Anne E Carpenter

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

61 18,858 164 137 h-index g-index citations papers 6.52 23,708 190 11.3 L-index ext. citations avg, IF ext. papers

#	Paper	IF	Citations
164	The new era of quantitative cell imaging-challenges and opportunities <i>Molecular Cell</i> , 2022 , 82, 241-24	47 ₁₇ .6	2
163	2020 BioImage Analysis Survey: Community experiences and needs for the future. 2022 , 1,		3
162	Predicting drug polypharmacology from cell morphology readouts using variational autoencoder latent space arithmetic <i>PLoS Computational Biology</i> , 2022 , 18, e1009888	5	2
161	Cell Painting predicts impact of lung cancer variants <i>Molecular Biology of the Cell</i> , 2022 , mbcE2111053	3 8 3.5	1
160	A New Image for Cell Sorting <i>New England Journal of Medicine</i> , 2022 , 386, 1755-1758	59.2	О
159	Molecular Diversity of Glutamatergic and GABAergic Synapses from Multiplexed Fluorescence Imaging. <i>ENeuro</i> , 2021 , 8,	3.9	2
158	A field guide to cultivating computational biology. <i>PLoS Biology</i> , 2021 , 19, e3001419	9.7	2
157	Open-source deep-learning software for bioimage segmentation. <i>Molecular Biology of the Cell</i> , 2021 , 32, 823-829	3.5	21
156	Developing open-source software for bioimage analysis: opportunities and challenges. <i>F1000Research</i> , 2021 , 10, 302	3.6	3
155	Predicting cell health phenotypes using image-based morphology profiling. <i>Molecular Biology of the Cell</i> , 2021 , 32, 995-1005	3.5	20
154	ImageJ and CellProfiler: Complements in Open-Source Bioimage Analysis. <i>Current Protocols</i> , 2021 , 1, e89		5
153	Resolving cell state in iPSC-derived human neural samples with multiplexed fluorescence imaging. <i>Communications Biology</i> , 2021 , 4, 786	6.7	1
152	Deepometry, a framework for applying supervised and weakly supervised deep learning to imaging cytometry. <i>Nature Protocols</i> , 2021 , 16, 3572-3595	18.8	3
151	Inter-laboratory automation of the in vitro micronucleus assay using imaging flow cytometry and deep learning. <i>Archives of Toxicology</i> , 2021 , 95, 3101-3115	5.8	2
150	Image-based profiling for drug discovery: due for a machine-learning upgrade?. <i>Nature Reviews Drug Discovery</i> , 2021 , 20, 145-159	64.1	43
149	CellProfiler Analyst 3.0: Accessible data exploration and machine learning for image analysis. <i>Bioinformatics</i> , 2021 ,	7.2	7
148	Genes in human obesity loci are causal obesity genes in C. elegans. <i>PLoS Genetics</i> , 2021 , 17, e1009736	6	6

147	CellProfiler 4: improvements in speed, utility and usability. BMC Bioinformatics, 2021, 22, 433	3.6	36
146	A Multiparametric Activity Profiling Platform for Neuron Disease Phenotyping and Drug Screening <i>Molecular Biology of the Cell</i> , 2021 , mbcE21100481	3.5	O
145	Label-Free Leukemia Monitoring by Computer Vision. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2020 , 97, 407-414	4.6	21
144	Artificial intelligence and cancer <i>Nature Cancer</i> , 2020 , 1, 149-152	15.4	9
143	Identification and local delivery of vasodilators for the reduction of ureteral contractions. <i>Nature Biomedical Engineering</i> , 2020 , 4, 28-39	19	3
142	High-content, label-free analysis of proplatelet production from megakaryocytes. <i>Journal of Thrombosis and Haemostasis</i> , 2020 , 18, 2701-2711	15.4	1
141	Keras R-CNN: library for cell detection in biological images using deep neural networks. <i>BMC Bioinformatics</i> , 2020 , 21, 300	3.6	15
140	On the correlation between material-induced cell shape and phenotypical response of human mesenchymal stem cells. <i>Scientific Reports</i> , 2020 , 10, 18988	4.9	9
139	A well-engineered path into cell biology and academia. <i>Molecular Biology of the Cell</i> , 2020 , 31, 2755-27	56 .5	
138	BIN1 protein isoforms are differentially expressed in astrocytes, neurons, and microglia: neuronal and astrocyte BIN1 are implicated in tau pathology. <i>Molecular Neurodegeneration</i> , 2020 , 15, 44	19	9
