

# John H Morris

## List of Publications by Year in Descending Order

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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	A biomedical open knowledge network harnesses the power of AI to understand deep human biology. <i>AI Magazine</i> , <b>2022</b> , 43, 46-58	6.1	1
53	Low-density lipoprotein receptor-related protein 1 (LRP1) is a novel receptor for apolipoprotein A4 (APOA4) in adipose tissue. <i>Scientific Reports</i> , <b>2021</b> , 11, 13289	4.9	3
52	UCSF ChimeraX: Structure visualization for researchers, educators, and developers. <i>Protein Science</i> , <b>2021</b> , 30, 70-82	6.3	775
51	Genetic interaction mapping informs integrative structure determination of protein complexes. <i>Science</i> , <b>2020</b> , 370,	33.3	11
50	Visualize omics data on networks with Omics Visualizer, a Cytoscape App. <i>F1000Research</i> , <b>2020</b> , 9, 157	3.6	20
49	Visualize omics data on networks with Omics Visualizer, a Cytoscape App. <i>F1000Research</i> , <b>2020</b> , 9, 157	3.6	14
48	Cytoscape Automation: empowering workflow-based network analysis. <i>Genome Biology</i> , <b>2019</b> , 20, 185	18.3	375
47	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data. <i>F1000Research</i> , <b>2019</b> , 8,	3.6	28
46	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data. <i>F1000Research</i> , <b>2019</b> , 8, 296	3.6	23
45	STRING v11: protein-protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, D607-D613	20.1	5966
44	Cytoscape StringApp: Network Analysis and Visualization of Proteomics Data. <i>Journal of Proteome Research</i> , <b>2019</b> , 18, 623-632	5.6	490
43	UCSF ChimeraX: Meeting modern challenges in visualization and analysis. <i>Protein Science</i> , <b>2018</b> , 27, 14-25.	5.3	1519
42	Copycat Layout: Network layout alignment via Cytoscape Automation. <i>F1000Research</i> , <b>2018</b> , 7, 822	3.6	2
41	Copycat Layout: Network layout alignment via Cytoscape Automation. <i>F1000Research</i> , <b>2018</b> , 7, 822	3.6	1
40	aMatReader: Importing adjacency matrices via Cytoscape Automation. <i>F1000Research</i> , <b>2018</b> , 7, 823	3.6	3
39	aMatReader: Importing adjacency matrices via Cytoscape Automation. <i>F1000Research</i> , <b>2018</b> , 7, 823	3.6	3
38	Prediction of enzymatic pathways by integrative pathway mapping. <i>ELife</i> , <b>2018</b> , 7,	8.9	22

37	An approach to functionally relevant clustering of the protein universe: Active site profile-based clustering of protein structures and sequences. <i>Protein Science</i> , <b>2017</b> , 26, 677-699	6.3	12
36	Biocuration in the structure-function linkage database: the anatomy of a superfamily. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2017</b> , 2017,	5	3
35	The STRING database in 2017: quality-controlled protein-protein association networks, made broadly accessible. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D362-D368	20.1	4068
34	Biocuration in the structure-function linkage database: the anatomy of a superfamily. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2017</b> , 2017,	5	2
33	An Atlas of Peroxiredoxins Created Using an Active Site Profile-Based Approach to Functionally Relevant Clustering of Proteins. <i>PLoS Computational Biology</i> , <b>2017</b> , 13, e1005284	5	16
32	DASP3: identification of protein sequences belonging to functionally relevant groups. <i>BMC Bioinformatics</i> , <b>2016</b> , 17, 458	3.6	6
31	cddApp: a Cytoscape app for accessing the NCBI conserved domain database. <i>Bioinformatics</i> , <b>2015</b> , 31, 134-6	7.2	3
30	CyAnimator: Simple Animations of Cytoscape Networks. <i>F1000Research</i> , <b>2015</b> , 4, 482	3.6	8
29	CyAnimator: Simple Animations of Cytoscape Networks. <i>F1000Research</i> , <b>2015</b> , 4, 482	3.6	8
28	Affinity purification-mass spectrometry and network analysis to understand protein-protein interactions. <i>Nature Protocols</i> , <b>2014</b> , 9, 2539-54	18.8	110
27	Enhancing UCSF Chimera through web services. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, W478-84	20.1	80
26	Integrative visual analysis of protein sequence mutations. <i>BMC Proceedings</i> , <b>2014</b> , 8, S2	2.3	10
25	Biological network exploration with Cytoscape 3. <i>Current Protocols in Bioinformatics</i> , <b>2014</b> , 47, 8.13.1-24	24.2	490
24	The Structure-Function Linkage Database. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, D521-30	20.1	169
23	setsApp: Set operations for Cytoscape Nodes and Edges. <i>F1000Research</i> , <b>2014</b> , 3, 149	3.6	11
22	enhancedGraphics: a Cytoscape app for enhanced node graphics. <i>F1000Research</i> , <b>2014</b> , 3, 147	3.6	30
21	The Cytoscape app article collection. <i>F1000Research</i> , <b>2014</b> , 3, 138	3.6	8
20	setsApp for Cytoscape: Set operations for Cytoscape Nodes and Edges. <i>F1000Research</i> , <b>2014</b> , 3, 149	3.6	6

