

Peter K Sorger

List of Publications by Year in descending order

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276
papers

40,168
citations

2544

96
h-index

3261

185
g-index

340
all docs

340
docs citations

340
times ranked

47107
citing authors

#	ARTICLE	IF	CITATIONS
1	Dissecting the multicellular ecosystem of metastatic melanoma by single-cell RNA-seq. <i>Science</i> , 2016, 352, 189-196.	12.6	3,421
2	Cells on chips. <i>Nature</i> , 2006, 442, 403-411.	27.8	2,022
3	Non-genetic origins of cell-to-cell variability in TRAIL-induced apoptosis. <i>Nature</i> , 2009, 459, 428-432.	27.8	993
4	A Cancer Cell Program Promotes T Cell Exclusion and Resistance to Checkpoint Blockade. <i>Cell</i> , 2018, 175, 984-997.e24.	28.9	892
5	Yeast heat shock factor is an essential DNA-binding protein that exhibits temperature-dependent phosphorylation. <i>Cell</i> , 1988, 54, 855-864.	28.9	863
6	SARS-CoV-2 infection protects against rechallenge in rhesus macaques. <i>Science</i> , 2020, 369, 812-817.	12.6	789
7	MAD2 haplo-insufficiency causes premature anaphase and chromosome instability in mammalian cells. <i>Nature</i> , 2001, 409, 355-359.	27.8	715
8	Sequential Application of Anticancer Drugs Enhances Cell Death by Rewiring Apoptotic Signaling Networks. <i>Cell</i> , 2012, 149, 780-794.	28.9	621
9	Heat shock factor and the heat shock response. <i>Cell</i> , 1991, 65, 363-366.	28.9	608
10	Physicochemical modelling of cell signalling pathways. <i>Nature Cell Biology</i> , 2006, 8, 1195-1203.	10.3	558
11	A role for the Adenomatous Polyposis Coli protein in chromosome segregation. <i>Nature Cell Biology</i> , 2001, 3, 429-432.	10.3	510
12	Heat shock factor is regulated differently in yeast and HeLa cells. <i>Nature</i> , 1987, 329, 81-84.	27.8	506
13	A Systems Model of Signaling Identifies a Molecular Basis Set for Cytokine-Induced Apoptosis. <i>Science</i> , 2005, 310, 1646-1653.	12.6	506
14	Systems biology and combination therapy in the quest for clinical efficacy. <i>Nature Chemical Biology</i> , 2006, 2, 458-466.	8.0	505
15	Growth rate inhibition metrics correct for confounders in measuring sensitivity to cancer drugs. <i>Nature Methods</i> , 2016, 13, 521-527.	19.0	489
16	Chromosome Missegregation and Apoptosis in Mice Lacking the Mitotic Checkpoint Protein Mad2. <i>Cell</i> , 2000, 101, 635-645.	28.9	484
17	Highly multiplexed immunofluorescence imaging of human tissues and tumors using t-CyCIF and conventional optical microscopes. <i>ELife</i> , 2018, 7, .	6.0	474
18	Combination Cancer Therapy Can Confer Benefit via Patient-to-Patient Variability without Drug Additivity or Synergy. <i>Cell</i> , 2017, 171, 1678-1691.e13.	28.9	467

