

Chris Sander

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.

340
papers

120,352
citations

136
h-index

346
g-index

366
ext. papers

145,412
ext. citations

15
avg, IF

7.96
L-index

#	Paper	IF	Citations
340	FcR-mediated SARS-CoV-2 infection of monocytes activates inflammation.. <i>Nature</i> , 2022 ,	50.4	20
339	A flexible search system for high-accuracy identification of biological entities and molecules. <i>Journal of Open Source Software</i> , 2021 , 6, 3756	5.2	0
338	Analyzing causal relationships in proteomic profiles using CausalPath. <i>STAR Protocols</i> , 2021 , 2, 100955	1.4	1
337	The reactome pathway knowledgebase 2022. <i>Nucleic Acids Research</i> , 2021 ,	20.1	57
336	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	5.5	0
335	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. <i>Molecular Systems Biology</i> , 2021 , 17, e10387	12.2	9
334	Disulfiram use is associated with lower risk of COVID-19: A retrospective cohort study. <i>PLoS ONE</i> , 2021 , 16, e0259061	3.7	8
333	Artificial Intelligence and Early Detection of Pancreatic Cancer: 2020 Summative Review. <i>Pancreas</i> , 2021 , 50, 251-279	2.6	12
332	Protein design and variant prediction using autoregressive generative models. <i>Nature Communications</i> , 2021 , 12, 2403	17.4	38
331	PredictProtein - Predicting Protein Structure and Function for 29 Years. <i>Nucleic Acids Research</i> , 2021 , 49, W535-W540	20.1	31
330	A pan-cancer survey of cell line tumor similarity by feature-weighted molecular profiles.. <i>Cell Reports Methods</i> , 2021 , 1, 100039		1
329	Causal interactions from proteomic profiles: Molecular data meet pathway knowledge. <i>Patterns</i> , 2021 , 2, 100257	5.1	13
328	CellMiner Cross-Database (CellMinerCDB) version 1.2: Exploration of patient-derived cancer cell line pharmacogenomics. <i>Nucleic Acids Research</i> , 2021 , 49, D1083-D1093	20.1	23
327	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	10.6	18
326	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020 , 578, 102-111	50.4	220
325	Pathway Commons 2019 Update: integration, analysis and exploration of pathway data. <i>Nucleic Acids Research</i> , 2020 , 48, D489-D497	20.1	71
324	AlignmentViewer: Sequence Analysis of Large Protein Families. <i>F1000Research</i> , 2020 , 9,	3.6	3

323	AlignmentViewer: Sequence Analysis of Large Protein Families. <i>F1000Research</i> , 2020 , 9, 213	3.6	4
322	netboxr: Automated discovery of biological process modules by network analysis in R. <i>PLoS ONE</i> , 2020 , 15, e0234669	3.7	1
321	Protein Structure from Experimental Evolution. <i>Cell Systems</i> , 2020 , 10, 15-24.e5	10.6	14
320	Perturbation biology links temporal protein changes to drug responses in a melanoma cell line. <i>PLoS Computational Biology</i> , 2020 , 16, e1007909	5	5
319	Diabetes, Weight Change, and Pancreatic Cancer Risk. <i>JAMA Oncology</i> , 2020 , 6, e202948	13.4	21
318	Perturbation biology links temporal protein changes to drug responses in a melanoma cell line 2020 , 16, e1007909		
317	Perturbation biology links temporal protein changes to drug responses in a melanoma cell line 2020 , 16, e1007909		
316	Perturbation biology links temporal protein changes to drug responses in a melanoma cell line 2020 , 16, e1007909		
315	Perturbation biology links temporal protein changes to drug responses in a melanoma cell line 2020 , 16, e1007909		
314	netboxr: Automated discovery of biological process modules by network analysis in R 2020 , 15, e0234669		
313	netboxr: Automated discovery of biological process modules by network analysis in R 2020 , 15, e0234669		
312	netboxr: Automated discovery of biological process modules by network analysis in R 2020 , 15, e0234669		
311	netboxr: Automated discovery of biological process modules by network analysis in R 2020 , 15, e0234669		
310	Inferring protein 3D structure from deep mutation scans. <i>Nature Genetics</i> , 2019 , 51, 1170-1176	36.3	66
309	LLGL2 rescues nutrient stress by promoting leucine uptake in ER breast cancer. <i>Nature</i> , 2019 , 569, 275-280.	30.4	58
308	Cancer-associated mutations in DICER1 RNase IIIa and IIIb domains exert similar effects on miRNA biogenesis. <i>Nature Communications</i> , 2019 , 10, 3682	17.4	23
307	Protein structure prediction assisted with sparse NMR data in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019 , 87, 1315-1332	4.2	9
306	Abnormal oxidative metabolism in a quiet genomic background underlies clear cell papillary renal cell carcinoma. <i>ELife</i> , 2019 , 8,	8.9	17

