

Emek Demir

List of Publications by Year in descending order

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Version: 2024-02-01

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	The reactome pathway knowledgebase 2022. <i>Nucleic Acids Research</i> , 2022, 50, D687-D692.	6.5	924
2	An omic and multidimensional spatial atlas from serial biopsies of an evolving metastatic breast cancer. <i>Cell Reports Medicine</i> , 2022, 3, 100525.	3.3	22
3	Newt: a comprehensive web-based tool for viewing, constructing and analyzing biological maps. <i>Bioinformatics</i> , 2021, 37, 1475-1477.	1.8	24
4	An expanded universe of cancer targets. <i>Cell</i> , 2021, 184, 1142-1155.	13.5	135
5	Systematic interrogation of mutation groupings reveals divergent downstream expression programs within key cancer genes. <i>BMC Bioinformatics</i> , 2021, 22, 233.	1.2	1
6	Ribavirin shows antiviral activity against SARS-CoV-2 and downregulates the activity of TMPRSS2 and the expression of ACE2 in vitro. <i>Canadian Journal of Physiology and Pharmacology</i> , 2021, 99, 449-460.	0.7	41
7	2D MXenes with antiviral and immunomodulatory properties: A pilot study against SARS-CoV-2. <i>Nano Today</i> , 2021, 38, 101136.	6.2	63
8	Causal interactions from proteomic profiles: Molecular data meet pathway knowledge. <i>Patterns</i> , 2021, 2, 100257.	3.1	44
9	The AML microenvironment catalyzes a stepwise evolution to gilteritinib resistance. <i>Cancer Cell</i> , 2021, 39, 999-1014.e8.	7.7	62
10	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. <i>Molecular Systems Biology</i> , 2021, 17, e10387.	3.2	53
11	A flexible search system for high-accuracy identification of biological entities and molecules. <i>Journal of Open Source Software</i> , 2021, 6, 3756.	2.0	1
12	Analyzing causal relationships in proteomic profiles using CausalPath. <i>STAR Protocols</i> , 2021, 2, 100955.	0.5	7
13	Author-sourced capture of pathway knowledge in computable form using Biofactoid. <i>ELife</i> , 2021, 10, .	2.8	11
14	3024 GERMLINE RUNX1 MUTATIONS -MEDIATED CHANGES COOPERATES WITH INFLAMMATORY MICROENVIRONMENT TO DRIVE DEFECTIVE HEMATOPOIESIS IN FAMILIAL PLATELET DISORDER. <i>Experimental Hematology</i> , 2021, 100, S55.	0.2	0
15	Pathway Commons 2019 Update: integration, analysis and exploration of pathway data. <i>Nucleic Acids Research</i> , 2020, 48, D489-D497.	6.5	161
16	COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms. <i>Scientific Data</i> , 2020, 7, 136.	2.4	99
17	Phosphoproteomic quantitation and causal analysis reveal pathways in GPVI/ITAM-mediated platelet activation programs. <i>Blood</i> , 2020, 136, 2346-2358.	0.6	53
18	Proteogenomic Characterization of Endometrial Carcinoma. <i>Cell</i> , 2020, 180, 729-748.e26.	13.5	296

