

John H Morris

List of Publications by Citations

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Version: 2024-04-28

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

54
papers

17,931
citations

23
h-index

58
g-index

58
ext. papers

28,065
ext. citations

9.3
avg, IF

7.14
L-index

#	Paper	IF	Citations
54	STRING v11: protein-protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. <i>Nucleic Acids Research</i> , 2019 , 47, D607-D613	20.1	5966
53	The STRING database in 2017: quality-controlled protein-protein association networks, made broadly accessible. <i>Nucleic Acids Research</i> , 2017 , 45, D362-D368	20.1	4068
52	Integration of biological networks and gene expression data using Cytoscape. <i>Nature Protocols</i> , 2007 , 2, 2366-82	18.8	1798
51	UCSF ChimeraX: Meeting modern challenges in visualization and analysis. <i>Protein Science</i> , 2018 , 27, 14-25	6.3	1519
50	UCSF ChimeraX: Structure visualization for researchers, educators, and developers. <i>Protein Science</i> , 2021 , 30, 70-82	6.3	775
49	Global landscape of HIV-human protein complexes. <i>Nature</i> , 2011 , 481, 365-70	50.4	507
48	Biological network exploration with Cytoscape 3. <i>Current Protocols in Bioinformatics</i> , 2014 , 47, 8.13.1-24	24.2	490
47	Cytoscape StringApp: Network Analysis and Visualization of Proteomics Data. <i>Journal of Proteome Research</i> , 2019 , 18, 623-632	5.6	490
46	Cytoscape Automation: empowering workflow-based network analysis. <i>Genome Biology</i> , 2019 , 20, 185	18.3	375
45	clusterMaker: a multi-algorithm clustering plugin for Cytoscape. <i>BMC Bioinformatics</i> , 2011 , 12, 436	3.6	337
44	Using sequence similarity networks for visualization of relationships across diverse protein superfamilies. <i>PLoS ONE</i> , 2009 , 4, e4345	3.7	287
43	The Structure-Function Linkage Database. <i>Nucleic Acids Research</i> , 2014 , 42, D521-30	20.1	169
42	GLayer: community structure analysis of biological networks. <i>Bioinformatics</i> , 2010 , 26, 3135-7	7.2	158
41	Leveraging enzyme structure-function relationships for functional inference and experimental design: the structure-function linkage database. <i>Biochemistry</i> , 2006 , 45, 2545-55	3.2	142
40	Affinity purification-mass spectrometry and network analysis to understand protein-protein interactions. <i>Nature Protocols</i> , 2014 , 9, 2539-54	18.8	110
39	From structure to systems: high-resolution, quantitative genetic analysis of RNA polymerase II. <i>Cell</i> , 2013 , 154, 775-88	56.2	102
38	Enhancing UCSF Chimera through web services. <i>Nucleic Acids Research</i> , 2014 , 42, W478-84	20.1	80