305	Quantitative Proteome Landscape of the NCI-60 Cancer Cell Lines. <i>Science</i> , 2019 , 21, 664-680	6.1	21
304	Combining Evolutionary Covariance and NMR Data for Protein Structure Determination. <i>Methods in Enzymology</i> , 2019 , 614, 363-392	1.7	5
303	The EVcouplings Python framework for coevolutionary sequence analysis. <i>Bioinformatics</i> , 2019 , 35, 1582-1584	6.1	61
302	Sequencing of prostate cancers identifies new cancer genes, routes of progression and drug targets. <i>Nature Genetics</i> , 2018 , 50, 682-692	36.3	112
301	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018 , 173, 371-385.e18	56.2	854
300	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	56.2	888
299	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018 , 173, 321-337.e10	56.2	1124
298	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , 2018 , 23, 282-296.e4	10.6	188
297	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , 2018 , 23, 227-238.e3	10.6	235
296	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	10.6	147
295	The Immune Landscape of Cancer. <i>Immunity</i> , 2018 , 48, 812-830.e14	32.3	1754
294	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , 2018 , 23, 172-180.e3	10.6	66
293	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. <i>Cell Reports</i> , 2018 , 23, 213-226.e3	26.6	56
292	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , 2018 , 23, 239-254.e6	10.6	405
291	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. <i>Cell Reports</i> , 2018 , 23, 255-269.e4	10.6	112
290	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , 2018 , 23, 270-281.e3	10.6	121
289	A Landscape of Metabolic Variation across Tumor Types. <i>Cell Systems</i> , 2018 , 6, 301-313.e3	10.6	73
288	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 2018 , 6, 271-281.e7	10.6	320

287	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	10.6	159
286	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	24.3	275
285	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018 , 34, 211-224.e6	24.3	327
284	Systems pharmacology using mass spectrometry identifies critical response nodes in prostate cancer. <i>Npj Systems Biology and Applications</i> , 2018 , 4, 26	5	7
283	Computer-guided design of optimal microbial consortia for immune system modulation. <i>ELife</i> , 2018 , 7,	8.9	44
282	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	3.6	6
281	CellMinerCDB for Integrative Cross-Database Genomics and Pharmacogenomics Analyses of Cancer Cell Lines. <i>IScience</i> , 2018 , 10, 247-264	6.1	78
280	3D clusters of somatic mutations in cancer reveal numerous rare mutations as functional targets. <i>Genome Medicine</i> , 2017 , 9, 4	14.4	117
279	Mutation effects predicted from sequence co-variation. <i>Nature Biotechnology</i> , 2017 , 35, 128-135	44.5	273
278	Analysis of renal cancer cell lines from two major resources enables genomics-guided cell line selection. <i>Nature Communications</i> , 2017 , 8, 15165	17.4	40
277	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017 , 169, 1327-1341.e23	56.2	1125
276	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,	5	12
275	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017 , 171, 950-965.e28	56.2	451
274	Mitochondrial respiratory gene expression is suppressed in many cancers. <i>ELife</i> , 2017 , 6,	8.9	64
273	Integrin-10 Dependency Identifies RAC and RICTOR as Therapeutic Targets in High-Grade Myxofibrosarcoma. <i>Cancer Discovery</i> , 2016 , 6, 1148-1165	24.4	40
272	Structured States of Disordered Proteins from Genomic Sequences. <i>Cell</i> , 2016 , 167, 158-170.e12	56.2	90
271	Human SRMATlas: A Resource of Targeted Assays to Quantify the Complete Human Proteome. <i>Cell</i> , 2016 , 166, 766-778	56.2	236
270	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	18.3	391

