

Ugur Dogrusoz

List of Publications by Year in descending order

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Version: 2024-02-01

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	The cBio Cancer Genomics Portal: An Open Platform for Exploring Multidimensional Cancer Genomics Data. <i>Cancer Discovery</i> , 2012, 2, 401-404.	7.7	12,801
2	Integrative Analysis of Complex Cancer Genomics and Clinical Profiles Using the cBioPortal. <i>Science Signaling</i> , 2013, 6, pl1.	1.6	11,344
3	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018, 173, 321-337.e10.	13.5	2,111
4	The Systems Biology Graphical Notation. <i>Nature Biotechnology</i> , 2009, 27, 735-741.	9.4	828
5	The BioPAX community standard for pathway data sharing. <i>Nature Biotechnology</i> , 2010, 28, 935-942.	9.4	613
6	Pathway Commons 2019 Update: integration, analysis and exploration of pathway data. <i>Nucleic Acids Research</i> , 2020, 48, D489-D497.	6.5	161
7	Systems medicine disease maps: community-driven comprehensive representation of disease mechanisms. <i>Npj Systems Biology and Applications</i> , 2018, 4, 21.	1.4	84
8	A layout algorithm for undirected compound graphs. <i>Information Sciences</i> , 2009, 179, 980-994.	4.0	74
9	Software support for SBGN maps: SBGN-ML and LibSBGN. <i>Bioinformatics</i> , 2012, 28, 2016-2021.	1.8	74
10	PathwayMapper: a collaborative visual web editor for cancer pathways and genomic data. <i>Bioinformatics</i> , 2017, 33, 2238-2240.	1.8	50
11	Community-driven roadmap for integrated disease maps. <i>Briefings in Bioinformatics</i> , 2019, 20, 659-670.	3.2	48
12	ChiBE: interactive visualization and manipulation of BioPAX pathway models. <i>Bioinformatics</i> , 2010, 26, 429-431.	1.8	46
13	Causal interactions from proteomic profiles: Molecular data meet pathway knowledge. <i>Patterns</i> , 2021, 2, 100257.	3.1	44
14	Systems Biology Graphical Notation: Process Description language Level 1 Version 2.0. <i>Journal of Integrative Bioinformatics</i> , 2019, 16, .	1.0	43
15	Discovering modulators of gene expression. <i>Nucleic Acids Research</i> , 2010, 38, 5648-5656.	6.5	34
16	SBGNviz: A Tool for Visualization and Complexity Management of SBGN Process Description Maps. <i>PLoS ONE</i> , 2015, 10, e0128985.	1.1	26
17	Algorithms for effective querying of compound graph-based pathway databases. <i>BMC Bioinformatics</i> , 2009, 10, 376.	1.2	25
18	Integrating biological pathways and genomic profiles with ChiBE 2. <i>BMC Genomics</i> , 2014, 15, 642.	1.2	24

#	ARTICLE	IF	CITATIONS
19	Newt: a comprehensive web-based tool for viewing, constructing and analyzing biological maps. <i>Bioinformatics</i> , 2021, 37, 1475-1477.	1.8	24
20	Systems biology graphical notation markup language (SBGNML) version 0.3. <i>Journal of Integrative Bioinformatics</i> , 2020, 17, .	1.0	21
21	On labeling in graph visualization. <i>Information Sciences</i> , 2007, 177, 2459-2472.	4.0	16
22	RSTrace+: Reviewer suggestion using software artifact traceability graphs. <i>Information and Software Technology</i> , 2021, 130, 106455.	3.0	16
23	Disconnected Graph Layout and the Polyomino Packing Approach. <i>Lecture Notes in Computer Science</i> , 2002, , 378-391.	1.0	14
24	VISBIOweb: visualization and layout services for BioPAX pathway models. <i>Nucleic Acids Research</i> , 2010, 38, W150-W154.	6.5	14
25	Abstract 5277: The cBioPortal for cancer genomics and its application in precision oncology. <i>Cancer Research</i> , 2016, 76, 5277-5277.	0.4	14
26	CiSE: A Circular Spring Embedder Layout Algorithm. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2013, 19, 953-966.	2.9	13
27	A Compound Graph Layout Algorithm for Biological Pathways. <i>Lecture Notes in Computer Science</i> , 2005, , 442-447.	1.0	12
28	Abstract 923: The cBioPortal for Cancer Genomics: An intuitive open-source platform for exploration, analysis and visualization of cancer genomics data. <i>Cancer Research</i> , 2018, 78, 923-923.	0.4	11
29	Two-dimensional packing algorithms for layout of disconnected graphs. <i>Information Sciences</i> , 2002, 143, 147-158.	4.0	10
30	cd2sbgnml: bidirectional conversion between CellDesigner and SBGN formats. <i>Bioinformatics</i> , 2020, 36, 2620-2622.	1.8	9
31	A Constrained, Force-Directed Layout Algorithm for Biological Pathways. <i>Lecture Notes in Computer Science</i> , 2004, , 314-319.	1.0	9
32	Abstract 3302: The molecular landscape of oncogenic signaling pathways in The Cancer Genome Atlas. , 2018, , .		9
33	PATIKAmad: Putting microarray data into pathway context. <i>Proteomics</i> , 2008, 8, 2196-2198.	1.3	8
34	Efficient methods and readily customizable libraries for managing complexity of large networks. <i>PLoS ONE</i> , 2018, 13, e0197238.	1.1	8
35	Reviewer Recommendation using Software Artifact Traceability Graphs. , 2019, , .		8
36	An algorithm for automated layout of process description maps drawn in SBGN. <i>Bioinformatics</i> , 2016, 32, 77-84.	1.8	7

#	ARTICLE	IF	CITATIONS
37	fCoSE: A Fast Compound Graph Layout Algorithm with Constraint Support. IEEE Transactions on Visualization and Computer Graphics, 2022, 28, 4582-4593.	2.9	7
38	Analyzing causal relationships in proteomic profiles using CausalPath. STAR Protocols, 2021, 2, 100955.	0.5	7
39	The Systems Biology Graphical Notation: Current Status and Applications in Systems Medicine. , 2021, , 372-381.		6
40	Triangle graphs. Applied Numerical Mathematics, 1995, 17, 85-96.	1.2	3
41	Edge Labeling in the Graph Layout Toolkit. Lecture Notes in Computer Science, 1998, , 356-363.	1.0	3
42	CoSEP: A compound spring embedder layout algorithm with support for ports. Information Visualization, 2021, 20, 151-169.	1.2	2
43	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
44	LibSBGN: Electronic Processing of SBGN maps. Nature Precedings, 2010, , .	0.1	0
45	Abstract 910: The cBioPortal for cancer genomics. , 2019, , .		0
46	Abstract 3209: The cBioPortal for Cancer Genomics. , 2020, , .		0
47	Hydra: detecting fraud in financial transactions via graph based representation and visual analysis. , 2020, , .		0