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19	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. <i>Cell</i> , 2020, 181, 236-249.	13.5	334
20	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , 2020, 16, e9110.	3.2	178
21	Cancer-associated mutations in DICER1 RNase IIIa and IIIb domains exert similar effects on miRNA biogenesis. <i>Nature Communications</i> , 2019, 10, 3682.	5.8	48
22	Systems Biology Graphical Notation: Process Description language Level 1 Version 2.0. <i>Journal of Integrative Bioinformatics</i> , 2019, 16, .	1.0	43
23	Large-scale automated machine reading discovers new cancer-driving mechanisms. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	1.4	40
24	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.	2.1	18
25	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.	2.1	21
26	Human SRMATlas: A Resource of Targeted Assays to Quantify the Complete Human Proteome. <i>Cell</i> , 2016, 166, 766-778.	13.5	295
27	PaxtoolsR: pathway analysis in R using Pathway Commons. <i>Bioinformatics</i> , 2016, 32, 1262-1264.	1.8	43
28	Systems Biology Graphical Notation: Process Description language Level 1 Version 1.3. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 213-280.	1.0	15
29	Systems Biology Graphical Notation: Activity Flow language Level 1 Version 1.2. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 340-381.	1.0	35
30	Promoting Coordinated Development of Community-Based Information Standards for Modeling in Biology: The COMBINE Initiative. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 19.	2.0	72
31	Crosstalk between Signaling Pathways Provided by Single and Multiple Protein Phosphorylation Sites. <i>Journal of Molecular Biology</i> , 2015, 427, 511-520.	2.0	47
32	Systematic identification of cancer driving signaling pathways based on mutual exclusivity of genomic alterations. <i>Genome Biology</i> , 2015, 16, 45.	3.8	145
33	SBCNViz: A Tool for Visualization and Complexity Management of SBCN Process Description Maps. <i>PLoS ONE</i> , 2015, 10, e0128985.	1.1	26
34	Perturbation biology nominates upstreamâ€“downstream drug combinations in RAF inhibitor resistant melanoma cells. <i>ELife</i> , 2015, 4, .	2.8	95
35	Prediction of individualized therapeutic vulnerabilities in cancer from genomic profiles. <i>Bioinformatics</i> , 2014, 30, 2051-2059.	1.8	30
36	Pattern search in BioPAX models. <i>Bioinformatics</i> , 2014, 30, 139-140.	1.8	45

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37	Integrating biological pathways and genomic profiles with ChiBE 2. BMC Genomics, 2014, 15, 642.	1.2	24
38	The BioPAX Validator. Bioinformatics, 2013, 29, 2659-2660.	1.8	9
39	Using Biological Pathway Data with Paxtools. PLoS Computational Biology, 2013, 9, e1003194.	1.5	57
40	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
41	Software support for SBCN maps: SBCN-ML and LibSBCN. Bioinformatics, 2012, 28, 2016-2021.	1.8	74
42	BioPAX support in CellDesigner. Bioinformatics, 2011, 27, 3437-3438.	1.8	18
43	Systems Biology Graphical Notation: Process Description language Level 1. Nature Precedings, 2011, , .	0.1	12
44	LibSBCN: Electronic Processing of SBCN maps. Nature Precedings, 2011, , .	0.1	0
45	Systems Biology Graphical Notation: Entity Relationship language Level 1 (Version 1.2). Nature Precedings, 2011, , .	0.1	5
46	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
47	Pathway Commons, a web resource for biological pathway data. Nucleic Acids Research, 2011, 39, D685-D690.	6.5	980
48	The BioPAX community standard for pathway data sharing. Nature Biotechnology, 2010, 28, 935-942.	9.4	613
49	LibSBCN: Electronic Processing of SBCN maps. Nature Precedings, 2010, , .	0.1	0
50	Automated Network Analysis Identifies Core Pathways in Glioblastoma. PLoS ONE, 2010, 5, e8918.	1.1	318
51	Discovering modulators of gene expression. Nucleic Acids Research, 2010, 38, 5648-5656.	6.5	34
52	ChiBE: interactive visualization and manipulation of BioPAX pathway models. Bioinformatics, 2010, 26, 429-431.	1.8	46
53	Algorithms for effective querying of compound graph-based pathway databases. BMC Bioinformatics, 2009, 10, 376.	1.2	25
54	The Systems Biology Graphical Notation. Nature Biotechnology, 2009, 27, 735-741.	9.4	828

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55	A layout algorithm for undirected compound graphs. Information Sciences, 2009, 179, 980-994.	4.0	74
56	PATIKAmad: Putting microarray data into pathway context. Proteomics, 2008, 8, 2196-2198.	1.3	8
57	A Compound Graph Layout Algorithm for Biological Pathways. Lecture Notes in Computer Science, 2005, , 442-447.	1.0	12
58	Systems Biology Graphical Notation: Entity Relationship language Level 1 (Version 1.2). Nature Precedings, 0, , .	0.1	2