19	From structure to systems: high-resolution, quantitative genetic analysis of RNA polymerase II. <i>Cell</i> , <b>2013</b> , 154, 775-88	56.2	102
18	Global landscape of HIV-human protein complexes. <i>Nature</i> , <b>2011</b> , 481, 365-70	50.4	507
17	clusterMaker: a multi-algorithm clustering plugin for Cytoscape. <i>BMC Bioinformatics</i> , <b>2011</b> , 12, 436	3.6	337
16	Improving the quality of protein similarity network clustering algorithms using the network edge weight distribution. <i>Bioinformatics</i> , <b>2011</b> , 27, 326-33	7.2	29
15	Partitioning biological data with transitivity clustering. <i>Nature Methods</i> , <b>2010</b> , 7, 419-20	21.6	73
14	Computational tools for the interactive exploration of proteomic and structural data. <i>Molecular and Cellular Proteomics</i> , <b>2010</b> , 9, 1703-15	7.6	7
13	GLay: community structure analysis of biological networks. <i>Bioinformatics</i> , <b>2010</b> , 26, 3135-7	7.2	158
12	Protein network prediction and topological analysis in <i>Leishmania major</i> as a tool for drug target selection. <i>BMC Bioinformatics</i> , <b>2010</b> , 11, 484	3.6	60
11	Using sequence similarity networks for visualization of relationships across diverse protein superfamilies. <i>PLoS ONE</i> , <b>2009</b> , 4, e4345	3.7	287
10	Integration of biological networks and gene expression data using Cytoscape. <i>Nature Protocols</i> , <b>2007</b> , 2, 2366-82	18.8	1798
9	structureViz: linking Cytoscape and UCSF Chimera. <i>Bioinformatics</i> , <b>2007</b> , 23, 2345-7	7.2	60
8	Leveraging enzyme structure-function relationships for functional inference and experimental design: the structure-function linkage database. <i>Biochemistry</i> , <b>2006</b> , 45, 2545-55	3.2	142
7	The 3-channel Lissajous trajectory of the auditory brain-stem response. II. Methodology. <i>Electroencephalography and Clinical Neurophysiology - Evoked Potentials</i> , <b>1987</b> , 68, 327-332		20
6	The 3-channel Lissajous trajectory of the auditory brain-stem response. VII. Planar segments in humans. <i>Electroencephalography and Clinical Neurophysiology - Evoked Potentials</i> , <b>1987</b> , 68, 368-379		20
5	Effects of acute nerve compression on conduction of impulse trains of increasing frequency. <i>Journal of the Neurological Sciences</i> , <b>1985</b> , 67, 187-99	3.2	4
4	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data. <i>F1000Research</i> , <b>8</b> , 296	3.6	2
3	Targeted phosphoproteomics of the Ras signaling network reveal regulatory mechanisms mediated by oncogenic KRAS		1
2	Cytoscape stringApp: Network analysis and visualization of proteomics data		5

1 Evaluation of methods to assign cell type labels to cell clusters from single-cell RNAsequencing data

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