269	Multilevel Genomics-Based Taxonomy of Renal Cell Carcinoma. <i>Cell Reports</i> , 2016 , 14, 2476-89	10.6	228
268	MutationAligner: a resource of recurrent mutation hotspots in protein domains in cancer. <i>Nucleic Acids Research</i> , 2016 , 44, D986-91	20.1	11
267	rCellMiner: exploring molecular profiles and drug response of the NCI-60 cell lines in R. <i>Bioinformatics</i> , 2016 , 32, 1272-4	7.2	30
266	An Integrated Metabolic Atlas of Clear Cell Renal Cell Carcinoma. <i>Cancer Cell</i> , 2016 , 29, 104-116	24.3	335
265	PaxtoolsR: pathway analysis in R using Pathway Commons. <i>Bioinformatics</i> , 2016 , 32, 1262-4	7.2	17
264	Genomic and transcriptomic hallmarks of poorly differentiated and anaplastic thyroid cancers. <i>Journal of Clinical Investigation</i> , 2016 , 126, 1052-66	15.9	576
263	Mitochondrial DNA copy number variation across human cancers. <i>ELife</i> , 2016 , 5,	8.9	255
262	A Multi-Method Approach for Proteomic Network Inference in 11 Human Cancers. <i>PLoS Computational Biology</i> , 2016 , 12, e1004765	5	23
261	3D RNA and Functional Interactions from Evolutionary Couplings. <i>Cell</i> , 2016 , 165, 963-75	56.2	108
260	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, 107-15	4.3	44
259	Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , 2015 , 161, 1681-96	56.2	1807
258	Extensive decoupling of metabolic genes in cancer. <i>PLoS Computational Biology</i> , 2015 , 11, e1004176	5	22
257	Pathway and network analysis of cancer genomes. <i>Nature Methods</i> , 2015 , 12, 615-621	21.6	235
256	Protein structure determination by combining sparse NMR data with evolutionary couplings. <i>Nature Methods</i> , 2015 , 12, 751-4	21.6	56
255	All-atom 3D structure prediction of transmembrane β -barrel proteins from sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 5413-8	11.5	44
254	Systematic identification of cancer driving signaling pathways based on mutual exclusivity of genomic alterations. <i>Genome Biology</i> , 2015 , 16, 45	18.3	101
253	Cancer immunology. Mutational landscape determines sensitivity to PD-1 blockade in non-small cell lung cancer. <i>Science</i> , 2015 , 348, 124-8	33.3	5003
252	Identifying actionable targets through integrative analyses of GEM model and human prostate cancer genomic profiling. <i>Molecular Cancer Therapeutics</i> , 2015 , 14, 278-88	6.1	24

251	Somatic POLE mutations cause an ultramutated giant cell high-grade glioma subtype with better prognosis. <i>Neuro-Oncology</i> , 2015 , 17, 1356-64	1	76
250	Applications of targeted proteomics in systems biology and translational medicine. <i>Proteomics</i> , 2015 , 15, 3193-208	4.8	134
249	The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , 2015 , 163, 1011-25	56.2	1713
248	Pan-Cancer Analysis of Mutation Hotspots in Protein Domains. <i>Cell Systems</i> , 2015 , 1, 197-209	10.6	72
247	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , 2015 , 163, 506-19	56.2	1055
246	Precision microbiome reconstitution restores bile acid mediated resistance to <i>Clostridium difficile</i> . <i>Nature</i> , 2015 , 517, 205-8	50.4	1064
245	GENO-15 IDENTIFICATION AND GENOMIC ANALYSIS OF HYPER-MUTATED AND ULTRA-MUTATED GBMS. <i>Neuro-Oncology</i> , 2015 , 17, v94.3-v94	1	78
244	TCEB1-mutated renal cell carcinoma: a distinct genomic and morphological subtype. <i>Modern Pathology</i> , 2015 , 28, 845-853	9.8	76
243	Inferring Pairwise Interactions from Biological Data Using Maximum-Entropy Probability Models. <i>PLoS Computational Biology</i> , 2015 , 11, e1004182	5	59
242	Perturbation biology nominates upstream-downstream drug combinations in RAF inhibitor resistant melanoma cells. <i>ELife</i> , 2015 , 4,	8.9	65
241	Exonuclease mutations in DNA polymerase epsilon reveal replication strand specific mutation patterns and human origins of replication. <i>Genome Research</i> , 2014 , 24, 1740-50	9.7	187
240	Integrating biological pathways and genomic profiles with ChiBE 2. <i>BMC Genomics</i> , 2014 , 15, 642	4.5	21
239	Genome-wide analysis of noncoding regulatory mutations in cancer. <i>Nature Genetics</i> , 2014 , 46, 1160-5	36.3	367
238	Collection, integration and analysis of cancer genomic profiles: from data to insight. <i>Current Opinion in Genetics and Development</i> , 2014 , 24, 92-8	4.9	17
237	Spatial normalization of reverse phase protein array data. <i>PLoS ONE</i> , 2014 , 9, e97213	3.7	18
236	Prediction of individualized therapeutic vulnerabilities in cancer from genomic profiles. <i>Bioinformatics</i> , 2014 , 30, 2051-9	7.2	28
235	Frequent disruption of the RB pathway in indolent follicular lymphoma suggests a new combination therapy. <i>Journal of Experimental Medicine</i> , 2014 , 211, 1379-91	16.6	26
234	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, 11139-44	11.5	218