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19	Timing and Checkpoints in the Regulation of Mitotic Progression. <i>Developmental Cell</i> , 2004, 7, 45-60.	7.0	434
20	Highly multiplexed imaging of single cells using a high-throughput cyclic immunofluorescence method. <i>Nature Communications</i> , 2015, 6, 8390.	12.8	428
21	Electronic detection of DNA by its intrinsic molecular charge. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 14142-14146.	7.1	420
22	Trimerization of a yeast transcriptional activator via a coiled-coil motif. <i>Cell</i> , 1989, 59, 807-813.	28.9	400
23	Quantitative Analysis of Pathways Controlling Extrinsic Apoptosis in Single Cells. <i>Molecular Cell</i> , 2008, 30, 11-25.	9.7	357
24	Measuring and Modeling Apoptosis in Single Cells. <i>Cell</i> , 2011, 144, 926-939.	28.9	354
25	Obesity Shapes Metabolism in the Tumor Microenvironment to Suppress Anti-Tumor Immunity. <i>Cell</i> , 2020, 183, 1848-1866.e26.	28.9	347
26	Towards a Rigorous Assessment of Systems Biology Models: The DREAM3 Challenges. <i>PLoS ONE</i> , 2010, 5, e9202.	2.5	337
27	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. <i>Cell</i> , 2020, 181, 236-249.	28.9	334
28	Anaphase initiation is regulated by antagonistic ubiquitination and deubiquitination activities. <i>Nature</i> , 2007, 446, 876-881.	27.8	333
29	Input-output behavior of ErbB signaling pathways as revealed by a mass action model trained against dynamic data. <i>Molecular Systems Biology</i> , 2009, 5, 239.	7.2	332
30	The Library of Integrated Network-Based Cellular Signatures NIH Program: System-Level Cataloging of Human Cells Response to Perturbations. <i>Cell Systems</i> , 2018, 6, 13-24.	6.2	327
31	Purification and characterization of a heat-shock element binding protein from yeast.. <i>EMBO Journal</i> , 1987, 6, 3035-3041.	7.8	311
32	S-phase feedback control in budding yeast independent of tyrosine phosphorylation of P34cdc28. <i>Nature</i> , 1992, 355, 365-368.	27.8	309
33	Discrete logic modelling as a means to link protein signalling networks with functional analysis of mammalian signal transduction. <i>Molecular Systems Biology</i> , 2009, 5, 331.	7.2	308
34	Logic-Based Models for the Analysis of Cell Signaling Networks. <i>Biochemistry</i> , 2010, 49, 3216-3224.	2.5	306
35	A Noncanonical Frizzled2 Pathway Regulates Epithelial-Mesenchymal Transition and Metastasis. <i>Cell</i> , 2014, 159, 844-856.	28.9	296
36	Discovery of Potent and Selective Covalent Inhibitors of JNK. <i>Chemistry and Biology</i> , 2012, 19, 140-154.	6.0	286

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37	Metrics other than potency reveal systematic variation in responses to cancer drugs. <i>Nature Chemical Biology</i> , 2013, 9, 708-714.	8.0	280
38	LINCS Canvas Browser: interactive web app to query, browse and interrogate LINCS L1000 gene expression signatures. <i>Nucleic Acids Research</i> , 2014, 42, W449-W460.	14.5	280
39	A single-cell landscape of high-grade serous ovarian cancer. <i>Nature Medicine</i> , 2020, 26, 1271-1279.	30.7	267
40	The yeast DASH complex forms closed rings on microtubules. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 138-143.	8.2	258
41	Yeast heat shock factor contains separable transient and sustained response transcriptional activators. <i>Cell</i> , 1990, 62, 793-805.	28.9	256
42	Transient Sister Chromatid Separation and Elastic Deformation of Chromosomes during Mitosis in Budding Yeast. <i>Cell</i> , 2000, 101, 763-775.	28.9	256
43	Hierarchical assembly of the budding yeast kinetochore from multiple subcomplexes. <i>Genes and Development</i> , 2003, 17, 2902-2921.	5.9	256
44	Classic and contemporary approaches to modeling biochemical reactions. <i>Genes and Development</i> , 2010, 24, 1861-1875.	5.9	255
45	The Open Microscopy Environment (OME) Data Model and XML file: open tools for informatics and quantitative analysis in biological imaging. <i>Genome Biology</i> , 2005, 6, R47.	9.6	254
46	Modeling a Snap-Action, Variable-Delay Switch Controlling Extrinsic Cell Death. <i>PLoS Biology</i> , 2008, 6, e299.	5.6	252
47	L1000CDS2: LINCS L1000 characteristic direction signatures search engine. <i>Npj Systems Biology and Applications</i> , 2016, 2, .	3.0	250
48	Informatics and Quantitative Analysis in Biological Imaging. <i>Science</i> , 2003, 300, 100-102.	12.6	249
49	Molecular organization of the Ndc80 complex, an essential kinetochore component. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 5363-5367.	7.1	243
50	Phylogenetic and structural analysis of centromeric DNA and kinetochore proteins. <i>Genome Biology</i> , 2006, 7, R23.	9.6	239
51	Profiling receptor tyrosine kinase activation by using Ab microarrays. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 9330-9335.	7.1	232
52	Molecular Analysis of Kinetochore-Microtubule Attachment in Budding Yeast. <i>Cell</i> , 2001, 106, 195-206.	28.9	231
53	Programming biological models in Python using PySB. <i>Molecular Systems Biology</i> , 2013, 9, 646.	7.2	216
54	Identification of essential components of the <i>S. cerevisiae</i> kinetochore. <i>Cell</i> , 1993, 73, 761-774.	28.9	215