137	Objective assessment of stored blood quality by deep learning. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 21381-21390	11.5	22
136	A High-Content Screen Identifies TPP1 and Aurora B as Regulators of Axonal Mitochondrial Transport. <i>Cell Reports</i> , 2019 , 28, 3224-3237.e5	10.6	17
135	Scientific Community Image Forum: A discussion forum for scientific image software. <i>PLoS Biology</i> , 2019 , 17, e3000340	9.7	10
134	DoGNet: A deep architecture for synapse detection in multiplexed fluorescence images. <i>PLoS Computational Biology</i> , 2019 , 15, e1007012	5	9
133	Label-Free Identification of White Blood Cells Using Machine Learning. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2019 , 95, 836-842	4.6	33
132	Capturing single-cell heterogeneity via data fusion improves image-based profiling. <i>Nature Communications</i> , 2019 , 10, 2082	17.4	16
131	Leveraging machine vision in cell-based diagnostics to do more with less. <i>Nature Materials</i> , 2019 , 18, 414-418	27	26
130	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	4.6	106

129	Nucleus segmentation across imaging experiments: the 2018 Data Science Bowl. <i>Nature Methods</i> , 2019 , 16, 1247-1253	21.6	165
128	Repurposing High-Throughput Image Assays Enables Biological Activity Prediction for Drug Discovery. <i>Cell Chemical Biology</i> , 2018 , 25, 611-618.e3	8.2	104
127	Opportunities and obstacles for deep learning in biology and medicine. <i>Journal of the Royal Society Interface</i> , 2018 , 15,	4.1	780
126	Diagnostic Potential of Imaging Flow Cytometry. <i>Trends in Biotechnology</i> , 2018 , 36, 649-652	15.1	70
125	Quality Control for High-Throughput Imaging Experiments Using Machine Learning in Cellprofiler. <i>Methods in Molecular Biology</i> , 2018 , 1683, 89-112	1.4	28
124	Designed Surface Topographies Control ICAM-1 Expression in Tonsil-Derived Human Stromal Cells. <i>Frontiers in Bioengineering and Biotechnology</i> , 2018 , 6, 87	5.8	10
123	CellProfiler 3.0: Next-generation image processing for biology. <i>PLoS Biology</i> , 2018 , 16, e2005970	9.7	775
122	Weakly Supervised Learning of Single-Cell Feature Embeddings. <i>Proceedings of the IEEE Computer Society Conference on Computer Vision and Pattern Recognition</i> , 2018 , 2018, 9309-9318	6	18
121	Combining morphological and migration profiles of in vitro time-lapse data 2018,		1
120	A dataset of images and morphological profiles of 30 000 small-molecule treatments using the Cell Painting assay. <i>GigaScience</i> , 2017 , 6, 1-5	7.6	59
119	Mining for osteogenic surface topographies: In silico design to in⊡ivo osseo-integration. <i>Biomaterials</i> , 2017 , 137, 49-60	15.6	49
118	Data-analysis strategies for image-based cell profiling. <i>Nature Methods</i> , 2017 , 14, 849-863	21.6	291
117	Reconstructing cell cycle and disease progression using deep learning. <i>Nature Communications</i> , 2017 , 8, 463	17.4	136
116	An open-source solution for advanced imaging flow cytometry data analysis using machine learning. <i>Methods</i> , 2017 , 112, 201-210	4.6	56
115	Systematic, multiparametric analysis of Mycobacterium tuberculosis intracellular infection offers insight into coordinated virulence. <i>PLoS Pathogens</i> , 2017 , 13, e1006363	7.6	59
114	Applying Faster R-CNN for Object Detection on Malaria Images <i>IEEE Computer Society Conference on Computer Vision and Pattern Recognition Workshops</i> , 2017 , 2017, 808-813	1.3	36
113	Systematic morphological profiling of human gene and allele function via Cell Painting. <i>ELife</i> , 2017 , 6,	8.9	65
112	Cell Painting, a high-content image-based assay for morphological profiling using multiplexed fluorescent dyes. <i>Nature Protocols</i> , 2016 , 11, 1757-74	18.8	286

(2015-2016)

High-Throughput Platform for Identifying Molecular Factors Involved in Phenotypic Stabilization of Primary Human Hepatocytes In Vitro. <i>Journal of Biomolecular Screening</i> , 2016 , 21, 897-911		7
