications, 2019, 10, 2082.	5.8	30
99	Nanoparticle vesicle encoding for imaging and tracking cell populations. Nature Methods, 2014, 11, 1177-1181.	9.0	29
100	Weakly Supervised Learning of Single-Cell Feature Embeddings. , 2018, 2018, 9309-9318.		29
101	Resolving clustered worms via probabilistic shape models. , 2010, 2010, 552-555.		28
102	Extracting Rich Information from Images. Methods in Molecular Biology, 2009, 486, 193-211.	0.4	27
103	Scientific Community Image Forum: A discussion forum for scientific image software. PLoS Biology, 2019, 17, e3000340.	2.6	27
104	Artificial intelligence and cancer. Nature Cancer, 2020, 1, 149-152.	5.7	26
105	Cell Painting predicts impact of lung cancer variants. Molecular Biology of the Cell, 2022, 33, mbcE21110538.	0.9	25
106	An open-source computational tool to automatically quantify immunolabeled retinal ganglion cells. Experimental Eye Research, 2016, 147, 50-56.	1.2	23
107	High-throughput screens for fluorescent dye discovery. Trends in Biotechnology, 2008, 26, 527-530.	4.9	22
108	Software opens the door to quantitative imaging. Nature Methods, 2007, 4, 120-121.	9.0	21

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109	Deepometry, a framework for applying supervised and weakly supervised deep learning to imaging cytometry. Nature Protocols, 2021, 16, 3572-3595.	5.5	21
110	An Intermittent Live Cell Imaging Screen for siRNA Enhancers and Suppressors of a Kinesin-5 Inhibitor. PLoS ONE, 2009, 4, e7339.	1.1	20
111	Developing open-source software for bioimage analysis: opportunities and challenges. F1000Research, 2021, 10, 302.	0.8	20
112	ImageJ and CellProfiler: Complements in Openâ€Source Bioimage Analysis. Current Protocols, 2021, 1, e89.	1.3	20
113	On the correlation between material-induced cell shape and phenotypical response of human mesenchymal stem cells. Scientific Reports, 2020, 10, 18988.	1.6	19
114	Ultrasome: efficient aberration caller for copy number studies of ultra-high resolution. Bioinformatics, 2009, 25, 1078-1079.	1.8	18
115	Screening Cellular Feature Measurements for Image-Based Assay Development. Journal of Biomolecular Screening, 2010, 15, 840-846.	2.6	18
116	Genes in human obesity loci are causal obesity genes in C. elegans. PLoS Genetics, 2021, 17, e1009736.	1.5	17
117	Predicting drug polypharmacology from cell morphology readouts using variational autoencoder latent space arithmetic. PLoS Computational Biology, 2022, 18, e1009888.	1.5	17
118	The antidepressant drug paroxetine as a new lead candidate in schistosome drug discovery. MedChemComm, 2016, 7, 1176-1182.	3.5	16
119	The new era of quantitative cell imagingâ€”challenges and opportunities. Molecular Cell, 2022, 82, 241-247.	4.5	16
120	2020 BioImage Analysis Survey: Community experiences and needs for the future. Biological Imaging, 2022, 1, .	1.0	15
121	Inter-laboratory automation of the in vitro micronucleus assay using imaging flow cytometry and deep learning. Archives of Toxicology, 2021, 95, 3101-3115.	1.9	14
122	DoGNet: A deep architecture for synapse detection in multiplexed fluorescence images. PLoS Computational Biology, 2019, 15, e1007012.	1.5	12
123	CDy6, a Photostable Probe for Long-Term Real-Time Visualization of Mitosis and Proliferating Cells. Chemistry and Biology, 2015, 22, 299-307.	6.2	11
124	Highâ€content, labelâ€free analysis of proplatelet production from megakaryocytes. Journal of Thrombosis and Haemostasis, 2020, 18, 2701-2711.	1.9	11
125	Designed Surface Topographies Control ICAM-1 Expression in Tonsil-Derived Human Stromal Cells. Frontiers in Bioengineering and Biotechnology, 2018, 6, 87.	2.0	10
126	ProtocolNavigator: emulation-based software for the design, documentation and reproduction biological experiments. Bioinformatics, 2014, 30, 3440-3442.	1.8	9

