

# Emek Demir

## List of Publications by Year in descending order

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Version: 2024-02-01

58  
papers

6,787  
citations

147801

31  
h-index

133252

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. <i>Nucleic Acids Research</i> , 2011, 39, D685-D690.	14.5	980
2	The reactome pathway knowledgebase 2022. <i>Nucleic Acids Research</i> , 2022, 50, D687-D692.	14.5	924
3	The Systems Biology Graphical Notation. <i>Nature Biotechnology</i> , 2009, 27, 735-741.	17.5	828
4	The BioPAX community standard for pathway data sharing. <i>Nature Biotechnology</i> , 2010, 28, 935-942.	17.5	613
5	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
6	Automated Network Analysis Identifies Core Pathways in Glioblastoma. <i>PLoS ONE</i> , 2010, 5, e8918.	2.5	318
7	Proteogenomic Characterization of Endometrial Carcinoma. <i>Cell</i> , 2020, 180, 729-748.e26.	28.9	296
8	Human SRMATlas: A Resource of Targeted Assays to Quantify the Complete Human Proteome. <i>Cell</i> , 2016, 166, 766-778.	28.9	295
9	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , 2020, 16, e9110.	7.2	178
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	Systematic identification of cancer driving signaling pathways based on mutual exclusivity of genomic alterations. <i>Genome Biology</i> , 2015, 16, 45.	8.8	145
12	An expanded universe of cancer targets. <i>Cell</i> , 2021, 184, 1142-1155.	28.9	135
13	COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms. <i>Scientific Data</i> , 2020, 7, 136.	5.3	99
14	Perturbation biology nominates upstreamâ€“downstream drug combinations in RAF inhibitor resistant melanoma cells. <i>ELife</i> , 2015, 4, .	6.0	95
15	A layout algorithm for undirected compound graphs. <i>Information Sciences</i> , 2009, 179, 980-994.	6.9	74
16	Software support for SBGN maps: SBGN-ML and LibSBGN. <i>Bioinformatics</i> , 2012, 28, 2016-2021.	4.1	74
17	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.	4.1	72
18	2D MXenes with antiviral and immunomodulatory properties: A pilot study against SARS-CoV-2. <i>Nano Today</i> , 2021, 38, 101136.	11.9	63

#	ARTICLE	IF	CITATIONS
19	The AML microenvironment catalyzes a stepwise evolution to gilteritinib resistance. <i>Cancer Cell</i> , 2021, 39, 999-1014.e8.	16.8	62
20	Using Biological Pathway Data with Paxtools. <i>PLoS Computational Biology</i> , 2013, 9, e1003194.	3.2	57
21	Phosphoproteomic quantitation and causal analysis reveal pathways in GPVI/ITAM-mediated platelet activation programs. <i>Blood</i> , 2020, 136, 2346-2358.	1.4	53
22	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. <i>Molecular Systems Biology</i> , 2021, 17, e10387.	7.2	53
23	Cancer-associated mutations in DICER1 RNase IIIa and IIIb domains exert similar effects on miRNA biogenesis. <i>Nature Communications</i> , 2019, 10, 3682.	12.8	48
24	Crosstalk between Signaling Pathways Provided by Single and Multiple Protein Phosphorylation Sites. <i>Journal of Molecular Biology</i> , 2015, 427, 511-520.	4.2	47
25	ChiBE: interactive visualization and manipulation of BioPAX pathway models. <i>Bioinformatics</i> , 2010, 26, 429-431.	4.1	46
26	Pattern search in BioPAX models. <i>Bioinformatics</i> , 2014, 30, 139-140.	4.1	45
27	Causal interactions from proteomic profiles: Molecular data meet pathway knowledge. <i>Patterns</i> , 2021, 2, 100257.	5.9	44
28	PaxtoolsR: pathway analysis in R using Pathway Commons. <i>Bioinformatics</i> , 2016, 32, 1262-1264.	4.1	43
29	Systems Biology Graphical Notation: Process Description language Level 1 Version 2.0. <i>Journal of Integrative Bioinformatics</i> , 2019, 16, .	1.5	43
30	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.	1.4	41
31	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
32	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
33	Discovering modulators of gene expression. <i>Nucleic Acids Research</i> , 2010, 38, 5648-5656.	14.5	34
34	Prediction of individualized therapeutic vulnerabilities in cancer from genomic profiles. <i>Bioinformatics</i> , 2014, 30, 2051-2059.	4.1	30
35	SBGNViz: A Tool for Visualization and Complexity Management of SBGN Process Description Maps. <i>PLoS ONE</i> , 2015, 10, e0128985.	2.5	26
36	Algorithms for effective querying of compound graph-based pathway databases. <i>BMC Bioinformatics</i> , 2009, 10, 376.	2.6	25

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37	Integrating biological pathways and genomic profiles with ChiBE 2. BMC Genomics, 2014, 15, 642.	2.8	24
38	Newt: a comprehensive web-based tool for viewing, constructing and analyzing biological maps. Bioinformatics, 2021, 37, 1475-1477.	4.1	24
39	An omic and multidimensional spatial atlas from serial biopsies of an evolving metastatic breast cancer. Cell Reports Medicine, 2022, 3, 100525.	6.5	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.	4.6	21
41	BioPAX support in CellDesigner. Bioinformatics, 2011, 27, 3437-3438.	4.1	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.	4.6	18
43	Systems Biology Graphical Notation: Process Description language Level 1 Version 1.3. Journal of Integrative Bioinformatics, 2015, 12, 213-280.	1.5	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.	1.3	12
46	Author-sourced capture of pathway knowledge in computable form using Biofactoid. ELife, 2021, 10, .	6.0	11
47	The BioPAX Validator. Bioinformatics, 2013, 29, 2659-2660.	4.1	9
48	PATIKAmad: Putting microarray data into pathway context. Proteomics, 2008, 8, 2196-2198.	2.2	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.	1.2	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.	2.6	1
54	A flexible search system for high-accuracy identification of biological entities and molecules. Journal of Open Source Software, 2021, 6, 3756.	4.6	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.	0.1	0
58	3024 " GERMLINE RUNX1 MUTATIONS -MEDIATED CHANGES COOPERATES WITH INFLAMMATORY MICROENVIRONMENT TO DRIVE DEFECTIVE HEMATOPOIESIS IN FAMILIAL PLATELET DISORDER. Experimental Hematology, 2021, 100, S55.	0.4	0