CP-CHARM: segmentation-free image classification made accessible. <i>BMC Bioinformatics</i> , 2016 , 17, 51	3.6	42
QSAR-Driven Discovery of Novel Chemical Scaffolds Active against Schistosoma mansoni. <i>Journal of Chemical Information and Modeling</i> , 2016 , 56, 1357-72	6.1	38
An open-source computational tool to automatically quantify immunolabeled retinal ganglion cells. <i>Experimental Eye Research</i> , 2016 , 147, 50-56	3.7	18
A Genome-wide RNAi Screen for Microtubule Bundle Formation and Lysosome Motility Regulation in Drosophila S2 Cells. <i>Cell Reports</i> , 2016 , 14, 611-620	10.6	3
Quantifying co-cultured cell phenotypes in high-throughput using pixel-based classification. <i>Methods</i> , 2016 , 96, 6-11	4.6	24
Label-free cell cycle analysis for high-throughput imaging flow cytometry. <i>Nature Communications</i> , 2016 , 7, 10256	17.4	156
Discovery of New Anti-Schistosomal Hits by Integration of QSAR-Based Virtual Screening and High Content Screening. <i>Journal of Medicinal Chemistry</i> , 2016 , 59, 7075-88	8.3	47
CellProfiler Analyst: interactive data exploration, analysis and classification of large biological image sets. <i>Bioinformatics</i> , 2016 , 32, 3210-3212	7.2	72
High-Throughput, Automated Image Processing for Large-Scale Fluorescence Microscopy Experiments. <i>Microscopy and Microanalysis</i> , 2016 , 22, 538-539	0.5	6
Imagining the future of bioimage analysis. <i>Nature Biotechnology</i> , 2016 , 34, 1250-1255	44.5	108
The antidepressant drug paroxetine as a new lead candidate in schistosome drug discovery. <i>MedChemComm</i> , 2016 , 7, 1176-1182	5	12
Applications in image-based profiling of perturbations. <i>Current Opinion in Biotechnology</i> , 2016 , 39, 134-	1 42 4	87
CellProfiler Tracer: exploring and validating high-throughput, time-lapse microscopy image data. <i>BMC Bioinformatics</i> , 2015 , 16, 368	3.6	24
Pharmacological HIF2IInhibition improves VHL disease-associated phenotypes in zebrafish model. Journal of Clinical Investigation, 2015 , 125, 1987-97	15.9	34
Increased expression of the immune modulatory molecule PD-L1 (CD274) in anaplastic meningioma. <i>Oncotarget</i> , 2015 , 6, 4704-16	3.3	92
Using CellProfiler for Automatic Identification and Measurement of Biological Objects in Images. <i>Current Protocols in Molecular Biology</i> , 2015 , 109, 14.17.1-14.17.13	2.9	44
CDy6, a photostable probe for long-term real-time visualization of mitosis and proliferating cells. <i>Chemistry and Biology</i> , 2015 , 22, 299-307		5
	Primary Human Hepatocytes In Vitro. Journal of Biomolecular Screening, 2016, 21, 897-911 CP-CHARM: segmentation-free image classification made accessible. BMC Bioinformatics, 2016, 17, 51 QSAR-Driven Discovery of Novel Chemical Scaffolds Active against Schistosoma mansoni. Journal of Chemical Information and Modeling, 2016, 56, 1357-72 An open-source computational tool to automatically quantify immunolabeled retinal ganglion cells. Experimental Eye Research, 2016, 147, 50-56 A Genome-wide RNAI Screen for Microtubule Bundle Formation and Lysosome Motility Regulation in Drosophila S2 Cells. Cell Reports, 2016, 14, 611-620 Quantifying co-cultured cell phenotypes in high-throughput using pixel-based classification. Methods, 2016, 96, 6-11 Label-free cell cycle analysis for high-throughput imaging flow cytometry. Nature Communications, 2016, 7, 10256 Discovery of New Anti-Schistosomal Hits by Integration of QSAR-Based Virtual Screening and High Content Screening. Journal of Medicinal Chemistry, 2016, 59, 7075-88 CellProfiler Analyst: interactive data exploration, analysis and classification of large biological image sets. Bioinformatics, 2016, 32, 3210-3212 High-Throughput, Automated Image Processing for Large-Scale Fluorescence Microscopy Experiments. Microscopy and Microanalysis, 2016, 22, 538-539 