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55	Structure and assembly of turnip crinkle virus. <i>Journal of Molecular Biology</i> , 1986, 191, 639-658.	4.2	203
56	Coupling cell division and cell death to microtubule dynamics. <i>Current Opinion in Cell Biology</i> , 1997, 9, 807-814.	5.4	202
57	Adaptive resistance of melanoma cells to <scp>RAF</scp> inhibition via reversible induction of a slowly dividing deâ€differentiated state. <i>Molecular Systems Biology</i> , 2017, 13, 905.	7.2	202
58	Non-genetic cell-to-cell variability and the consequences for pharmacology. <i>Current Opinion in Chemical Biology</i> , 2009, 13, 556-561.	6.1	200
59	BID Preferentially Activates BAK while BIM Preferentially Activates BAX, Affecting Chemotherapy Response. <i>Molecular Cell</i> , 2013, 51, 751-765.	9.7	200
60	A dual role for Bub1 in the spindle checkpoint and chromosome congression. <i>EMBO Journal</i> , 2005, 24, 1621-1633.	7.8	192
61	Discovering causal pathways linking genomic events to transcriptional states using Tied Diffusion Through Interacting Events (TieDIE). <i>Bioinformatics</i> , 2013, 29, 2757-2764.	4.1	189
62	The Response of Human Epithelial Cells to TNF Involves an Inducible Autocrine Cascade. <i>Cell</i> , 2006, 124, 1225-1239.	28.9	188
63	Genetic Selection of Peptide Inhibitors of Biological Pathways. <i>Science</i> , 1999, 285, 591-595.	12.6	185
64	Structure, Function, and Regulation of Budding Yeast Kinetochores. <i>Annual Review of Cell and Developmental Biology</i> , 2003, 19, 519-539.	9.4	184
65	Vascular Disease and Thrombosis in SARS-CoV-2-Infected Rhesus Macaques. <i>Cell</i> , 2020, 183, 1354-1366.e13.	28.9	184
66	Automatic fluorescent tag detection in 3D with super-resolution: application to the analysis of chromosome movement. <i>Journal of Microscopy</i> , 2002, 208, 49-64.	1.8	183
67	Immunogenomic profiling determines responses to combined PARP and PD-1 inhibition in ovarian cancer. <i>Nature Communications</i> , 2020, 11, 1459.	12.8	176
68	Spindle checkpoint proteins and chromosomeâ€™microtubule attachment in budding yeast. <i>Journal of Cell Biology</i> , 2004, 164, 535-546.	5.2	166
69	The Logic of EGFR/ErbB Signaling: Theoretical Properties and Analysis of High-Throughput Data. <i>PLoS Computational Biology</i> , 2009, 5, e1000438.	3.2	164
70	The glucose-regulated protein grp94 is related to heat shock protein hsp90. <i>Journal of Molecular Biology</i> , 1987, 194, 341-344.	4.2	161
71	Purification and characterization of a heat-shock element binding protein from yeast. <i>EMBO Journal</i> , 1987, 6, 3035-41.	7.8	157
72	Multomics Profiling Establishes the Polypharmacology of FDA-Approved CDK4/6 Inhibitors and the Potential for Differential Clinical Activity. <i>Cell Chemical Biology</i> , 2019, 26, 1067-1080.e8.	5.2	151

