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List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

8,260
citations

201674

27
h-index

243625

44
g-index

58
all docs

58
docs citations

58
times ranked

15524
citing authors

#	ARTICLE	IF	CITATIONS
1	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018, 173, 321-337.e10.	28.9	2,111
2	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018, 173, 371-385.e18.	28.9	1,670
3	The Systems Biology Graphical Notation. <i>Nature Biotechnology</i> , 2009, 27, 735-741.	17.5	828
4	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.	8.8	746
5	The BioPAX community standard for pathway data sharing. <i>Nature Biotechnology</i> , 2010, 28, 935-942.	17.5	613
6	An Integrated Metabolic Atlas of Clear Cell Renal Cell Carcinoma. <i>Cancer Cell</i> , 2016, 29, 104-116.	16.8	531
7	Pathway Commons 2019 Update: integration, analysis and exploration of pathway data. <i>Nucleic Acids Research</i> , 2020, 48, D489-D497.	14.5	161
8	A Landscape of Metabolic Variation across Tumor Types. <i>Cell Systems</i> , 2018, 6, 301-313.e3.	6.2	123
9	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 172-180.e3.	6.4	119
10	CellMinerCDB for Integrative Cross-Database Genomics and Pharmacogenomics Analyses of Cancer Cell Lines. <i>IScience</i> , 2018, 10, 247-264.	4.1	117
11	CellMiner Cross-Database (CellMinerCDB) version 1.2: Exploration of patient-derived cancer cell line pharmacogenomics. <i>Nucleic Acids Research</i> , 2021, 49, D1083-D1093.	14.5	104
12	LLGL2 rescues nutrient stress by promoting leucine uptake in ER+ breast cancer. <i>Nature</i> , 2019, 569, 275-279.	27.8	99
13	Evidence of statistical epistasis between DISC1, CIT and NDEL1 impacting risk for schizophrenia: biological validation with functional neuroimaging. <i>Human Genetics</i> , 2010, 127, 441-452.	3.8	93
14	SCLC-CellMiner: A Resource for Small Cell Lung Cancer Cell Line Genomics and Pharmacology Based on Genomic Signatures. <i>Cell Reports</i> , 2020, 33, 108296.	6.4	86
15	Software support for SBGN maps: SBGN-ML and LibSBGN. <i>Bioinformatics</i> , 2012, 28, 2016-2021.	4.1	74
16	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.	6.2	67
17	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.	2.8	55
18	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. <i>Molecular Systems Biology</i> , 2021, 17, e10387.	7.2	53

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19	Quantitative Proteome Landscape of the NCI-60 Cancer Cell Lines. <i>IScience</i> , 2019, 21, 664-680.	4.1	52
20	The NCI-60 Methylome and Its Integration into CellMiner. <i>Cancer Research</i> , 2017, 77, 601-612.	0.9	48
21	Causal interactions from proteomic profiles: Molecular data meet pathway knowledge. <i>Patterns</i> , 2021, 2, 100257.	5.9	44
22	PaxtoolsR: pathway analysis in R using Pathway Commons. <i>Bioinformatics</i> , 2016, 32, 1262-1264.	4.1	43
23	Systems Biology Graphical Notation: Process Description language Level 1 Version 2.0. <i>Journal of Integrative Bioinformatics</i> , 2019, 16, .	1.5	43
24	The digital revolution in phenotyping. <i>Briefings in Bioinformatics</i> , 2016, 17, 819-830.	6.5	41
25	rCellMiner: exploring molecular profiles and drug response of the NCI-60 cell lines in R. <i>Bioinformatics</i> , 2016, 32, 1272-1274.	4.1	39
26	Systems Biology Graphical Notation: Activity Flow language Level 1 Version 1.2. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 340-381.	1.5	35
27	Communicating Structure and Function in Synthetic Biology Diagrams. <i>ACS Synthetic Biology</i> , 2019, 8, 1818-1825.	3.8	30
28	Gene Expression Profiles of the NCI-60 Human Tumor Cell Lines Define Molecular Interaction Networks Governing Cell Migration Processes. <i>PLoS ONE</i> , 2012, 7, e35716.	2.5	28
29	Using drug response data to identify molecular effectors, and molecular "omic" data to identify candidate drugs in cancer. <i>Human Genetics</i> , 2015, 134, 3-11.	3.8	27
30	Synthetic Biology Open Language Visual (SBOL Visual) Version 2.0. <i>Journal of Integrative Bioinformatics</i> , 2018, 15, .	1.5	21
31	Systems biology graphical notation markup language (SBGNML) version 0.3. <i>Journal of Integrative Bioinformatics</i> , 2020, 17, .	1.5	21
32	Predicted Role of NAD Utilization in the Control of Circadian Rhythms during DNA Damage Response. <i>PLoS Computational Biology</i> , 2015, 11, e1004144.	3.2	15
33	An Evaluation of Power and Type I Error of Single-Nucleotide Polymorphism Transmission/Disequilibrium-Based Statistical Methods under Different Family Structures, Missing Parental Data, and Population Stratification. <i>American Journal of Human Genetics</i> , 2007, 80, 178-185.	6.2	13
34	Author-sourced capture of pathway knowledge in computable form using Biofactoid. <i>ELife</i> , 2021, 10, .	6.0	11
35	Synthetic Biology Open Language Visual (SBOL Visual) Version 2.1. <i>Journal of Integrative Bioinformatics</i> , 2019, 16, .	1.5	8
36	A pan-cancer survey of cell line tumor similarity by feature-weighted molecular profiles. <i>Cell Reports Methods</i> , 2021, 1, 100039.	2.9	8

#	ARTICLE	IF	CITATIONS
37	AlignmentViewer: Sequence Analysis of Large Protein Families. F1000Research, 2020, 9, 213.	1.6	7
38	Synthetic biology open language visual (SBOL visual) version 2.2. Journal of Integrative Bioinformatics, 2020, 17, .	1.5	7
39	Analyzing causal relationships in proteomic profiles using CausalPath. STAR Protocols, 2021, 2, 100955.	1.2	7
40	Synthetic biology open language visual (SBOL Visual) version 2.3. Journal of Integrative Bioinformatics, 2021, 18, .	1.5	6
41	AlignmentViewer: Sequence Analysis of Large Protein Families. F1000Research, 2020, 9, 213.	1.6	5
42	netboxr: Automated discovery of biological process modules by network analysis in R. PLoS ONE, 2020, 15, e0234669.	2.5	2
43	netboxr: Automated discovery of biological process modules by network analysis in R. , 2020, 15, e0234669.		0
44	netboxr: Automated discovery of biological process modules by network analysis in R. , 2020, 15, e0234669.		0
45	netboxr: Automated discovery of biological process modules by network analysis in R. , 2020, 15, e0234669.		0
46	netboxr: Automated discovery of biological process modules by network analysis in R. , 2020, 15, e0234669.		0
47	Exploring causal relationships in proteomic profiles in Cytoscape using the CausalPath App. F1000Research, 0, 11, 458.	1.6	0