Imagining the future of bioimage analysis. Nature Biotechnology, 2016, 34, 1250-1255 The antidepressant drug paroxetine as a new lead candidate in schistosome drug discovery. MedChemComm, 2016, 7, 1176-1182 Applications in image-based profiling of perturbations. Current Opinion in Biotechnology, 2016, 39, 134-CellProfiler Tracer: exploring and validating high-throughput, time-lapse microscopy image data. BMC Bioinformatics, 2015, 16, 368 Pharmacological HIP2Inhibition improves VHL disease-associated phenotypes in zebrafish model. Journal of Clinical Investigation, 2015, 125, 1987-97 Increased expression of the immune modulatory molecule PD-L1 (CD274) in anaplastic meningioma. Oncotarget, 2015, 6, 4704-16 U	Primary Human Hepatocytes In Vitro. Journal of Biomolecular Screening, 2016, 21, 897-911 CP-CHARM: segmentation-free image classification made accessible. BMC Bioinformatics, 2016, 17, 51 3.6 QSAR-Driven Discovery of Novel Chemical Scaffolds Active against Schistosoma mansoni. Journal of Chemical Information and Modeling, 2016, 56, 1357-72 An open-source computational tool to automatically quantify immunolabeled retinal ganglion cells. Experimental Eye Research, 2016, 147, 50-56 A Genome-wide RNAi Screen for Microtubule Bundle Formation and Lysosome Motility Regulation in Drosophila SZ Cells. Cell Reports, 2016, 14, 611-620 Quantifying co-cultured cell phenotypes in high-throughput using pixel-based classification. Methods, 2016, 96, 6-11 Label-free cell cycle analysis for high-throughput imaging flow cytometry. Nature Communications, 2016, 7, 10256 Discovery of New Anti-Schistosomal Hits by Integration of QSAR-Based Virtual Screening and High Content Screening. Journal of Medicinal Chemistry, 2016, 59, 7075-88 CellProfiler Analyst: interactive data exploration, analysis and classification of large biological image sets. Bioinformatics, 2016, 32, 3210-3212 High-Throughput, Automated Image Processing for Large-Scale Fluorescence Microscopy Experiments. Microscopy and Microanalysis, 2016, 22, 538-539 Imagining the future of bioimage analysis. Nature Biotechnology, 2016, 34, 1250-1255 445 The antidepressant drug paroxetine as a new lead candidate in schistosome drug discovery. MedChemComm, 2016, 7, 1176-1182 Applications in image-based profilling of perturbations. Current Opinion in Biotechnology, 2016, 39, 134-1424 CellProfiler Tracer: exploring and validating high-throughput, time-lapse microscopy image data. BMC Bioinformatics, 2015, 16, 368 Pharmacological HiF2Ihhibition improves VHL disease-associated phenotypes in zebrafish model. Journal of Clinical Investigation, 2015, 125, 1987-97 Increased expression of the immune modulatory molecule PD-L1 (CD274) in anaplastic meningiona. Oncotarget, 201

93	Morphological Profiles of RNAi-Induced Gene Knockdown Are Highly Reproducible but Dominated by Seed Effects. <i>PLoS ONE</i> , 2015 , 10, e0131370	3.7	24
92	Pipeline for illumination correction of images for high-throughput microscopy. <i>Journal of Microscopy</i> , 2014 , 256, 231-6	1.9	47
91	Toward performance-diverse small-molecule libraries for cell-based phenotypic screening using multiplexed high-dimensional profiling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 10911-6	11.5	141
90	Nanoparticle vesicle encoding for imaging and tracking cell populations. <i>Nature Methods</i> , 2014 , 11, 117	7 <u>-</u> 816	26
89	High- and low-throughput scoring of fat mass and body fat distribution in C. elegans. <i>Methods</i> , 2014 , 68, 492-9	4.6	37
88	ZFHX4 interacts with the NuRD core member CHD4 and regulates the glioblastoma tumor-initiating cell state. <i>Cell Reports</i> , 2014 , 6, 313-24	10.6	77
87	High content image analysis identifies novel regulators of synaptogenesis in a high-throughput RNAi screen of primary neurons. <i>PLoS ONE</i> , 2014 , 9, e91744	3.7	32
86	Increasing the Content of High-Content Screening: An Overview. <i>Journal of Biomolecular Screening</i> , 2014 , 19, 640-50		136