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73	Misorientation and reduced stretching of aligned sister kinetochores promote chromosome missegregation in EB1- or APC-depleted cells. <i>EMBO Journal</i> , 2006, 25, 2814-2827.	7.8	150
74	Chromosome segregation and genomic stability. <i>Current Opinion in Genetics and Development</i> , 2004, 14, 120-125.	3.3	149
75	Analysis of Mitosis and Antimitotic Drug Responses in Tumors by <i>In Vivo</i> Microscopy and Single-Cell Pharmacodynamics. <i>Cancer Research</i> , 2011, 71, 4608-4616.	0.9	146
76	Fuzzy Logic Analysis of Kinase Pathway Crosstalk in TNF/EGF/Insulin-Induced Signaling. <i>PLoS Computational Biology</i> , 2009, 5, e1000340.	3.2	145
77	Regulating the Yeast Kinetochore by Ubiquitin-Dependent Degradation and Skp1p-Mediated Phosphorylation. <i>Cell</i> , 1997, 91, 491-500.	28.9	144
78	Cyclic Immunofluorescence (CyclF), A Highly Multiplexed Method for Single-Cell Imaging. <i>Current Protocols in Chemical Biology</i> , 2016, 8, 251-264.	1.7	142
79	From word models to executable models of signaling networks using automated assembly. <i>Molecular Systems Biology</i> , 2017, 13, 954.	7.2	137
80	Regulation of <i>Saccharomyces cerevisiae</i> kinetochores by the type 1 \hat{A} phosphatase Glc7p. <i>Genes and Development</i> , 1999, 13, 545-555.	5.9	135
81	A Compendium of Signals and Responses Triggered by Prodeath and Prosurvival Cytokines. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1569-1590.	3.8	134
82	Comparing Signaling Networks between Normal and Transformed Hepatocytes Using Discrete Logical Models. <i>Cancer Research</i> , 2011, 71, 5400-5411.	0.9	132
83	Fractional killing arises from cell-to-cell variability in overcoming a caspase activity threshold. <i>Molecular Systems Biology</i> , 2015, 11, 803.	7.2	132
84	Analysis of kinesin motor function at budding yeast kinetochores. <i>Journal of Cell Biology</i> , 2006, 172, 861-874.	5.2	127
85	Synergistic drug-cytokine induction of hepatocellular death as an <i>in vitro</i> approach for the study of inflammation-associated idiosyncratic drug hepatotoxicity. <i>Toxicology and Applied Pharmacology</i> , 2009, 237, 317-330.	2.8	127
86	Targeting immunosuppressive macrophages overcomes PARP inhibitor resistance in BRCA1-associated triple-negative breast cancer. <i>Nature Cancer</i> , 2021, 2, 66-82.	13.2	126
87	Machine learning identifies candidates for drug repurposing in Alzheimer's disease. <i>Nature Communications</i> , 2021, 12, 1033.	12.8	124
88	Surviving apoptosis: life-death signaling in single cells. <i>Trends in Cell Biology</i> , 2015, 25, 446-458.	7.9	120
89	Conservation of protein abundance patterns reveals the regulatory architecture of the EGFR-MAPK pathway. <i>Science Signaling</i> , 2016, 9, rs6.	3.6	119
90	Rapid Phospho-Turnover by Receptor Tyrosine Kinases Impacts Downstream Signaling and Drug Binding. <i>Molecular Cell</i> , 2011, 43, 723-737.	9.7	118