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127	A New Image for Cell Sorting. New England Journal of Medicine, 2022, 386, 1755-1758.	13.9	9
128	High-Throughput, Automated Image Processing for Large-Scale Fluorescence Microscopy Experiments. Microscopy and Microanalysis, 2016, 22, 538-539.	0.2	8
129	High-Throughput Platform for Identifying Molecular Factors Involved in Phenotypic Stabilization of Primary Human Hepatocytes In Vitro. Journal of Biomolecular Screening, 2016, 21, 897-911.	2.6	8
130	Harnessing the power of microscopy images to accelerate drug discovery: what are the possibilities?. Expert Opinion on Drug Discovery, 2020, 15, 639-642.	2.5	8
131	Direct Visualization of Transcription Factor-Induced Chromatin Remodeling and Cofactor Recruitment In Vivo. Methods in Enzymology, 2003, 375, 366-381.	0.4	7
132	Resolving cell state in iPSC-derived human neural samples with multiplexed fluorescence imaging. Communications Biology, 2021, 4, 786.	2.0	7
133	Molecular Diversity of Glutamatergic and GABAergic Synapses from Multiplexed Fluorescence Imaging. ENeuro, 2021, 8, ENEURO.0286-20.2020.	0.9	7
134	Automated microscopy identifies estrogen receptor subdomains with large-scale chromatin structure unfolding activity. Cytometry, 2004, 58A, 157-166.	1.8	6
135	Correction for Unadkat et al., An algorithm-based topographical biomaterials library to instruct cell fate. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 5905-5905.	3.3	6
136	A Genome-wide RNAi Screen for Microtubule Bundle Formation and Lysosome Motility Regulation in Drosophila S2 Cells. Cell Reports, 2016, 14, 611-620.	2.9	6
137	Identification and local delivery of vasodilators for the reduction of ureteral contractions. Nature Biomedical Engineering, 2020, 4, 28-39.	11.6	6
138	A field guide to cultivating computational biology. PLoS Biology, 2021, 19, e3001419.	2.6	6
139	Automated image-based assay for evaluation of HIV neutralization and cell-to-cell fusion inhibition. BMC Infectious Diseases, 2014, 14, 472.	1.3	4
140	A multiparametric activity profiling platform for neuron disease phenotyping and drug screening. Molecular Biology of the Cell, 2022, 33, mbcE21100481.	0.9	4
141	Automated tracking of yeast cell lineages. Proceedings of SPIE, 2010, , .	0.8	2
142	Combining morphological and migration profiles of in vitro time-lapse data. , 2018, , .		2
143	Bridging Domain and Data. Patterns, 2020, 1, 100064.	3.1	2
144	Extracting biomedically important information from large, automated imaging experiments. , 2011, , 1723-1726.		1

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145	Which image-based phenotypes are most promising for using AI to understand cellular functions and why?. Cell Systems, 2021, 12, 384-387.	2.9	1
146	CellProfiler: Open-Source Software to Automatically Quantify Images. Microscopy Today, 2008, 16, 38-39.	0.2	0
147	PI-09 PRECLINICAL TESTING OF SMALL MOLECULE HIF2Î± INHIBITOR IN ZEBRAFISH AND MOUSE MODELS OF VHL-DEFICIENT RENAL CELL CARCINOMA.. Journal of Urology, 2015, 193, .	0.2	0
148	A well-engineered path into cell biology and academia. Molecular Biology of the Cell, 2020, 31, 2755-2756.	0.9	0
149	A Kinome shRNA Screen to Identify Pathways That Regulate Megakaryocyte Polyploidization and New Targets for Differentiation Therapy. Blood, 2010, 116, 89-89.	0.6	0
150	Distinct Metabolic Dependency of Normal and Leukemic Cells in a Mouse Model. Blood, 2011, 118, 759-759.	0.6	0
151	Niche-Based Screening Reveals Leukemia Stem Cell Specific Therapeutics. Blood, 2011, 118, 760-760.	0.6	0
152	Aldehyde Dehydrogenase 3a2 (Aldh3a2) Represents a Distinct Metabolic Vulnerability in MLL-AF9 AML Leukemia Initiating Cells. Blood, 2012, 120, 208-208.	0.6	0