85	Identification of host-targeted small molecules that restrict intracellular Mycobacterium tuberculosis growth. <i>PLoS Pathogens</i> , 2014 , 10, e1003946	7.6	172
84	ProtocolNavigator: emulation-based software for the design, documentation and reproduction biological experiments. <i>Bioinformatics</i> , 2014 , 30, 3440-2	7.2	7
83	Automated image-based assay for evaluation of HIV neutralization and cell-to-cell fusion inhibition. <i>BMC Infectious Diseases</i> , 2014 , 14, 472	4	1
82	A microscale human liver platform that supports the hepatic stages of Plasmodium falciparum and vivax. <i>Cell Host and Microbe</i> , 2013 , 14, 104-15	23.4	152
81	Niche-based screening identifies small-molecule inhibitors of leukemia stem cells. <i>Nature Chemical Biology</i> , 2013 , 9, 840-848	11.7	96
80	Identification of small molecules for human hepatocyte expansion and iPS differentiation. <i>Nature Chemical Biology</i> , 2013 , 9, 514-20	11.7	201
79	The bromodomain protein Brd4 insulates chromatin from DNA damage signalling. <i>Nature</i> , 2013 , 498, 246-50	50.4	214
78	Comparison of methods for image-based profiling of cellular morphological responses to small-molecule treatment. <i>Journal of Biomolecular Screening</i> , 2013 , 18, 1321-9		113
77	Multiplex cytological profiling assay to measure diverse cellular states. <i>PLoS ONE</i> , 2013 , 8, e80999	3.7	136
76	Identification of regulators of polyploidization presents therapeutic targets for treatment of AMKL. <i>Cell</i> , 2012 , 150, 575-89	56.2	107

75	Annotated high-throughput microscopy image sets for validation. <i>Nature Methods</i> , 2012 , 9, 637	21.6	230
74	An image analysis toolbox for high-throughput C. elegans assays. <i>Nature Methods</i> , 2012 , 9, 714-6	21.6	112
73	A chemical screen probing the relationship between mitochondrial content and cell size. <i>PLoS ONE</i> , 2012 , 7, e33755	3.7	41
72	Biological imaging software tools. <i>Nature Methods</i> , 2012 , 9, 697-710	21.6	377
71	A call for bioimaging software usability. <i>Nature Methods</i> , 2012 , 9, 666-70	21.6	92
70	Workflow and metrics for image quality control in large-scale high-content screens. <i>Journal of Biomolecular Screening</i> , 2012 , 17, 266-74		68
69	Correction for Unadkat et al., An algorithm-based topographical biomaterials library to instruct cell fate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 5905-5	9 05 .5	5
68	Aldehyde Dehydrogenase 3a2 (Aldh3a2) Represents a Distinct Metabolic Vulnerability in MLL-AF9 AML Leukemia Initiating Cells. <i>Blood</i> , 2012 , 120, 208-208	2.2	
67	mTOR complex 1 regulates lipin 1 localization to control the SREBP pathway. <i>Cell</i> , 2011 , 146, 408-20	56.2	774
66	Visualization of parameter space for image analysis. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2011 , 17, 2402-11	4	40
66		9.7	40 31
	Computer Graphics, 2011, 17, 2402-11 Genome-scale RNAi on living-cell microarrays identifies novel regulators of Drosophila	9.7	
65	Computer Graphics, 2011, 17, 2402-11 Genome-scale RNAi on living-cell microarrays identifies novel regulators of Drosophila melanogaster TORC1-S6K pathway signaling. Genome Research, 2011, 21, 433-46 EXTRACTING BIOMEDICALLY IMPORTANT INFORMATION FROM LARGE, AUTOMATED IMAGING		
65 64	Computer Graphics, 2011, 17, 2402-11 Genome-scale RNAi on living-cell microarrays identifies novel regulators of Drosophila melanogaster TORC1-S6K pathway signaling. Genome Research, 2011, 21, 433-46 EXTRACTING BIOMEDICALLY IMPORTANT INFORMATION FROM LARGE, AUTOMATED IMAGING EXPERIMENTS 2011, 1723-1726 An algorithm-based topographical biomaterials library to instruct cell fate. Proceedings of the	1.5	31