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91	Mps1 at kinetochores is essential for female mouse meiosis I. <i>Development (Cambridge)</i> , 2011, 138, 2261-2271.	2.5	114
92	Training Signaling Pathway Maps to Biochemical Data with Constrained Fuzzy Logic: Quantitative Analysis of Liver Cell Responses to Inflammatory Stimuli. <i>PLoS Computational Biology</i> , 2011, 7, e1001099.	3.2	113
93	Image metrics in the statistical analysis of DNA microarray data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 8944-8949.	7.1	111
94	Cue-Signal-Response Analysis of TNF-Induced Apoptosis by Partial Least Squares Regression of Dynamic Multivariate Data. <i>Journal of Computational Biology</i> , 2004, 11, 544-561.	1.6	106
95	Generating chromosome instability through the simultaneous deletion of Mad2 and p53. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 11296-11301.	7.1	106
96	Fundamental trade-offs between information flow in single cells and cellular populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 5755-5760.	7.1	106
97	Changing Mad2 Levels Affects Chromosome Segregation and Spindle Assembly Checkpoint Control in Female Mouse Meiosis I. <i>PLoS ONE</i> , 2007, 2, e1165.	2.5	104
98	Development of a Selective CDK7 Covalent Inhibitor Reveals Predominant Cell-Cycle Phenotype. <i>Cell Chemical Biology</i> , 2019, 26, 792-803.e10.	5.2	103
99	Crowdsourcing Network Inference: The DREAM Predictive Signaling Network Challenge Meeting Information: The DREAM4 Predictive Signaling Network Challenge took place in the summer of 2009. Results were presented at the DREAM4 conference, December 2009, The Broad Institute of MIT and Harvard, Cambridge, Massachusetts.. <i>Science Signaling</i> , 2011, 4, nr7.	3.6	102
100	MCMICRO: a scalable, modular image-processing pipeline for multiplexed tissue imaging. <i>Nature Methods</i> , 2022, 19, 311-315.	19.0	102
101	Concurrent Dexamethasone Limits the Clinical Benefit of Immune Checkpoint Blockade in Glioblastoma. <i>Clinical Cancer Research</i> , 2021, 27, 276-287.	7.0	100
102	Collecting and organizing systematic sets of protein data. <i>Nature Reviews Molecular Cell Biology</i> , 2006, 7, 803-812.	37.0	98
103	The Unstable F-box Protein p58-Ctf13 Forms the Structural Core of the CBF3 Kinetochores Complex. <i>Journal of Cell Biology</i> , 1999, 145, 933-950.	5.2	96
104	A functional genomic screen identifies a role for TAO1 kinase in spindle-checkpoint signalling. <i>Nature Cell Biology</i> , 2007, 9, 556-564.	10.3	95
105	Networks Inferred from Biochemical Data Reveal Profound Differences in Toll-like Receptor and Inflammatory Signaling between Normal and Transformed Hepatocytes. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1849-1865.	3.8	95
106	A Multi-center Study on the Reproducibility of Drug-Response Assays in Mammalian Cell Lines. <i>Cell Systems</i> , 2019, 9, 35-48.e5.	6.2	95
107	Independent Drug Action in Combination Therapy: Implications for Precision Oncology. <i>Cancer Discovery</i> , 2022, 12, 606-624.	9.4	93
108	Qualifying antibodies for image-based immune profiling and multiplexed tissue imaging. <i>Nature Protocols</i> , 2019, 14, 2900-2930.	12.0	92

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109	Structure and Function of Kinetochores in Budding Yeast. Annual Review of Cell and Developmental Biology, 1995, 11, 471-495.	9.4	91
110	Factors required for the binding of reassembled yeast kinetochores to microtubules in vitro.. Journal of Cell Biology, 1994, 127, 995-1008.	5.2	90
111	Profiles of Basal and Stimulated Receptor Signaling Networks Predict Drug Response in Breast Cancer Lines. Science Signaling, 2013, 6, ra84.	3.6	90
112	A High-throughput Quantitative Multiplex Kinase Assay for Monitoring Information Flow in Signaling Networks. Molecular and Cellular Proteomics, 2003, 2, 463-473.	3.8	89
113	Kinome-wide Selectivity Profiling of ATP-competitive Mammalian Target of Rapamycin (mTOR) Inhibitors and Characterization of Their Binding Kinetics. Journal of Biological Chemistry, 2012, 287, 9742-9752.	3.4	89
114	Properties of cell death models calibrated and compared using Bayesian approaches. Molecular Systems Biology, 2013, 9, 644.	7.2	89
115	Retention of the Bub3 checkpoint protein on lagging chromosomes. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 8493-8498.	7.1	88
116	Centromeric Chromatin and Epigenetic Effects in Kinetochores Assembly. Cell, 1998, 93, 313-316.	28.9	87
117	The Spatial Landscape of Progression and Immunoediting in Primary Melanoma at Single-Cell Resolution. Cancer Discovery, 2022, 12, 1518-1541.	9.4	87
118	Structure of a Central Component of the Yeast Kinetochores: The Spc24p/Spc25p Globular Domain. Structure, 2006, 14, 1003-1009.	3.3	86
119	Cell Stimulus and Lysis in a Microfluidic Device with Segmented Gas-Liquid Flow. Analytical Chemistry, 2005, 77, 3629-3636.	6.5	84
120	Cells surviving fractional killing by TRAIL exhibit transient but sustainable resistance and inflammatory phenotypes. Molecular Biology of the Cell, 2013, 24, 2186-2200.	2.1	84
121	Systematic analysis of BRAF ^{V600E} melanomas reveals a role for JNK/c-Jun pathway in adaptive resistance to drug-induced apoptosis. Molecular Systems Biology, 2015, 11, 797.	7.2	84
122	Chromosome instability induced by Mps1 and p53 mutation generates aggressive lymphomas exhibiting aneuploidy-induced stress. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13427-13432.	7.1	82
123	Structural and Functional Dissection of Mif2p, a Conserved DNA-binding Kinetochores Protein. Molecular Biology of the Cell, 2008, 19, 4480-4491.	2.1	80
124	Exploring the Contextual Sensitivity of Factors that Determine Cell-to-Cell Variability in Receptor-Mediated Apoptosis. PLoS Computational Biology, 2012, 8, e1002482.	3.2	79
125	Common and cell-type specific responses to anti-cancer drugs revealed by high throughput transcript profiling. Nature Communications, 2017, 8, 1186.	12.8	78
126	A curative combination cancer therapy achieves high fractional cell killing through low cross-resistance and drug additivity. ELife, 2019, 8, .	6.0	78