233	PconsFold: improved contact predictions improve protein models. <i>Bioinformatics</i> , 2014 , 30, i482-8	7.2	76
232	PredictProtein--an open resource for online prediction of protein structural and functional features. <i>Nucleic Acids Research</i> , 2014 , 42, W337-43	20.1	433
231	Integrated genomic characterization of papillary thyroid carcinoma. <i>Cell</i> , 2014 , 159, 676-90	56.2	1660
230	Pattern search in BioPAX models. <i>Bioinformatics</i> , 2014 , 30, 139-40	7.2	36
229	Sequence co-evolution gives 3D contacts and structures of protein complexes. <i>ELife</i> , 2014 , 3,	8.9	324
228	Author response: Sequence co-evolution gives 3D contacts and structures of protein complexes 2014 ,		2
227	Evaluating cell lines as tumour models by comparison of genomic profiles. <i>Nature Communications</i> , 2013 , 4, 2126	17.4	831
226	Computational approaches to identify functional genetic variants in cancer genomes. <i>Nature Methods</i> , 2013 , 10, 723-9	21.6	129
225	Analysis of microRNA-target interactions across diverse cancer types. <i>Nature Structural and Molecular Biology</i> , 2013 , 20, 1325-32	17.6	153
224	The somatic genomic landscape of glioblastoma. <i>Cell</i> , 2013 , 155, 462-77	56.2	2900
223	Prevalence and co-occurrence of actionable genomic alterations in high-grade bladder cancer. <i>Journal of Clinical Oncology</i> , 2013 , 31, 3133-40	2.2	226
222	The Cancer Genome Atlas Pan-Cancer analysis project. <i>Nature Genetics</i> , 2013 , 45, 1113-20	36.3	3933
221	Emerging landscape of oncogenic signatures across human cancers. <i>Nature Genetics</i> , 2013 , 45, 1127-33	36.3	889
220	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, 4245-50	11.5	250
219	SQSTM1 is a pathogenic target of 5q copy number gains in kidney cancer. <i>Cancer Cell</i> , 2013 , 24, 738-50	24.3	111
218	Using MEMo to discover mutual exclusivity modules in cancer. <i>Current Protocols in Bioinformatics</i> , 2013 , Chapter 8, Unit 8.17	24.2	26
217	Integrative analysis of complex cancer genomics and clinical profiles using the cBioPortal. <i>Science Signaling</i> , 2013 , 6, pl1	8.8	7715
216	The mutational landscape of adenoid cystic carcinoma. <i>Nature Genetics</i> , 2013 , 45, 791-8	36.3	311

