Emek Demir

List of Publications by Year
in descending order

58 papers	6,787 citations	147566 31 h-index	133063 59 g-index
78 all docs	78 docs citations	78 times ranked	9494 citing authors

#	Article	IF	Citations
1	Pathway Commons, a web resource for biological pathway data. Nucleic Acids Research, 2011, 39, D685-D690.	6.5	980
2	The reactome pathway knowledgebase 2022. Nucleic Acids Research, 2022, 50, D687-D692.	6.5	924
3	The Systems Biology Graphical Notation. Nature Biotechnology, 2009, 27, 735-741.	9.4	828
4	The BioPAX community standard for pathway data sharing. Nature Biotechnology, 2010, 28, 935-942.	9.4	613
5	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. Cell, 2020, 181, 236-249.	13.5	334
6	Automated Network Analysis Identifies Core Pathways in Glioblastoma. PLoS ONE, 2010, 5, e8918.	1.1	318
7	Proteogenomic Characterization of Endometrial Carcinoma. Cell, 2020, 180, 729-748.e26.	13.5	296
8	Human SRMAtlas: A Resource of Targeted Assays to Quantify the Complete Human Proteome. Cell, 2016, 166, 766-778.	13.5	295
9	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110.	3.2	178
10	Pathway Commons 2019 Update: integration, analysis and exploration of pathway data. Nucleic Acids Research, 2020, 48, D489-D497.	6.5	161
11	Systematic identification of cancer driving signaling pathways based on mutual exclusivity of genomic alterations. Genome Biology, 2015, 16, 45.	3.8	145
12	An expanded universe of cancer targets. Cell, 2021, 184, 1142-1155.	13.5	135
13	COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms. Scientific Data, 2020, 7, 136.	2.4	99
14	Perturbation biology nominates upstream–downstream drug combinations in RAF inhibitor resistant melanoma cells. ELife, 2015, 4, .	2.8	95
15	A layout algorithm for undirected compound graphs. Information Sciences, 2009, 179, 980-994.	4.0	74
16	Software support for SBGN maps: SBGN-ML and LibSBGN. Bioinformatics, 2012, 28, 2016-2021.	1.8	74
17	Promoting Coordinated Development of Community-Based Information Standards for Modeling in Biology: The COMBINE Initiative. Frontiers in Bioengineering and Biotechnology, 2015, 3, 19.	2.0	72
18	2D MXenes with antiviral and immunomodulatory properties: A pilot study against SARS-CoV-2. Nano Today, 2021, 38, 101136.	6.2	63

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19	The AML microenvironment catalyzes a stepwise evolution to gilteritinib resistance. Cancer Cell, 2021, 39, 999-1014.e8.	7.7	62
20	Using Biological Pathway Data with Paxtools. PLoS Computational Biology, 2013, 9, e1003194.	1.5	57
21	Phosphoproteomic quantitation and causal analysis reveal pathways in GPVI/ITAM-mediated platelet activation programs. Blood, 2020, 136, 2346-2358.	0.6	53
22	COVID19 Disease Map, a computational knowledge repository of virus–host interaction mechanisms. Molecular Systems Biology, 2021, 17, e10387.	3.2	53
23	Cancer-associated mutations in DICER1 RNase IIIa and IIIb domains exert similar effects on miRNA biogenesis. Nature Communications, 2019, 10, 3682.	5.8	48
24	Crosstalk between Signaling Pathways Provided by Single and Multiple Protein Phosphorylation Sites. Journal of Molecular Biology, 2015, 427, 511-520.	2.0	47
25	ChiBE: interactive visualization and manipulation of BioPAX pathway models. Bioinformatics, 2010, 26, 429-431.	1.8	46
26	Pattern search in BioPAX models. Bioinformatics, 2014, 30, 139-140.	1.8	45
27	Causal interactions from proteomic profiles: Molecular data meet pathway knowledge. Patterns, 2021, 2, 100257.	3.1	44
28	PaxtoolsR: pathway analysis in R using Pathway Commons. Bioinformatics, 2016, 32, 1262-1264.	1.8	43
29	Systems Biology Graphical Notation: Process Description language Level 1 Version 2.0. Journal of Integrative Bioinformatics, 2019, 16, .	1.0	43
30	Ribavirin shows antiviral activity against SARS-CoV-2 and downregulates the activity of TMPRSS2 and the expression of ACE2 in vitro. Canadian Journal of Physiology and Pharmacology, 2021, 99, 449-460.	0.7	41
31	Large-scale automated machine reading discovers new cancer-driving mechanisms. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	40
32	Systems Biology Graphical Notation: Activity Flow language Level 1 Version 1.2. Journal of Integrative Bioinformatics, 2015, 12, 340-381.	1.0	35
33	Discovering modulators of gene expression. Nucleic Acids Research, 2010, 38, 5648-5656.	6.5	34
34	Prediction of individualized therapeutic vulnerabilities in cancer from genomic profiles. Bioinformatics, 2014, 30, 2051-2059.	1.8	30
35	SBGNViz: A Tool for Visualization and Complexity Management of SBGN Process Description Maps. PLoS ONE, 2015, 10, e0128985.	1.1	26
36	Algorithms for effective querying of compound graph-based pathway databases. BMC Bioinformatics, 2009, 10, 376.	1.2	25