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127	The Dark Kinase Knowledgebase: an online compendium of knowledge and experimental results of understudied kinases. <i>Nucleic Acids Research</i> , 2021, 49, D529-D535.	14.5	75
128	Probing the Architecture of a Simple Kinetochore Using DNA-Protein Crosslinking. <i>Journal of Cell Biology</i> , 1997, 139, 1383-1396.	5.2	74
129	Creating and analyzing pathway and protein interaction compendia for modelling signal transduction networks. <i>BMC Systems Biology</i> , 2012, 6, 29.	3.0	71
130	Receptor-Driven ERK Pulses Reconfigure MAPK Signaling and Enable Persistence of Drug-Adapted BRAF-Mutant Melanoma Cells. <i>Cell Systems</i> , 2020, 11, 478-494.e9.	6.2	71
131	The human kinetochore proteins Nnf1R and Mcm21R are required for accurate chromosome segregation. <i>EMBO Journal</i> , 2006, 25, 4033-4049.	7.8	70
132	Profiling phospho-signaling networks in breast cancer using reverse-phase protein arrays. <i>Oncogene</i> , 2013, 32, 3470-3476.	5.9	70
133	Roles for the Conserved Spc105p/Kre28p Complex in Kinetochore-Microtubule Binding and the Spindle Assembly Checkpoint. <i>PLoS ONE</i> , 2009, 4, e7640.	2.5	70
134	Selective USP7 inhibition elicits cancer cell killing through a p53-dependent mechanism. <i>Scientific Reports</i> , 2020, 10, 5324.	3.3	69
135	Discovery and resistance mechanism of a selective CDK12 degrader. <i>Nature Chemical Biology</i> , 2021, 17, 675-683.	8.0	69
136	Alternative drug sensitivity metrics improve preclinical cancer pharmacogenomics. <i>Nature Biotechnology</i> , 2017, 35, 500-502.	17.5	68
137	Development and Characterization of a Wee1 Kinase Degradator. <i>Cell Chemical Biology</i> , 2020, 27, 57-65.e9.	5.2	68
138	Biophysical prediction of protein-peptide interactions and signaling networks using machine learning. <i>Nature Methods</i> , 2020, 17, 175-183.	19.0	68
139	Multiplexed immunofluorescence reveals potential PD-1/PD-L1 pathway vulnerabilities in craniopharyngioma. <i>Neuro-Oncology</i> , 2018, 20, 1101-1112.	1.2	67
140	Evolution of delayed resistance to immunotherapy in a melanoma responder. <i>Nature Medicine</i> , 2021, 27, 985-992.	30.7	67
141	HSF1 phase transition mediates stress adaptation and cell fate decisions. <i>Nature Cell Biology</i> , 2020, 22, 151-158.	10.3	67
142	Microfluidics closes in on point-of-care assays. <i>Nature Biotechnology</i> , 2008, 26, 1345-1346.	17.5	65
143	Adaptive informatics for multifactorial and high-content biological data. <i>Nature Methods</i> , 2011, 8, 487-492.	19.0	65
144	Flexible informatics for linking experimental data to mathematical models via <i>DataRail</i> . <i>Bioinformatics</i> , 2008, 24, 840-847.	4.1	64