37	Partitioning biological data with transitivity clustering. <i>Nature Methods</i> , 2010 , 7, 419-20	21.6	73
36	Protein network prediction and topological analysis in <i>Leishmania major</i> as a tool for drug target selection. <i>BMC Bioinformatics</i> , 2010 , 11, 484	3.6	60
35	structureViz: linking Cytoscape and UCSF Chimera. <i>Bioinformatics</i> , 2007 , 23, 2345-7	7.2	60
34	enhancedGraphics: a Cytoscape app for enhanced node graphics. <i>F1000Research</i> , 2014 , 3, 147	3.6	30
33	Improving the quality of protein similarity network clustering algorithms using the network edge weight distribution. <i>Bioinformatics</i> , 2011 , 27, 326-33	7.2	29
32	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data. <i>F1000Research</i> , 2019 , 8,	3.6	28
31	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data. <i>F1000Research</i> , 2019 , 8, 296	3.6	23
30	Prediction of enzymatic pathways by integrative pathway mapping. <i>ELife</i> , 2018 , 7,	8.9	22
29	The 3-channel Lissajous trajectory of the auditory brain-stem response. II. Methodology. <i>Electroencephalography and Clinical Neurophysiology - Evoked Potentials</i> , 1987 , 68, 327-332		20
28	The 3-channel Lissajous trajectory of the auditory brain-stem response. VII. Planar segments in humans. <i>Electroencephalography and Clinical Neurophysiology - Evoked Potentials</i> , 1987 , 68, 368-379		20
27	Visualize omics data on networks with Omics Visualizer, a Cytoscape App. <i>F1000Research</i> , 2020 , 9, 157	3.6	20
26	An Atlas of Peroxiredoxins Created Using an Active Site Profile-Based Approach to Functionally Relevant Clustering of Proteins. <i>PLoS Computational Biology</i> , 2017 , 13, e1005284	5	16
25	Visualize omics data on networks with Omics Visualizer, a Cytoscape App. <i>F1000Research</i> , 2020 , 9, 157	3.6	14
24	An approach to functionally relevant clustering of the protein universe: Active site profile-based clustering of protein structures and sequences. <i>Protein Science</i> , 2017 , 26, 677-699	6.3	12
23	Genetic interaction mapping informs integrative structure determination of protein complexes. <i>Science</i> , 2020 , 370,	33.3	11
22	setsApp: Set operations for Cytoscape Nodes and Edges. <i>F1000Research</i> , 2014 , 3, 149	3.6	11
21	Integrative visual analysis of protein sequence mutations. <i>BMC Proceedings</i> , 2014 , 8, S2	2.3	10
20	The Cytoscape app article collection. <i>F1000Research</i> , 2014 , 3, 138	3.6	8

19	CyAnimator: Simple Animations of Cytoscape Networks. <i>F1000Research</i> , 2015 , 4, 482	3.6	8
18	CyAnimator: Simple Animations of Cytoscape Networks. <i>F1000Research</i> , 2015 , 4, 482	3.6	8
17	Computational tools for the interactive exploration of proteomic and structural data. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 1703-15	7.6	7
16	setsApp for Cytoscape: Set operations for Cytoscape Nodes and Edges. <i>F1000Research</i> , 2014 , 3, 149	3.6	6
15	DASP3: identification of protein sequences belonging to functionally relevant groups. <i>BMC Bioinformatics</i> , 2016 , 17, 458	3.6	6
14	Cytoscape stringApp: Network analysis and visualization of proteomics data		5
13	Effects of acute nerve compression on conduction of impulse trains of increasing frequency. <i>Journal of the Neurological Sciences</i> , 1985 , 67, 187-99	3.2	4
12	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNAsequencing data		4
11	Biocuration in the structure-function linkage database: the anatomy of a superfamily. <i>Database: the Journal of Biological Databases and Curation</i> , 2017 , 2017,	5	3
10	cddApp: a Cytoscape app for accessing the NCBI conserved domain database. <i>Bioinformatics</i> , 2015 , 31, 134-6	7.2	3
9	aMatReader: Importing adjacency matrices via Cytoscape Automation. <i>F1000Research</i> , 2018 , 7, 823	3.6	3
8	aMatReader: Importing adjacency matrices via Cytoscape Automation. <i>F1000Research</i> , 2018 , 7, 823	3.6	3
7	Low-density lipoprotein receptor-related protein 1 (LRP1) is a novel receptor for apolipoprotein A4 (APOA4) in adipose tissue. <i>Scientific Reports</i> , 2021 , 11, 13289	4.9	3
6	Biocuration in the structure-function linkage database: the anatomy of a superfamily. <i>Database: the Journal of Biological Databases and Curation</i> , 2017 , 2017,	5	2
5	Copycat Layout: Network layout alignment via Cytoscape Automation. <i>F1000Research</i> , 2018 , 7, 822	3.6	2
4	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data. <i>F1000Research</i> , 8 , 296	3.6	2
3	Copycat Layout: Network layout alignment via Cytoscape Automation. <i>F1000Research</i> , 2018 , 7, 822	3.6	1
2	Targeted phosphoproteomics of the Ras signaling network reveal regulatory mechanisms mediated by oncogenic KRAS		1

- 1 A biomedical open knowledge network harnesses the power of AI to understand deep human biology. *AI Magazine*, **2022**, 43, 46-58 6.1 1