656463	Genome-scale RNAi on living-cell microarrays identifies novel regulators of Drosophila melanogaster TORC1-S6K pathway signaling. <i>Genome Research</i> , 2011 , 21, 433-46 EXTRACTING BIOMEDICALLY IMPORTANT INFORMATION FROM LARGE, AUTOMATED IMAGING EXPERIMENTS 2011 , 1723-1726 An algorithm-based topographical biomaterials library to instruct cell fate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 16565-70 Improved structure, function and compatibility for CellProfiler: modular high-throughput image	1.5	31 1 310
65646362	Genome-scale RNAi on living-cell microarrays identifies novel regulators of Drosophila melanogaster TORC1-S6K pathway signaling. <i>Genome Research</i> , 2011 , 21, 433-46 EXTRACTING BIOMEDICALLY IMPORTANT INFORMATION FROM LARGE, AUTOMATED IMAGING EXPERIMENTS 2011 , 1723-1726 An algorithm-based topographical biomaterials library to instruct cell fate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 16565-70 Improved structure, function and compatibility for CellProfiler: modular high-throughput image analysis software. <i>Bioinformatics</i> , 2011 , 27, 1179-80 Human tumors instigate granulin-expressing hematopoietic cells that promote malignancy by	1.5 11.5 7.2 15.9	31 1 310 741
65 64 63 62 61	Genome-scale RNAi on living-cell microarrays identifies novel regulators of Drosophila melanogaster TORC1-S6K pathway signaling. <i>Genome Research</i> , 2011 , 21, 433-46 EXTRACTING BIOMEDICALLY IMPORTANT INFORMATION FROM LARGE, AUTOMATED IMAGING EXPERIMENTS 2011 , 1723-1726 An algorithm-based topographical biomaterials library to instruct cell fate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 16565-70 Improved structure, function and compatibility for CellProfiler: modular high-throughput image analysis software. <i>Bioinformatics</i> , 2011 , 27, 1179-80 Human tumors instigate granulin-expressing hematopoietic cells that promote malignancy by activating stromal fibroblasts in mice. <i>Journal of Clinical Investigation</i> , 2011 , 121, 784-99	1.5 11.5 7.2 15.9	31 1 310 741

57	Visualization of image data from cells to organisms. <i>Nature Methods</i> , 2010 , 7, S26-41	21.6	189
56	Automated tracking of yeast cell lineages 2010 ,		1
55	RESOLVING CLUSTERED WORMS VIA PROBABILISTIC SHAPE MODELS 2010 , 2010, 552-555	1.5	25
54	Screening cellular feature measurements for image-based assay development. <i>Journal of Biomolecular Screening</i> , 2010 , 15, 840-6		16
53	Abnormalities in mitochondrial structure in cells from patients with bipolar disorder. <i>American Journal of Pathology</i> , 2010 , 177, 575-85	5.8	170
52	A Kinome shRNA Screen to Identify Pathways That Regulate Megakaryocyte Polyploidization and New Targets for Differentiation Therapy. <i>Blood</i> , 2010 , 116, 89-89	2.2	
51	An intermittent live cell imaging screen for siRNA enhancers and suppressors of a kinesin-5 inhibitor. <i>PLoS ONE</i> , 2009 , 4, e7339	3.7	20
50	Ultrasome: efficient aberration caller for copy number studies of ultra-high resolution. <i>Bioinformatics</i> , 2009 , 25, 1078-9	7.2	17
49	Introduction to the quantitative analysis of two-dimensional fluorescence microscopy images for cell-based screening. <i>PLoS Computational Biology</i> , 2009 , 5, e1000603	5	75
48	Scoring diverse cellular morphologies in image-based screens with iterative feedback and machine learning. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 18	26-35	29 0
47	High-throughput screen for novel antimicrobials using a whole animal infection model. <i>ACS Chemical Biology</i> , 2009 , 4, 527-33	4.9	167
46	Extracting rich information from images. <i>Methods in Molecular Biology</i> , 2009 , 486, 193-211	1.4	26
45	CellProfiler Analyst: data exploration and analysis software for complex image-based screens. <i>BMC Bioinformatics</i> , 2008 , 9, 482	3.6	375
44	High-throughput screens for fluorescent dye discovery. <i>Trends in Biotechnology</i> , 2008 , 26, 527-30	15.1	22
43	Using CellProfiler for automatic identification and measurement of biological objects in images. <i>Current Protocols in Molecular Biology</i> , 2008 , Chapter 14, Unit 14.17	2.9	24