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145	GRcalculator: an online tool for calculating and mining dose-response data. BMC Cancer, 2017, 17, 698.	2.6	64
146	Opposing immune and genetic mechanisms shape oncogenic programs in synovial sarcoma. Nature Medicine, 2021, 27, 289-300.	30.7	64
147	Myeloid antigen-presenting cell niches sustain antitumor T cells and license PD-1 blockade via CD28 costimulation. Cancer Cell, 2021, 39, 1623-1642.e20.	16.8	64
148	A reductionist's systems biology Opinion. Current Opinion in Cell Biology, 2005, 17, 9-11.	5.4	63
149	Intra- and Interdimeric Caspase-8 Self-Cleavage Controls Strength and Timing of CD95-Induced Apoptosis. Science Signaling, 2014, 7, ra23.	3.6	63
150	Lyapunov exponents and phase diagrams reveal multifactorial control over TRAIL-induced apoptosis. Molecular Systems Biology, 2011, 7, 553.	7.2	62
151	A multiscale statistical mechanical framework integrates biophysical and genomic data to assemble cancer networks. Nature Genetics, 2014, 46, 1363-1371.	21.4	60
152	Dissecting Variability in Responses to Cancer Chemotherapy Through Systems Pharmacology. Clinical Pharmacology and Therapeutics, 2010, 88, 34-38.	4.7	59
153	Cheminformatics Tools for Analyzing and Designing Optimized Small-Molecule Collections and Libraries. Cell Chemical Biology, 2019, 26, 765-777.e3.	5.2	59
154	Cloning and expression of a gene encoding hsc73, the major hsp70-like protein in unstressed rat cells. EMBO Journal, 1987, 6, 993-8.	7.8	58
155	Yeast Kinetochores Microtubule Dynamics Analyzed by High-Resolution Three-Dimensional Microscopy. Biophysical Journal, 2005, 89, 2835-2854.	0.5	57
156	Direct Lyapunov exponent analysis enables parametric study of transient signalling governing cell behaviour. IET Systems Biology, 2006, 153, 425.	2.0	56
157	Profiling drugs for rheumatoid arthritis that inhibit synovial fibroblast activation. Nature Chemical Biology, 2017, 13, 38-45.	8.0	56
158	Deletion of the MAD2L1 spindle assembly checkpoint gene is tolerated in mouse models of acute T-cell lymphoma and hepatocellular carcinoma. ELife, 2017, 6, .	6.0	56
159	Impaired SHP2-Mediated Extracellular Signal-Regulated Kinase Activation Contributes to Gefitinib Sensitivity of Lung Cancer Cells with Epidermal Growth Factor Receptor-Activating Mutations. Cancer Research, 2010, 70, 3843-3850.	0.9	55
160	Cytokine-associated drug toxicity in human hepatocytes is associated with signaling network dysregulation. Molecular BioSystems, 2010, 6, 1195.	2.9	55
161	Automatic fluorescent tag localization II: improvement in super-resolution by relative tracking. Journal of Microscopy, 2003, 211, 230-248.	1.8	51
162	p31 ^{comet} acts to ensure timely spindle checkpoint silencing subsequent to kinetochore attachment. Molecular Biology of the Cell, 2011, 22, 4236-4246.	2.1	51

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163	Two genes required for the binding of an essential <i>Saccharomyces cerevisiae</i> kinetochore complex to DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 12026-12030.	7.1	50
164	A human breast atlas integrating single-cell proteomics and transcriptomics. <i>Developmental Cell</i> , 2022, 57, 1400-1420.e7.	7.0	50
165	Adaptation of Human iPSC-Derived Cardiomyocytes to Tyrosine Kinase Inhibitors Reduces Acute Cardiotoxicity via Metabolic Reprogramming. <i>Cell Systems</i> , 2019, 8, 412-426.e7.	6.2	49
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