215	The BioPAX Validator. <i>Bioinformatics</i> , 2013 , 29, 2659-60	7.2	4
214	Using biological pathway data with paxtools. <i>PLoS Computational Biology</i> , 2013 , 9, e1003194	5	47
213	Perturbation biology: inferring signaling networks in cellular systems. <i>PLoS Computational Biology</i> , 2013 , 9, e1003290	5	98
212	Drug synergy screen and network modeling in dedifferentiated liposarcoma identifies CDK4 and IGF1R as synergistic drug targets. <i>Science Signaling</i> , 2013 , 6, ra85	8.8	61
211	Ecological modeling from time-series inference: insight into dynamics and stability of intestinal microbiota. <i>PLoS Computational Biology</i> , 2013 , 9, e1003388	5	329
210	PiHelper: an open source framework for drug-target and antibody-target data. <i>Bioinformatics</i> , 2013 , 29, 2071-2	7.2	10
209	Adverse outcomes in clear cell renal cell carcinoma with mutations of 3p21 epigenetic regulators BAP1 and SETD2: a report by MSKCC and the KIRC TCGA research network. <i>Clinical Cancer Research</i> , 2013 , 19, 3259-67	12.9	233
208	Protein structure prediction from sequence variation. <i>Nature Biotechnology</i> , 2012 , 30, 1072-80	44.5	432
207	The cBio cancer genomics portal: an open platform for exploring multidimensional cancer genomics data. <i>Cancer Discovery</i> , 2012 , 2, 401-4	24.4	8578
206	Genome sequencing identifies a basis for everolimus sensitivity. <i>Science</i> , 2012 , 338, 221	33.3	546
205	A role for neuronal piRNAs in the epigenetic control of memory-related synaptic plasticity. <i>Cell</i> , 2012 , 149, 693-707	56.2	399
204	Three-dimensional structures of membrane proteins from genomic sequencing. <i>Cell</i> , 2012 , 149, 1607-21	56.2	395
203	miR-34a repression in proneural malignant gliomas upregulates expression of its target PDGFRA and promotes tumorigenesis. <i>PLoS ONE</i> , 2012 , 7, e33844	3.7	90
202	Integrated analyses of microRNAs demonstrate their widespread influence on gene expression in high-grade serous ovarian carcinoma. <i>PLoS ONE</i> , 2012 , 7, e34546	3.7	94
201	Distinct patterns of dysregulated expression of enzymes involved in androgen synthesis and metabolism in metastatic prostate cancer tumors. <i>Cancer Research</i> , 2012 , 72, 6142-52	10.1	152
200	Genomic complexity and AKT dependence in serous ovarian cancer. <i>Cancer Discovery</i> , 2012 , 2, 56-67	24.4	89
199	Mutual exclusivity analysis identifies oncogenic network modules. <i>Genome Research</i> , 2012 , 22, 398-406	9.7	452
198	Integrative subtype discovery in glioblastoma using iCluster. <i>PLoS ONE</i> , 2012 , 7, e35236	3.7	140

197	The nuclear deubiquitinase BAP1 is commonly inactivated by somatic mutations and 3p21.1 losses in malignant pleural mesothelioma. <i>Nature Genetics</i> , 2011 , 43, 668-72	36.3	512
196	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, 2173-86	12.6	143
195	Time to recurrence and survival in serous ovarian tumors predicted from integrated genomic profiles. <i>PLoS ONE</i> , 2011 , 6, e24709	3.7	72
194	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, 173-86	24.3	131
193	Small RNA sequencing and functional characterization reveals MicroRNA-143 tumor suppressor activity in liposarcoma. <i>Cancer Research</i> , 2011 , 71, 5659-69	10.1	92
192	Frequent alterations and epigenetic silencing of differentiation pathway genes in structurally rearranged liposarcomas. <i>Cancer Discovery</i> , 2011 , 1, 587-97	24.4	88
191	Off-target effects dominate a large-scale RNAi screen for modulators of the TGF- β pathway and reveal microRNA regulation of TGFBR2. <i>Silence: A Journal of RNA Regulation</i> , 2011 , 2, 3		67
190	Network modeling of the transcriptional effects of copy number aberrations in glioblastoma. <i>Molecular Systems Biology</i> , 2011 , 7, 486	12.2	67
189	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	11.5	837
188	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, 16375-80	11.5	89
187	Predicting the functional impact of protein mutations: application to cancer genomics. <i>Nucleic Acids Research</i> , 2011 , 39, e118	20.1	1237
186	Pathway Commons, a web resource for biological pathway data. <i>Nucleic Acids Research</i> , 2011 , 39, D685-90	20.1	786
185	A series of PDB related databases for everyday needs. <i>Nucleic Acids Research</i> , 2011 , 39, D411-9	20.1	487
184	MYC cooperates with AKT in prostate tumorigenesis and alters sensitivity to mTOR inhibitors. <i>PLoS ONE</i> , 2011 , 6, e17449	3.7	68
183	Protein 3D structure computed from evolutionary sequence variation. <i>PLoS ONE</i> , 2011 , 6, e28766	3.7	709
182	International network of cancer genome projects. <i>Nature</i> , 2010 , 464, 993-8	50.4	1613
181	The BioPAX community standard for pathway data sharing. <i>Nature Biotechnology</i> , 2010 , 28, 935-42	44.5	499
180	Somatic mutations of the Parkinson disease-associated gene PARK2 in glioblastoma and other human malignancies. <i>Nature Genetics</i> , 2010 , 42, 77-82	36.3	280