42	A novel small molecule regulator of guanine nucleotide exchange activity of the ADP-ribosylation factor and golgi membrane trafficking. <i>Journal of Biological Chemistry</i> , 2008 , 283, 31087-96	5.4	39
41	CellProfiler: Open-Source Software to Automatically Quantify Images. <i>Microscopy Today</i> , 2008 , 16, 38-3	39 0.4	
40	CellProfiler: free, versatile software for automated biological image analysis. <i>BioTechniques</i> , 2007 , 42, 71-5	2.5	633

39	Image-based chemical screening. <i>Nature Chemical Biology</i> , 2007 , 3, 461-5	11.7	124
38	Long-range directional movement of an interphase chromosome site. <i>Current Biology</i> , 2006 , 16, 825-31	6.3	444
37	Genetic architecture of Hsp90-dependent drug resistance. Eukaryotic Cell, 2006, 5, 2184-8		126
36	The Spemann organizer gene, Goosecoid, promotes tumor metastasis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 18969-74	11.5	172
35	CellProfiler: image analysis software for identifying and quantifying cell phenotypes. <i>Genome Biology</i> , 2006 , 7, R100	18.3	3203
34	A lentiviral RNAi library for human and mouse genes applied to an arrayed viral high-content screen. <i>Cell</i> , 2006 , 124, 1283-98	56.2	1340
33	In germ cells of mouse embryonic ovaries, the decision to enter meiosis precedes premeiotic DNA replication. <i>Nature Genetics</i> , 2006 , 38, 1430-4	36.3	390
32	Microarrays of lentiviruses for gene function screens in immortalized and primary cells. <i>Nature Methods</i> , 2006 , 3, 117-22	21.6	115
31	Dynamic proteomics in individual human cells uncovers widespread cell-cycle dependence of nuclear proteins. <i>Nature Methods</i> , 2006 , 3, 525-31	21.6	117
30	Cell microarrays and RNA interference chip away at gene function. <i>Nature Genetics</i> , 2005 , 37 Suppl, S25	-36 .3	193
29	In vivo HP1 targeting causes large-scale chromatin condensation and enhanced histone lysine methylation. <i>Molecular and Cellular Biology</i> , 2005 , 25, 4552-64	4.8	147
28	Distinctive actions of membrane-targeted versus nuclear localized estrogen receptors in breast cancer cells. <i>Molecular Endocrinology</i> , 2005 , 19, 1606-17		62
27	Voronoi-Based Segmentation of Cells on Image Manifolds. Lecture Notes in Computer Science, 2005, 535	5- 5 . 4)3	95
26	Common effects of acidic activators on large-scale chromatin structure and transcription. <i>Molecular and Cellular Biology</i> , 2005 , 25, 958-68	4.8	56
25	RNAi living-cell microarrays for loss-of-function screens in Drosophila melanogaster cells. <i>Nature Methods</i> , 2004 , 1, 127-32	21.6	123
24	Systematic genome-wide screens of gene function. <i>Nature Reviews Genetics</i> , 2004 , 5, 11-22	30.1	261
23	Automated microscopy identifies estrogen receptor subdomains with large-scale chromatin structure unfolding activity. <i>Cytometry</i> , 2004 , 58, 157-66		5

21	Regulation of nuclear receptor transcriptional activity by a novel DEAD box RNA helicase (DP97). Journal of Biological Chemistry, 2003 , 278, 4628-38	5.4	45
20	Alteration of large-scale chromatin structure by estrogen receptor. <i>Molecular and Cellular Biology</i> , 2002 , 22, 3437-49	4.8	85
19	Ligand-mediated assembly and real-time cellular dynamics of estrogen receptor alpha-coactivator complexes in living cells. <i>Molecular and Cellular Biology</i> , 2001 , 21, 4404-12	4.8	129
18	BRCA1-induced large-scale chromatin unfolding and allele-specific effects of cancer-predisposing mutations. <i>Journal of Cell Biology</i> , 2001 , 155, 911-21	7.3	164
17	Large-scale chromatin structure and function. Current Opinion in Cell Biology, 1999, 11, 307-11	9	114
16	Morphology and gene expression profiling provide complementary information for mapping cell state		4
15	Reconstructing cell cycle and disease progression using deep learning		4
14	Automating Morphological Profiling with Generic Deep Convolutional Networks		27
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