

# Chris Sander

## List of Publications by Year in descending order

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Version: 2024-02-01

331  
papers

162,563  
citations

288

144  
h-index

236

313  
g-index

366  
all docs

366  
docs citations

366  
times ranked

158124  
citing authors

#	ARTICLE	IF	CITATIONS
1	The reactome pathway knowledgebase 2022. <i>Nucleic Acids Research</i> , 2022, 50, D687-D692.	6.5	924
2	Fc $\gamma$ R-mediated SARS-CoV-2 infection of monocytes activates inflammation. <i>Nature</i> , 2022, 606, 576-584.	13.7	314
3	Precision Combination Therapies Based on Recurrent Oncogenic Coalterations. <i>Cancer Discovery</i> , 2022, 12, 1542-1559.	7.7	17
4	CellMiner Cross-Database (CellMinerCDB) version 1.2: Exploration of patient-derived cancer cell line pharmacogenomics. <i>Nucleic Acids Research</i> , 2021, 49, D1083-D1093.	6.5	104
5	CellBox: Interpretable Machine Learning for Perturbation Biology with Application to the Design of Cancer Combination Therapy. <i>Cell Systems</i> , 2021, 12, 128-140.e4.	2.9	67
6	Artificial Intelligence and Early Detection of Pancreatic Cancer. <i>Pancreas</i> , 2021, 50, 251-279.	0.5	71
7	Protein design and variant prediction using autoregressive generative models. <i>Nature Communications</i> , 2021, 12, 2403.	5.8	168
8	PredictProtein - Predicting Protein Structure and Function for 29 Years. <i>Nucleic Acids Research</i> , 2021, 49, W535-W540.	6.5	135
9	A pan-cancer survey of cell line tumor similarity by feature-weighted molecular profiles. <i>Cell Reports Methods</i> , 2021, 1, 100039.	1.4	8
10	Causal interactions from proteomic profiles: Molecular data meet pathway knowledge. <i>Patterns</i> , 2021, 2, 100257.	3.1	44
11	Molecular response to PARP1 inhibition in ovarian cancer cells as determined by mass spectrometry based proteomics. <i>Journal of Ovarian Research</i> , 2021, 14, 140.	1.3	8
12	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. <i>Molecular Systems Biology</i> , 2021, 17, e10387.	3.2	53
13	Disulfiram use is associated with lower risk of COVID-19: A retrospective cohort study. <i>PLoS ONE</i> , 2021, 16, e0259061.	1.1	32
14	A flexible search system for high-accuracy identification of biological entities and molecules. <i>Journal of Open Source Software</i> , 2021, 6, 3756.	2.0	1
15	Analyzing causal relationships in proteomic profiles using CausalPath. <i>STAR Protocols</i> , 2021, 2, 100955.	0.5	7
16	Author-sourced capture of pathway knowledge in computable form using Biofactoid. <i>ELife</i> , 2021, 10, .	2.8	11
17	Pathway Commons 2019 Update: integration, analysis and exploration of pathway data. <i>Nucleic Acids Research</i> , 2020, 48, D489-D497.	6.5	161
18	Protein Structure from Experimental Evolution. <i>Cell Systems</i> , 2020, 10, 15-24.e5.	2.9	39

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19	Perturbation biology links temporal protein changes to drug responses in a melanoma cell line. PLoS Computational Biology, 2020, 16, e1007909.	1.5	15
20	Diabetes, Weight Change, and Pancreatic Cancer Risk. JAMA Oncology, 2020, 6, e202948.	3.4	72
21	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. Nature, 2020, 578, 102-111.	13.7	424
22	AlignmentViewer: Sequence Analysis of Large Protein Families. F1000Research, 2020, 9, 213.	0.8	5
23	AlignmentViewer: Sequence Analysis of Large Protein Families. F1000Research, 2020, 9, 213.	0.8	7
24	netboxr: Automated discovery of biological process modules by network analysis in R. PLoS ONE, 2020, 15, e0234669.	1.1	2
25	Perturbation biology links temporal protein changes to drug responses in a melanoma cell line. , 2020, 16, e1007909.		0
26	Perturbation biology links temporal protein changes to drug responses in a melanoma cell line. , 2020, 16, e1007909.		0
27	Perturbation biology links temporal protein changes to drug responses in a melanoma cell line. , 2020, 16, e1007909.		0
28	Perturbation biology links temporal protein changes to drug responses in a melanoma cell line. , 2020, 16, e1007909.		0
29	netboxr: Automated discovery of biological process modules by network analysis in R. , 2020, 15, e0234669.		0
30	netboxr: Automated discovery of biological process modules by network analysis in R. , 2020, 15, e0234669.		0
31	netboxr: Automated discovery of biological process modules by network analysis in R. , 2020, 15, e0234669.		0
32	netboxr: Automated discovery of biological process modules by network analysis in R. , 2020, 15, e0234669.		0
33	Cancer-associated mutations in DICER1 RNase IIIa and IIIb domains exert similar effects on miRNA biogenesis. Nature Communications, 2019, 10, 3682.	5.8	48
34	Protein structure prediction assisted with sparse NMR data in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1315-1332.	1.5	21
35	Inferring protein 3D structure from deep mutation scans. Nature Genetics, 2019, 51, 1170-1176.	9.4	124
36	LLGL2 rescues nutrient stress by promoting leucine uptake in ER+ breast cancer. Nature, 2019, 569, 275-279.	13.7	99