179	Subtype-specific genomic alterations define new targets for soft-tissue sarcoma therapy. <i>Nature Genetics</i> , 2010 , 42, 715-21	36.3	521
178	Automated network analysis identifies core pathways in glioblastoma. <i>PLoS ONE</i> , 2010 , 5, e8918	3.7	268
177	ZIC1 overexpression is oncogenic in liposarcoma. <i>Cancer Research</i> , 2010 , 70, 6891-901	10.1	34
176	mRNA turnover rate limits siRNA and microRNA efficacy. <i>Molecular Systems Biology</i> , 2010 , 6, 454	12.2	11
175	Discovering modulators of gene expression. <i>Nucleic Acids Research</i> , 2010 , 38, 5648-56	20.1	26
174	ChiBE: interactive visualization and manipulation of BioPAX pathway models. <i>Bioinformatics</i> , 2010 , 26, 429-31	7.2	37
173	mRNA turnover rate limits siRNA and microRNA efficacy. <i>Molecular Systems Biology</i> , 2010 , 6, 433	12.2	78
172	Target mRNA abundance dilutes microRNA and siRNA activity. <i>Molecular Systems Biology</i> , 2010 , 6, 363	12.2	264
171	Comprehensive modeling of microRNA targets predicts functional non-conserved and non-canonical sites. <i>Genome Biology</i> , 2010 , 11, R90	18.3	1143
170	NetPath: a public resource of curated signal transduction pathways. <i>Genome Biology</i> , 2010 , 11, R3	18.3	331
169	Integrative genomic profiling of human prostate cancer. <i>Cancer Cell</i> , 2010 , 18, 11-22	24.3	2666
168	(V600E)BRAF is associated with disabled feedback inhibition of RAF-MEK signaling and elevated transcriptional output of the pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 4519-24	11.5	444
167	The tyrosine phosphatase PTPRD is a tumor suppressor that is frequently inactivated and mutated in glioblastoma and other human cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 9435-40	11.5	196
166	DGCR8-dependent microRNA biogenesis is essential for skin development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 498-502	11.5	190
165	Genetic dissection of the miR-17~92 cluster of microRNAs in Myc-induced B-cell lymphomas. <i>Genes and Development</i> , 2009 , 23, 2806-11	12.6	379
164	Transfection of small RNAs globally perturbs gene regulation by endogenous microRNAs. <i>Nature Biotechnology</i> , 2009 , 27, 549-55	44.5	393
163	The Systems Biology Graphical Notation. <i>Nature Biotechnology</i> , 2009 , 27, 735-41	44.5	651
162	Cooperativity of TMPRSS2-ERG with PI3-kinase pathway activation in prostate oncogenesis. <i>Nature Genetics</i> , 2009 , 41, 524-6	36.3	386

161	Characterization of small RNAs in <i>Aplysia</i> reveals a role for miR-124 in constraining synaptic plasticity through CREB. <i>Neuron</i> , 2009 , 63, 803-17	13.9	320
160	Predicting cancer involvement of genes from heterogeneous data. <i>BMC Bioinformatics</i> , 2008 , 9, 172	3.6	56
159	Introducing meta-services for biomedical information extraction. <i>Genome Biology</i> , 2008 , 9 Suppl 2, S6	18.3	49
158	A specificity map for the PDZ domain family. <i>PLoS Biology</i> , 2008 , 6, e239	9.7	348
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7	Adaptive response to BET inhibition induces therapeutic vulnerability to MCL1 inhibitors in breast cancer		1
6	Protein Design and Variant Prediction Using Autoregressive Generative Models		17
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