John H Morris

List of Publications by Year
in descending order

54 papers	34,986 citations	218381 26 h-index	168136 53 g-index
58 all docs	58 docs citations	58 times ranked	55584 citing authors

#	Article	IF	Citations
1	STRING v11: protein–protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. Nucleic Acids Research, 2019, 47, D607-D613.	6.5	12,237
2	The STRING database in 2017: quality-controlled protein–protein association networks, made broadly accessible. Nucleic Acids Research, 2017, 45, D362-D368.	6.5	6,303
3	<scp>UCSF ChimeraX</scp>: Structure visualization for researchers, educators, and developers. Protein Science, 2021, 30, 70-82.	3.1	4,478
4	UCSF ChimeraX: Meeting modern challenges in visualization and analysis. Protein Science, 2018, 27, 14-25.	3.1	3,377
5	Integration of biological networks and gene expression data using Cytoscape. Nature Protocols, 2007, 2, 2366-2382.	5.5	2,275
6	Cytoscape StringApp: Network Analysis and Visualization of Proteomics Data. Journal of Proteome Research, 2019, 18, 623-632.	1.8	1,228
7	Cytoscape Automation: empowering workflow-based network analysis. Genome Biology, 2019, 20, 185.	3.8	888
8	Biological Network Exploration with Cytoscape 3. Current Protocols in Bioinformatics, 2014, 47, 8.13.1-24.	25.8	780
9	Global landscape of HIV–human protein complexes. Nature, 2012, 481, 365-370.	13.7	651
10	clusterMaker: a multi-algorithm clustering plugin for Cytoscape. BMC Bioinformatics, 2011, 12, 436.	1.2	541
11	Using Sequence Similarity Networks for Visualization of Relationships Across Diverse Protein Superfamilies. PLoS ONE, 2009, 4, e4345.	1.1	385
12	GLay: community structure analysis of biological networks. Bioinformatics, 2010, 26, 3135-3137.	1.8	241
13	The Structure–Function Linkage Database. Nucleic Acids Research, 2014, 42, D521-D530.	6.5	210
14	Affinity purification–mass spectrometry and network analysis to understand protein-protein interactions. Nature Protocols, 2014, 9, 2539-2554.	5.5	169
15	Leveraging Enzyme Structure˜Function Relationships for Functional Inference and Experimental Design:‰ The Structure˜Function Linkage Database. Biochemistry, 2006, 45, 2545-2555.	1.2	157
16	From Structure to Systems: High-Resolution, Quantitative Genetic Analysis of RNA Polymerase II. Cell, 2013, 154, 775-788.	13.5	132
17	Enhancing UCSF Chimera through web services. Nucleic Acids Research, 2014, 42, W478-W484.	6.5	116
18	Partitioning biological data with transitivity clustering. Nature Methods, 2010, 7, 419-420.	9.0	84

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19	Protein network prediction and topological analysis in Leishmania major as a tool for drug target selection. BMC Bioinformatics, 2010, 11, 484.	1.2	81
20	structureViz: linking Cytoscape and UCSF Chimera. Bioinformatics, 2007, 23, 2345-2347.	1.8	71
21	Visualize omics data on networks with Omics Visualizer, a Cytoscape App. F1000Research, 2020, 9, 157.	0.8	54
22	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data. F1000Research, 2019, 8, 296.	0.8	49
23	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data. F1000Research, 2019, 8, 296.	0.8	45
24	enhancedGraphics: a Cytoscape app for enhanced node graphics. F1000Research, 2014, 3, 147.	0.8	45
25	Improving the quality of protein similarity network clustering algorithms using the network edge weight distribution. Bioinformatics, 2011, 27, 326-333.	1.8	36
26	Visualize omics data on networks with Omics Visualizer, a Cytoscape App. F1000Research, 2020, 9, 157.	0.8	35
27	Prediction of enzymatic pathways by integrative pathway mapping. ELife, 2018, 7, .	2.8	30
28	Genetic interaction mapping informs integrative structure determination of protein complexes. Science, 2020, 370, .	6.0	24
29	The 3-channel Lissajous' trajectory of the auditory brain-stem response. II. Methodology. Electroencephalography and Clinical Neurophysiology - Evoked Potentials, 1987, 68, 327-332.	2.0	21
30	The 3-channel Lissajous' trajectory of the auditory brain-stem response. VII. Planar segments in humans. Electroencephalography and Clinical Neurophysiology - Evoked Potentials, 1987, 68, 368-379.	2.0	21
31	Ten simple rules to create biological network figures for communication. PLoS Computational Biology, 2019, 15, e1007244.	1.5	21
32	An Atlas of Peroxiredoxins Created Using an Active Site Profile-Based Approach to Functionally Relevant Clustering of Proteins. PLoS Computational Biology, 2017, 13, e1005284.	1.5	19
33	The Cytoscape Automation app article collection. F1000Research, 2018, 7, 800.	0.8	17
34	Low-density lipoprotein receptor-related protein 1 (LRP1) is a novel receptor for apolipoprotein A4 (APOA4) in adipose tissue. Scientific Reports, 2021, 11, 13289.	1.6	16
35	setsApp: Set operations for Cytoscape Nodes and Edges. F1000Research, 2014, 3, 149.	0.8	14
36	Integrative visual analysis of protein sequence mutations. BMC Proceedings, 2014, 8, S2.	1.8	13

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37	An approach to functionally relevant clustering of the protein universe: Active site profile–based clustering of protein structures and sequences. Protein Science, 2017, 26, 677-699.	3.1	13
38	CyAnimator: Simple Animations of Cytoscape Networks. F1000Research, 2015, 4, 482.	0.8	11
39	The Cytoscape app article collection. F1000Research, 2014, 3, 138.	0.8	10
40	CyAnimator: Simple Animations of Cytoscape Networks. F1000Research, 2015, 4, 482.	0.8	10
41	Computational Tools for the Interactive Exploration of Proteomic and Structural Data. Molecular and Cellular Proteomics, 2010, 9, 1703-1715.	2.5	9
42	setsApp for Cytoscape: Set operations for Cytoscape Nodes and Edges. F1000Research, 2014, 3, 149.	0.8	8
43	DASP3: identification of protein sequences belonging to functionally relevant groups. BMC Bioinformatics, 2016, 17, 458.	1.2	6
44	Biocuration in the structure–function linkage database: the anatomy of a superfamily. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	6
45	aMatReader: Importing adjacency matrices via Cytoscape Automation. F1000Research, 2018, 7, 823.	0.8	6
46	aMatReader: Importing adjacency matrices via Cytoscape Automation. F1000Research, 2018, 7, 823.	0.8	5
47	A biomedical open knowledge network harnesses the power of AI to understand deep human biology. AI Magazine, 2022, 43, 46-58.	1.4	5
48	Effects of acute nerve compression on conduction of impulse trains of increasing frequency. Journal of the Neurological Sciences, 1985, 67, 187-199.	0.3	4
49	cddApp: a Cytoscape app for accessing the NCBI conserved domain database. Bioinformatics, 2015, 31, 134-136.	1.8	4
50	Copycat Layout: Network layout alignment via Cytoscape Automation. F1000Research, 2018, 7, 822.	0.8	3
51	Biocuration in the structure–function linkage database: the anatomy of a superfamily. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	2
52	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data. F1000Research, 0, 8, 296.	0.8	2
53	scNetViz: from single cells to networks using Cytoscape. F1000Research, 2021, 10, 448.	0.8	1
54	Copycat Layout: Network layout alignment via Cytoscape Automation. F1000Research, 2018, 7, 822.	0.8	1