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37	Quantitative Proteome Landscape of the NCI-60 Cancer Cell Lines. <i>IScience</i> , 2019, 21, 664-680.	1.9	52
38	Combining Evolutionary Covariance and NMR Data for Protein Structure Determination. <i>Methods in Enzymology</i> , 2019, 614, 363-392.	0.4	8
39	The Evcouplings Python framework for coevolutionary sequence analysis. <i>Bioinformatics</i> , 2019, 35, 1582-1584.	1.8	180
40	Abnormal oxidative metabolism in a quiet genomic background underlies clear cell papillary renal cell carcinoma. <i>ELife</i> , 2019, 8, .	2.8	31
41	Sequencing of prostate cancers identifies new cancer genes, routes of progression and drug targets. <i>Nature Genetics</i> , 2018, 50, 682-692.	9.4	182
42	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018, 173, 371-385.e18.	13.5	1,670
43	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. <i>Cell</i> , 2018, 173, 291-304.e6.	13.5	1,718
44	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018, 173, 321-337.e10.	13.5	2,111
45	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , 2018, 23, 282-296.e4.	2.9	333
46	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , 2018, 23, 227-238.e3.	2.9	407
47	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. <i>Cell Reports</i> , 2018, 23, 297-312.e12.	2.9	205
48	The Immune Landscape of Cancer. <i>Immunity</i> , 2018, 48, 812-830.e14.	6.6	3,706
49	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 172-180.e3.	2.9	119
50	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. <i>Cell Reports</i> , 2018, 23, 213-226.e3.	2.9	83
51	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 239-254.e6.	2.9	801
52	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. <i>Cell Reports</i> , 2018, 23, 255-269.e4.	2.9	204
53	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , 2018, 23, 270-281.e3.	2.9	177
54	A Landscape of Metabolic Variation across Tumor Types. <i>Cell Systems</i> , 2018, 6, 301-313.e3.	2.9	123

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55	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 2018, 6, 271-281.e7.	2.9	605
56	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. <i>Cell Systems</i> , 2018, 6, 282-300.e2.	2.9	284
57	lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. <i>Cancer Cell</i> , 2018, 33, 706-720.e9.	7.7	400
58	A Hybrid Approach for Protein Structure Determination Combining Sparse NMR with Evolutionary Coupling Sequence Data. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1105, 153-169.	0.8	7
59	CellMinerCDB for Integrative Cross-Database Genomics and Pharmacogenomics Analyses of Cancer Cell Lines. <i>IScience</i> , 2018, 10, 247-264.	1.9	117
60	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018, 34, 211-224.e6.	7.7	623
61	Systems pharmacology using mass spectrometry identifies critical response nodes in prostate cancer. <i>Npj Systems Biology and Applications</i> , 2018, 4, 26.	1.4	13
62	Computer-guided design of optimal microbial consortia for immune system modulation. <i>ELife</i> , 2018, 7, .	2.8	65
63	3D clusters of somatic mutations in cancer reveal numerous rare mutations as functional targets. <i>Genome Medicine</i> , 2017, 9, 4.	3.6	170
64	Mutation effects predicted from sequence co-variation. <i>Nature Biotechnology</i> , 2017, 35, 128-135.	9.4	543
65	Analysis of renal cancer cell lines from two major resources enables genomics-guided cell line selection. <i>Nature Communications</i> , 2017, 8, 15165.	5.8	61
66	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017, 169, 1327-1341.e23.	13.5	1,794
67	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017, 171, 950-965.e28.	13.5	738
68	CTD2 Dashboard: a searchable web interface to connect validated results from the Cancer Target Discovery and Development Network. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	23
69	Mitochondrial respiratory gene expression is suppressed in many cancers. <i>ELife</i> , 2017, 6, .	2.8	102
70	Mitochondrial DNA copy number variation across human cancers. <i>ELife</i> , 2016, 5, .	2.8	384
71	A Multi-Method Approach for Proteomic Network Inference in 11 Human Cancers. <i>PLoS Computational Biology</i> , 2016, 12, e1004765.	1.5	32
72	3D RNA and Functional Interactions from Evolutionary Couplings. <i>Cell</i> , 2016, 165, 963-975.	13.5	152

