Ugur Dogrusoz

List of Publications by Year in descending order

47 papers	28,717 citations	430754 18 h-index	265120 42 g-index
54 all docs	54 docs citations	54 times ranked	38733 citing authors

#	Article	IF	Citations
1	fCoSE: A Fast Compound Graph Layout Algorithm with Constraint Support. IEEE Transactions on Visualization and Computer Graphics, 2022, 28, 4582-4593.	2.9	7
2	Newt: a comprehensive web-based tool for viewing, constructing and analyzing biological maps. Bioinformatics, 2021, 37, 1475-1477.	1.8	24
3	RSTrace+: Reviewer suggestion using software artifact traceability graphs. Information and Software Technology, 2021, 130, 106455.	3.0	16
4	Causal interactions from proteomic profiles: Molecular data meet pathway knowledge. Patterns, 2021, 2, 100257.	3.1	44
5	CoSEP: A compound spring embedder layout algorithm with support for ports. Information Visualization, 2021, 20, 151-169.	1.2	2
6	The Systems Biology Graphical Notation: Current Status and Applications in Systems Medicine. , 2021, , 372-381.		6
7	Analyzing causal relationships in proteomic profiles using CausalPath. STAR Protocols, 2021, 2, 100955.	0.5	7
8	Pathway Commons 2019 Update: integration, analysis and exploration of pathway data. Nucleic Acids Research, 2020, 48, D489-D497.	6.5	161
9	cd2sbgnml: bidirectional conversion between CellDesigner and SBGN formats. Bioinformatics, 2020, 36, 2620-2622.	1.8	9
10	Systems biology graphical notation markup language (SBGNML) version 0.3. Journal of Integrative Bioinformatics, 2020, 17, .	1.0	21
11	Abstract 3209: The cBioPortal for Cancer Genomics. , 2020, , .		0
12	Hydra: detecting fraud in financial transactions via graph based representation and visual analysis. , 2020, , .		0
13	Systems Biology Graphical Notation: Process Description language Level 1 Version 2.0. Journal of Integrative Bioinformatics, 2019, 16, .	1.0	43
14	Reviewer Recommendation using Software Artifact Traceability Graphs. , 2019, , .		8
15	Community-driven roadmap for integrated disease maps. Briefings in Bioinformatics, 2019, 20, 659-670.	3.2	48
16	Abstract 910: The cBioPortal for cancer genomics. , 2019, , .		0
17	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	13.5	2,111
18	Efficient methods and readily customizable libraries for managing complexity of large networks. PLoS ONE, 2018, 13, e0197238.	1.1	8

#	Article	IF	Citations
19	Systems medicine disease maps: community-driven comprehensive representation of disease mechanisms. Npj Systems Biology and Applications, 2018, 4, 21.	1.4	84
20	Abstract 3302: The molecular landscape of oncogenic signaling pathways in The Cancer Genome Atlas. , 2018, , .		9
21	Abstract 923: The cBioPortal for Cancer Genomics: An intuitive open-source platform for exploration, analysis and visualization of cancer genomics data. Cancer Research, 2018, 78, 923-923.	0.4	11
22	PathwayMapper: a collaborative visual web editor for cancer pathways and genomic data. Bioinformatics, 2017, 33, 2238-2240.	1.8	50
23	Abstract 2607: The cBioPortal for Cancer Genomics: an open source platform for accessing and interpreting complex cancer genomics data in the era of precision medicine. , 2017, , .		1
24	An algorithm for automated layout of process description maps drawn in SBGN. Bioinformatics, 2016, 32, 77-84.	1.8	7
25	Abstract 5277: The cBioPortal for cancer genomics and its application in precision oncology. Cancer Research, 2016, 76, 5277-5277.	0.4	14
26	SBGNViz: A Tool for Visualization and Complexity Management of SBGN Process Description Maps. PLoS ONE, 2015, 10, e0128985.	1.1	26
27	Integrating biological pathways and genomic profiles with ChiBE 2. BMC Genomics, 2014, 15, 642.	1.2	24
28	Integrative Analysis of Complex Cancer Genomics and Clinical Profiles Using the cBioPortal. Science Signaling, 2013, 6, pl1.	1.6	11,344
29	CiSE: A Circular Spring Embedder Layout Algorithm. IEEE Transactions on Visualization and Computer Graphics, 2013, 19, 953-966.	2.9	13
30	Software support for SBGN maps: SBGN-ML and LibSBGN. Bioinformatics, 2012, 28, 2016-2021.	1.8	74
31	The cBio Cancer Genomics Portal: An Open Platform for Exploring Multidimensional Cancer Genomics Data. Cancer Discovery, 2012, 2, 401-404.	7.7	12,801
32	The BioPAX community standard for pathway data sharing. Nature Biotechnology, 2010, 28, 935-942.	9.4	613
33	LibSBGN: Electronic Processing of SBGN maps. Nature Precedings, 2010, , .	0.1	0
34	Discovering modulators of gene expression. Nucleic Acids Research, 2010, 38, 5648-5656.	6.5	34
35	VISIBIOweb: visualization and layout services for BioPAX pathway models. Nucleic Acids Research, 2010, 38, W150-W154.	6.5	14
36	ChiBE: interactive visualization and manipulation of BioPAX pathway models. Bioinformatics, 2010, 26, 429-431.	1.8	46

#	Article	IF	Citations
37	Algorithms for effective querying of compound graph-based pathway databases. BMC Bioinformatics, 2009, 10, 376.	1.2	25
38	The Systems Biology Graphical Notation. Nature Biotechnology, 2009, 27, 735-741.	9.4	828
39	A layout algorithm for undirected compound graphs. Information Sciences, 2009, 179, 980-994.	4.0	74
40	PATIKAmad: Putting microarray data into pathway context. Proteomics, 2008, 8, 2196-2198.	1.3	8
41	On labeling in graph visualization. Information Sciences, 2007, 177, 2459-2472.	4.0	16
42	A Compound Graph Layout Algorithm for Biological Pathways. Lecture Notes in Computer Science, 2005, , 442-447.	1.0	12
43	A Constrained, Force-Directed Layout Algorithm for Biological Pathways. Lecture Notes in Computer Science, 2004, , 314-319.	1.0	9
44	Disconnected Graph Layout and the Polyomino Packing Approach. Lecture Notes in Computer Science, 2002, , 378-391.	1.0	14
45	Two-dimensional packing algorithms for layout of disconnected graphs. Information Sciences, 2002, 143, 147-158.	4.0	10
46	Edge Labeling in the Graph Layout Toolkit. Lecture Notes in Computer Science, 1998, , 356-363.	1.0	3
47	Triangle graphs. Applied Numerical Mathematics, 1995, 17, 85-96.	1.2	3