Ozgun Babur

List of Publications by Year
in descending order

34 papers	4,334 citations	304743 22 h-index	345221 36 g-index
46 all docs	46 docs citations	46 times ranked	7866 citing authors

#	Article	IF	Citations
1	Pathway Commons, a web resource for biological pathway data. Nucleic Acids Research, 2011, 39, D685-D690.	14.5	980
2	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. Cancer Cell, 2017, 32, 204-220.e15.	16.8	642
3	The BioPAX community standard for pathway data sharing. Nature Biotechnology, 2010, 28, 935-942.	17.5	613
4	Integrated Analysis of TP53 Gene and Pathway Alterations in The Cancer Genome Atlas. Cell Reports, 2019, 28, 1370-1384.e5.	6.4	382
5	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. Cell, 2020, 181, 236-249.	28.9	334
6	A proteogenomic portrait of lung squamous cell carcinoma. Cell, 2021, 184, 4348-4371.e40.	28.9	170
7	Pathway Commons 2019 Update: integration, analysis and exploration of pathway data. Nucleic Acids Research, 2020, 48, D489-D497.	14.5	161
8	Systematic identification of cancer driving signaling pathways based on mutual exclusivity of genomic alterations. Genome Biology, 2015, 16, 45.	8.8	145
9	Perturbation biology nominates upstream–downstream drug combinations in RAF inhibitor resistant melanoma cells. ELife, 2015, 4, .	6.0	95
10	The AML microenvironment catalyzes a stepwise evolution to gilteritinib resistance. Cancer Cell, 2021, 39, 999-1014.e8.	16.8	62
11	Using Biological Pathway Data with Paxtools. PLoS Computational Biology, 2013, 9, e1003194.	3.2	57
12	Phosphoproteomic quantitation and causal analysis reveal pathways in GPVI/ITAM-mediated platelet activation programs. Blood, 2020, 136, 2346-2358.	1.4	53
13	COVID19 Disease Map, a computational knowledge repository of virus–host interaction mechanisms. Molecular Systems Biology, 2021, 17, e10387.	7.2	53
14	PathwayMapper: a collaborative visual web editor for cancer pathways and genomic data. Bioinformatics, 2017, 33, 2238-2240.	4.1	50
15	ChiBE: interactive visualization and manipulation of BioPAX pathway models. Bioinformatics, 2010, 26, 429-431.	4.1	46
16	Pattern search in BioPAX models. Bioinformatics, 2014, 30, 139-140.	4.1	45
17	Causal interactions from proteomic profiles: Molecular data meet pathway knowledge. Patterns, 2021, 2, 100257.	5.9	44
18	PaxtoolsR: pathway analysis in R using Pathway Commons. Bioinformatics, 2016, 32, 1262-1264.	4.1	43

#	Article	IF	Citations
19	Large-scale automated machine reading discovers new cancer-driving mechanisms. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	40
20	Discovering modulators of gene expression. Nucleic Acids Research, 2010, 38, 5648-5656.	14.5	34
21	Prediction of individualized therapeutic vulnerabilities in cancer from genomic profiles. Bioinformatics, 2014, 30, 2051-2059.	4.1	30
22	SBGNViz: A Tool for Visualization and Complexity Management of SBGN Process Description Maps. PLoS ONE, 2015, 10, e0128985.	2.5	26
23	Algorithms for effective querying of compound graph-based pathway databases. BMC Bioinformatics, 2009, 10, 376.	2.6	25
24	Integrating biological pathways and genomic profiles with ChiBE 2. BMC Genomics, 2014, 15, 642.	2.8	24
25	Newt: a comprehensive web-based tool for viewing, constructing and analyzing biological maps. Bioinformatics, 2021, 37, 1475-1477.	4.1	24
26	PPM1D mutations are oncogenic drivers of de novo diffuse midline glioma formation. Nature Communications, 2022, 13, 604.	12.8	22
27	Assessment of roles for the Rho-specific guanine nucleotide dissociation inhibitor Ly-GDI in platelet function: a spatial systems approach. American Journal of Physiology - Cell Physiology, 2017, 312, C527-C536.	4.6	21
28	Platelet procoagulant phenotype is modulated by a p38-MK2 axis that regulates RTN4/Nogo proximal to the endoplasmic reticulum: utility of pathway analysis. American Journal of Physiology - Cell Physiology, 2018, 314, C603-C615.	4.6	18
29	A highly multiplexed quantitative phosphosite assay for biology and preclinical studies. Molecular Systems Biology, 2021, 17, e10156.	7.2	12
30	Author-sourced capture of pathway knowledge in computable form using Biofactoid. ELife, 2021, 10, .	6.0	11
31	PATIKAmad: Putting microarray data into pathway context. Proteomics, 2008, 8, 2196-2198.	2.2	8
32	Identification, Quantification, and System Analysis of Protein Nâ€¦µ Lysine Methylation in Anucleate Blood Platelets. Proteomics, 2019, 19, e1900001.	2.2	7
33	Analyzing causal relationships in proteomic profiles using CausalPath. STAR Protocols, 2021, 2, 100955.	1.2	7
34	Exploring causal relationships in proteomic profiles in Cytoscape using the CausalPath App. F1000Research, 0, 11, 458.	1.6	0