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73	Integrin- $\beta$ 10 Dependency Identifies RAC and RICTOR as Therapeutic Targets in High-Grade Myxofibrosarcoma. <i>Cancer Discovery</i> , 2016, 6, 1148-1165.	7.7	62
74	Structured States of Disordered Proteins from Genomic Sequences. <i>Cell</i> , 2016, 167, 158-170.e12.	13.5	127
75	Human SRMATlas: A Resource of Targeted Assays to Quantify the Complete Human Proteome. <i>Cell</i> , 2016, 166, 766-778.	13.5	295
76	Tumor immune microenvironment characterization in clear cell renal cell carcinoma identifies prognostic and immunotherapeutically relevant messenger RNA signatures. <i>Genome Biology</i> , 2016, 17, 231.	3.8	746
77	Multilevel Genomics-Based Taxonomy of Renal Cell Carcinoma. <i>Cell Reports</i> , 2016, 14, 2476-2489.	2.9	298
78	MutationAligner: a resource of recurrent mutation hotspots in protein domains in cancer. <i>Nucleic Acids Research</i> , 2016, 44, D986-D991.	6.5	21
79	rCellMiner: exploring molecular profiles and drug response of the NCI-60 cell lines in R. <i>Bioinformatics</i> , 2016, 32, 1272-1274.	1.8	39
80	An Integrated Metabolic Atlas of Clear Cell Renal Cell Carcinoma. <i>Cancer Cell</i> , 2016, 29, 104-116.	7.7	531
81	PaxtoolsR: pathway analysis in R using Pathway Commons. <i>Bioinformatics</i> , 2016, 32, 1262-1264.	1.8	43
82	Genomic and transcriptomic hallmarks of poorly differentiated and anaplastic thyroid cancers. <i>Journal of Clinical Investigation</i> , 2016, 126, 1052-1066.	3.9	874
83	GENO-15 IDENTIFICATION AND GENOMIC ANALYSIS OF HYPER-MUTATED AND ULTRA-MUTATED GBMS. <i>Neuro-Oncology</i> , 2015, 17, v94.3-v94.	0.6	0
84	TCEB1-mutated renal cell carcinoma: a distinct genomic and morphological subtype. <i>Modern Pathology</i> , 2015, 28, 845-853.	2.9	127
85	Alterations of DNA repair genes in the NCI-60 cell lines and their predictive value for anticancer drug activity. <i>DNA Repair</i> , 2015, 28, 107-115.	1.3	55
86	Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , 2015, 161, 1681-1696.	13.5	2,562
87	Extensive Decoupling of Metabolic Genes in Cancer. <i>PLoS Computational Biology</i> , 2015, 11, e1004176.	1.5	29
88	Pathway and network analysis of cancer genomes. <i>Nature Methods</i> , 2015, 12, 615-621.	9.0	297
89	Protein structure determination by combining sparse NMR data with evolutionary couplings. <i>Nature Methods</i> , 2015, 12, 751-754.	9.0	75
90	All-atom 3D structure prediction of transmembrane $\beta$ -barrel proteins from sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5413-5418.	3.3	53

