

Ozgun Babur

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

4,334
citations

304743

22
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345221

36
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46
all docs

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docs citations

46
times ranked

7866
citing authors

#	ARTICLE	IF	CITATIONS
1	PPM1D mutations are oncogenic drivers of de novo diffuse midline glioma formation. <i>Nature Communications</i> , 2022, 13, 604.	12.8	22
2	Newt: a comprehensive web-based tool for viewing, constructing and analyzing biological maps. <i>Bioinformatics</i> , 2021, 37, 1475-1477.	4.1	24
3	Causal interactions from proteomic profiles: Molecular data meet pathway knowledge. <i>Patterns</i> , 2021, 2, 100257.	5.9	44
4	The AML microenvironment catalyzes a stepwise evolution to gilteritinib resistance. <i>Cancer Cell</i> , 2021, 39, 999-1014.e8.	16.8	62
5	A proteogenomic portrait of lung squamous cell carcinoma. <i>Cell</i> , 2021, 184, 4348-4371.e40.	28.9	170
6	A highly multiplexed quantitative phosphosite assay for biology and preclinical studies. <i>Molecular Systems Biology</i> , 2021, 17, e10156.	7.2	12
7	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. <i>Molecular Systems Biology</i> , 2021, 17, e10387.	7.2	53
8	Analyzing causal relationships in proteomic profiles using CausalPath. <i>STAR Protocols</i> , 2021, 2, 100955.	1.2	7
9	Author-sourced capture of pathway knowledge in computable form using Biofactoid. <i>ELife</i> , 2021, 10, .	6.0	11
10	Pathway Commons 2019 Update: integration, analysis and exploration of pathway data. <i>Nucleic Acids Research</i> , 2020, 48, D489-D497.	14.5	161
11	Phosphoproteomic quantitation and causal analysis reveal pathways in GPVI/ITAM-mediated platelet activation programs. <i>Blood</i> , 2020, 136, 2346-2358.	1.4	53
12	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
13	Integrated Analysis of TP53 Gene and Pathway Alterations in The Cancer Genome Atlas. <i>Cell Reports</i> , 2019, 28, 1370-1384.e5.	6.4	382
14	Identification, Quantification, and System Analysis of Protein N-epsilon Lysine Methylation in Anucleate Blood Platelets. <i>Proteomics</i> , 2019, 19, e1900001.	2.2	7
15	Large-scale automated machine reading discovers new cancer-driving mechanisms. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	40
16	Platelet procoagulant phenotype is modulated by a p38-MK2 axis that regulates RTN4/Nogo proximal to the endoplasmic reticulum: utility of pathway analysis. <i>American Journal of Physiology - Cell Physiology</i> , 2018, 314, C603-C615.	4.6	18
17	Assessment of roles for the Rho-specific guanine nucleotide dissociation inhibitor Ly-GDI in platelet function: a spatial systems approach. <i>American Journal of Physiology - Cell Physiology</i> , 2017, 312, C527-C536.	4.6	21
18	PathwayMapper: a collaborative visual web editor for cancer pathways and genomic data. <i>Bioinformatics</i> , 2017, 33, 2238-2240.	4.1	50

#	ARTICLE	IF	CITATIONS
19	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017, 32, 204-220.e15.	16.8	642
20	PaxtoolsR: pathway analysis in R using Pathway Commons. <i>Bioinformatics</i> , 2016, 32, 1262-1264.	4.1	43
21	Systematic identification of cancer driving signaling pathways based on mutual exclusivity of genomic alterations. <i>Genome Biology</i> , 2015, 16, 45.	8.8	145
22	SBGNViz: A Tool for Visualization and Complexity Management of SBGN Process Description Maps. <i>PLoS ONE</i> , 2015, 10, e0128985.	2.5	26
23	Perturbation biology nominates upstreamâ€“downstream drug combinations in RAF inhibitor resistant melanoma cells. <i>ELife</i> , 2015, 4, .	6.0	95
24	Prediction of individualized therapeutic vulnerabilities in cancer from genomic profiles. <i>Bioinformatics</i> , 2014, 30, 2051-2059.	4.1	30
25	Pattern search in BioPAX models. <i>Bioinformatics</i> , 2014, 30, 139-140.	4.1	45
26	Integrating biological pathways and genomic profiles with ChiBE 2. <i>BMC Genomics</i> , 2014, 15, 642.	2.8	24
27	Using Biological Pathway Data with Paxtools. <i>PLoS Computational Biology</i> , 2013, 9, e1003194.	3.2	57
28	Pathway Commons, a web resource for biological pathway data. <i>Nucleic Acids Research</i> , 2011, 39, D685-D690.	14.5	980
29	The BioPAX community standard for pathway data sharing. <i>Nature Biotechnology</i> , 2010, 28, 935-942.	17.5	613
30	Discovering modulators of gene expression. <i>Nucleic Acids Research</i> , 2010, 38, 5648-5656.	14.5	34
31	ChiBE: interactive visualization and manipulation of BioPAX pathway models. <i>Bioinformatics</i> , 2010, 26, 429-431.	4.1	46
32	Algorithms for effective querying of compound graph-based pathway databases. <i>BMC Bioinformatics</i> , 2009, 10, 376.	2.6	25
33	PATIKAmad: Putting microarray data into pathway context. <i>Proteomics</i> , 2008, 8, 2196-2198.	2.2	8
34	Exploring causal relationships in proteomic profiles in Cytoscape using the CausalPath App. <i>F1000Research</i> , 0, 11, 458.	1.6	0