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37	Integrating biological pathways and genomic profiles with ChiBE 2. BMC Genomics, 2014, 15, 642.	1.2	24
38	Newt: a comprehensive web-based tool for viewing, constructing and analyzing biological maps. Bioinformatics, 2021, 37, 1475-1477.	1.8	24
39	An omic and multidimensional spatial atlas from serial biopsies of an evolving metastatic breast cancer. Cell Reports Medicine, 2022, 3, 100525.	3.3	22
40	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.	2.1	21
41	BioPAX support in CellDesigner. Bioinformatics, 2011, 27, 3437-3438.	1.8	18
42	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.	2.1	18
43	Systems Biology Graphical Notation: Process Description language Level 1 Version 1.3. Journal of Integrative Bioinformatics, 2015, 12, 213-280.	1.0	15
44	Systems Biology Graphical Notation: Process Description language Level 1. Nature Precedings, 2011, , .	0.1	12
45	A Compound Graph Layout Algorithm for Biological Pathways. Lecture Notes in Computer Science, 2005, , 442-447.	1.0	12
46	Author-sourced capture of pathway knowledge in computable form using Biofactoid. ELife, 2021, 10, .	2.8	11
47	The BioPAX Validator. Bioinformatics, 2013, 29, 2659-2660.	1.8	9
48	PATIKAmad: Putting microarray data into pathway context. Proteomics, 2008, 8, 2196-2198.	1.3	8
49	Meeting report from the first meetings of the Computational Modeling in Biology Network (COMBINE). Standards in Genomic Sciences, 2011, 5, 230-242.	1.5	7
50	Analyzing causal relationships in proteomic profiles using CausalPath. STAR Protocols, 2021, 2, 100955.	0.5	7
51	Systems Biology Graphical Notation: Entity Relationship language Level 1 (Version 1.2). Nature Precedings, 2011, , .	0.1	5
52	Systems Biology Graphical Notation: Entity Relationship language Level 1 (Version 1.2). Nature Precedings, 0, , .	0.1	2
53	Systematic interrogation of mutation groupings reveals divergent downstream expression programs within key cancer genes. BMC Bioinformatics, 2021, 22, 233.	1.2	1
54	A flexible search system for high-accuracy identification of biological entities and molecules. Journal of Open Source Software, 2021, 6, 3756.	2.0	1

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55	LibSBGN: Electronic Processing of SBGN maps. Nature Precedings, 2010, , .	0.1	0
56	LibSBGN: Electronic Processing of SBGN maps. Nature Precedings, 2011, , .	0.1	0
57	1P271 Crosstalk between signaling pathways revealed by database analysis of human phosphorylation sites(22B. Bioinformatics: Functional genomics,Poster). Seibutsu Butsuri, 2013, 53, S150.	0.0	0
58	3024 â€" GERMLINE RUNX1 MUTATIONS -MEDIATED CHANGES COOPERATES WITH INFLAMMATORY MICROENVIRONMENT TO DRIVE DEFECTIVE HEMATOPOIESIS IN FAMILIAL PLATELET DISORDER. Experimental Hematology, 2021, 100, S55.	0.2	0