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91	Systematic identification of cancer driving signaling pathways based on mutual exclusivity of genomic alterations. <i>Genome Biology</i> , 2015, 16, 45.	3.8	145
92	Mutational landscape determines sensitivity to PD-1 blockade in nonâ€“small cell lung cancer. <i>Science</i> , 2015, 348, 124-128.	6.0	6,756
93	Identifying Actionable Targets through Integrative Analyses of GEM Model and Human Prostate Cancer Genomic Profiling. <i>Molecular Cancer Therapeutics</i> , 2015, 14, 278-288.	1.9	29
94	Somatic <i>POLE</i> mutations cause an ultramutated giant cell high-grade glioma subtype with better prognosis. <i>Neuro-Oncology</i> , 2015, 17, 1356-1364.	0.6	94
95	Applications of targeted proteomics in systems biology and translational medicine. <i>Proteomics</i> , 2015, 15, 3193-3208.	1.3	182
96	The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , 2015, 163, 1011-1025.	13.5	2,435
97	Pan-Cancer Analysis of Mutation Hotspots in Protein Domains. <i>Cell Systems</i> , 2015, 1, 197-209.	2.9	94
98	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , 2015, 163, 506-519.	13.5	1,485
99	Precision microbiome reconstitution restores bile acid mediated resistance to <i>Clostridium difficile</i> . <i>Nature</i> , 2015, 517, 205-208.	13.7	1,506
100	Inferring Pairwise Interactions from Biological Data Using Maximum-Entropy Probability Models. <i>PLoS Computational Biology</i> , 2015, 11, e1004182.	1.5	97
101	Perturbation biology nominates upstreamâ€“downstream drug combinations in RAF inhibitor resistant melanoma cells. <i>ELife</i> , 2015, 4, .	2.8	95
102	Spatial Normalization of Reverse Phase Protein Array Data. <i>PLoS ONE</i> , 2014, 9, e97213.	1.1	23
103	Prediction of individualized therapeutic vulnerabilities in cancer from genomic profiles. <i>Bioinformatics</i> , 2014, 30, 2051-2059.	1.8	30
104	Frequent disruption of the RB pathway in indolent follicular lymphoma suggests a new combination therapy. <i>Journal of Experimental Medicine</i> , 2014, 211, 1379-1391.	4.2	32
105	Copy number alteration burden predicts prostate cancer relapse. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 11139-11144.	3.3	299
106	PconsFold: improved contact predictions improve protein models. <i>Bioinformatics</i> , 2014, 30, i482-i488.	1.8	92
107	PredictProteinâ€“an open resource for online prediction of protein structural and functional features. <i>Nucleic Acids Research</i> , 2014, 42, W337-W343.	6.5	589
108	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. <i>Cell</i> , 2014, 159, 676-690.	13.5	2,318

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109	Pattern search in BioPAX models. <i>Bioinformatics</i> , 2014, 30, 139-140.	1.8	45
110	Exonuclease mutations in DNA polymerase epsilon reveal replication strand specific mutation patterns and human origins of replication. <i>Genome Research</i> , 2014, 24, 1740-1750.	2.4	244
111	Integrating biological pathways and genomic profiles with ChiBE 2. <i>BMC Genomics</i> , 2014, 15, 642.	1.2	24
112	Genome-wide analysis of noncoding regulatory mutations in cancer. <i>Nature Genetics</i> , 2014, 46, 1160-1165.	9.4	469
113	Collection, integration and analysis of cancer genomic profiles: from data to insight. <i>Current Opinion in Genetics and Development</i> , 2014, 24, 92-98.	1.5	22
114	Sequence co-evolution gives 3D contacts and structures of protein complexes. <i>ELife</i> , 2014, 3, .	2.8	452
115	Evaluating cell lines as tumour models by comparison of genomic profiles. <i>Nature Communications</i> , 2013, 4, 2126.	5.8	1,108
116	Computational approaches to identify functional genetic variants in cancer genomes. <i>Nature Methods</i> , 2013, 10, 723-729.	9.0	161
117	Analysis of microRNA-target interactions across diverse cancer types. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1325-1332.	3.6	184
118	The Somatic Genomic Landscape of Glioblastoma. <i>Cell</i> , 2013, 155, 462-477.	13.5	3,979
119	Prevalence and Co-Occurrence of Actionable Genomic Alterations in High-Grade Bladder Cancer. <i>Journal of Clinical Oncology</i> , 2013, 31, 3133-3140.	0.8	282
120	The Cancer Genome Atlas Pan-Cancer analysis project. <i>Nature Genetics</i> , 2013, 45, 1113-1120.	9.4	6,265
121	Emerging landscape of oncogenic signatures across human cancers. <i>Nature Genetics</i> , 2013, 45, 1127-1133.	9.4	1,190
122	Pattern discovery and cancer gene identification in integrated cancer genomic data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 4245-4250.	3.3	361
123	SQSTM1 Is a Pathogenic Target of 5q Copy Number Gains in Kidney Cancer. <i>Cancer Cell</i> , 2013, 24, 738-750.	7.7	135
124	Using MEMo to Discover Mutual Exclusivity Modules in Cancer. <i>Current Protocols in Bioinformatics</i> , 2013, 41, Unit 8.17.	25.8	29
125	Integrative Analysis of Complex Cancer Genomics and Clinical Profiles Using the cBioPortal. <i>Science Signaling</i> , 2013, 6, p1.	1.6	11,344
126	The mutational landscape of adenoid cystic carcinoma. <i>Nature Genetics</i> , 2013, 45, 791-798.	9.4	394



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127	The BioPAX Validator. <i>Bioinformatics</i> , 2013, 29, 2659-2660.	1.8	9
128	Using Biological Pathway Data with Paxtools. <i>PLoS Computational Biology</i> , 2013, 9, e1003194.	1.5	57
129	Perturbation Biology: Inferring Signaling Networks in Cellular Systems. <i>PLoS Computational Biology</i> , 2013, 9, e1003290.	1.5	128
130	Drug Synergy Screen and Network Modeling in Dedifferentiated Liposarcoma Identifies CDK4 and IGF1R as Synergistic Drug Targets. <i>Science Signaling</i> , 2013, 6, ra85.	1.6	97
131	Ecological Modeling from Time-Series Inference: Insight into Dynamics and Stability of Intestinal Microbiota. <i>PLoS Computational Biology</i> , 2013, 9, e1003388.	1.5	487
132	PiHelper: an open source framework for drug-target and antibody-target data. <i>Bioinformatics</i> , 2013, 29, 2071-2072.	1.8	13
133	Adverse Outcomes in Clear Cell Renal Cell Carcinoma with Mutations of 3p21 Epigenetic Regulators <i>BAP1</i> and <i>SETD2</i> : A Report by MSKCC and the KIRC TCGA Research Network. <i>Clinical Cancer Research</i> , 2013, 19, 3259-3267.	3.2	301
134	Distinct Patterns of Dysregulated Expression of Enzymes Involved in Androgen Synthesis and Metabolism in Metastatic Prostate Cancer Tumors. <i>Cancer Research</i> , 2012, 72, 6142-6152.	0.4	175
135	Genomic Complexity and AKT Dependence in Serous Ovarian Cancer. <i>Cancer Discovery</i> , 2012, 2, 56-67.	7.7	109
136	Mutual exclusivity analysis identifies oncogenic network modules. <i>Genome Research</i> , 2012, 22, 398-406.	2.4	597
137	Protein structure prediction from sequence variation. <i>Nature Biotechnology</i> , 2012, 30, 1072-1080.	9.4	569
138	The cBio Cancer Genomics Portal: An Open Platform for Exploring Multidimensional Cancer Genomics Data. <i>Cancer Discovery</i> , 2012, 2, 401-404.	7.7	12,801
139	Genome Sequencing Identifies a Basis for Everolimus Sensitivity. <i>Science</i> , 2012, 338, 221-221.	6.0	681
140	A Role for Neuronal piRNAs in the Epigenetic Control of Memory-Related Synaptic Plasticity. <i>Cell</i> , 2012, 149, 693-707.	13.5	474
141	Three-Dimensional Structures of Membrane Proteins from Genomic Sequencing. <i>Cell</i> , 2012, 149, 1607-1621.	13.5	478
142	miR-34a Repression in Proneural Malignant Gliomas Upregulates Expression of Its Target PDGFRA and Promotes Tumorigenesis. <i>PLoS ONE</i> , 2012, 7, e33844.	1.1	106
143	Integrated Analyses of microRNAs Demonstrate Their Widespread Influence on Gene Expression in High-Grade Serous Ovarian Carcinoma. <i>PLoS ONE</i> , 2012, 7, e34546.	1.1	104
144	Integrative Subtype Discovery in Glioblastoma Using iCluster. <i>PLoS ONE</i> , 2012, 7, e35236.	1.1	196

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145	Network modeling of the transcriptional effects of copy number aberrations in glioblastoma. <i>Molecular Systems Biology</i> , 2011, 7, 486.	3.2	80
146	The nuclear deubiquitinase BAP1 is commonly inactivated by somatic mutations and 3p21.1 losses in malignant pleural mesothelioma. <i>Nature Genetics</i> , 2011, 43, 668-672.	9.4	617
147	Genome-wide identification of microRNA targets in human ES cells reveals a role for miR-302 in modulating BMP response. <i>Genes and Development</i> , 2011, 25, 2173-2186.	2.7	175
148	Time to Recurrence and Survival in Serous Ovarian Tumors Predicted from Integrated Genomic Profiles. <i>PLoS ONE</i> , 2011, 6, e24709.	1.1	88
149	Identification of PHLPP1 as a Tumor Suppressor Reveals the Role of Feedback Activation in PTEN-Mutant Prostate Cancer Progression. <i>Cancer Cell</i> , 2011, 20, 173-186.	7.7	158
150	Small RNA Sequencing and Functional Characterization Reveals MicroRNA-143 Tumor Suppressor Activity in Liposarcoma. <i>Cancer Research</i> , 2011, 71, 5659-5669.	0.4	106
151	Frequent Alterations and Epigenetic Silencing of Differentiation Pathway Genes in Structurally Rearranged Liposarcomas. <i>Cancer Discovery</i> , 2011, 1, 587-597.	7.7	108
152	Off-target effects dominate a large-scale RNAi screen for modulators of the TGF- $\beta$ 2 pathway and reveal microRNA regulation of TGFBR2. <i>Silence: A Journal of RNA Regulation</i> , 2011, 2, 3.	8.0	78
153	Direct-coupling analysis of residue coevolution captures native contacts across many protein families. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E1293-301.	3.3	1,231
154	Superoxide dismutase 1 (SOD1) is a target for a small molecule identified in a screen for inhibitors of the growth of lung adenocarcinoma cell lines. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 16375-16380.	3.3	124
155	Predicting the functional impact of protein mutations: application to cancer genomics. <i>Nucleic Acids Research</i> , 2011, 39, e118-e118.	6.5	1,622
156	Pathway Commons, a web resource for biological pathway data. <i>Nucleic Acids Research</i> , 2011, 39, D685-D690.	6.5	980
157	A series of PDB related databases for everyday needs. <i>Nucleic Acids Research</i> , 2011, 39, D411-D419.	6.5	837
158	MYC Cooperates with AKT in Prostate Tumorigenesis and Alters Sensitivity to mTOR Inhibitors. <i>PLoS ONE</i> , 2011, 6, e17449.	1.1	77
159	Protein 3D Structure Computed from Evolutionary Sequence Variation. <i>PLoS ONE</i> , 2011, 6, e28766.	1.1	975
160	Integrative Genomic Profiling of Human Prostate Cancer. <i>Cancer Cell</i> , 2010, 18, 11-22.	7.7	3,151
161	International network of cancer genome projects. <i>Nature</i> , 2010, 464, 993-998.	13.7	2,114
162	The BioPAX community standard for pathway data sharing. <i>Nature Biotechnology</i> , 2010, 28, 935-942.	9.4	613

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163	Somatic mutations of the Parkinson's disease-associated gene PARK2 in glioblastoma and other human malignancies. <i>Nature Genetics</i> , 2010, 42, 77-82.	9.4	336
164	Subtype-specific genomic alterations define new targets for soft-tissue sarcoma therapy. <i>Nature Genetics</i> , 2010, 42, 715-721.	9.4	642
165	Automated Network Analysis Identifies Core Pathways in Glioblastoma. <i>PLoS ONE</i> , 2010, 5, e8918.	1.1	318
166	ZIC1 Overexpression Is Oncogenic in Liposarcoma. <i>Cancer Research</i> , 2010, 70, 6891-6901.	0.4	41
167	mRNA turnover rate limits siRNA and microRNA efficacy. <i>Molecular Systems Biology</i> , 2010, 6, 454.	3.2	14
168	Discovering modulators of gene expression. <i>Nucleic Acids Research</i> , 2010, 38, 5648-5656.	6.5	34
169	ChiBE: interactive visualization and manipulation of BioPAX pathway models. <i>Bioinformatics</i> , 2010, 26, 429-431.	1.8	46
170	mRNA turnover rate limits siRNA and microRNA efficacy. <i>Molecular Systems Biology</i> , 2010, 6, 433.	3.2	94
171	Target mRNA abundance dilutes microRNA and siRNA activity. <i>Molecular Systems Biology</i> , 2010, 6, 363.	3.2	299
172	Comprehensive modeling of microRNA targets predicts functional non-conserved and non-canonical sites. <i>Genome Biology</i> , 2010, 11, R90.	13.9	1,478
173	NetPath: a public resource of curated signal transduction pathways. <i>Genome Biology</i> , 2010, 11, R3.	13.9	456
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