

John H Morris

List of Publications by Year in descending order

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Version: 2024-02-01

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	A biomedical open knowledge network harnesses the power of AI to understand deep human biology. AI Magazine, 2022, 43, 46-58.	1.4	5
2	<scp>UCSF ChimeraX</scp>: Structure visualization for researchers, educators, and developers. Protein Science, 2021, 30, 70-82.	3.1	4,478
3	scNetViz: from single cells to networks using Cytoscape. F1000Research, 2021, 10, 448.	0.8	1
4	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
5	Genetic interaction mapping informs integrative structure determination of protein complexes. Science, 2020, 370, .	6.0	24
6	Visualize omics data on networks with Omics Visualizer, a Cytoscape App. F1000Research, 2020, 9, 157.	0.8	54
7	Visualize omics data on networks with Omics Visualizer, a Cytoscape App. F1000Research, 2020, 9, 157.	0.8	35
8	Cytoscape Automation: empowering workflow-based network analysis. Genome Biology, 2019, 20, 185.	3.8	888
9	Ten simple rules to create biological network figures for communication. PLoS Computational Biology, 2019, 15, e1007244.	1.5	21
10	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
11	Cytoscape StringApp: Network Analysis and Visualization of Proteomics Data. Journal of Proteome Research, 2019, 18, 623-632.	1.8	1,228
12	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data. F1000Research, 2019, 8, 296.	0.8	49
13	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data. F1000Research, 2019, 8, 296.	0.8	45
14	UCSF ChimeraX: Meeting modern challenges in visualization and analysis. Protein Science, 2018, 27, 14-25.	3.1	3,377
15	Prediction of enzymatic pathways by integrative pathway mapping. ELife, 2018, 7, .	2.8	30
16	Copycat Layout: Network layout alignment via Cytoscape Automation. F1000Research, 2018, 7, 822.	0.8	3
17	Copycat Layout: Network layout alignment via Cytoscape Automation. F1000Research, 2018, 7, 822.	0.8	1
18	aMatReader: Importing adjacency matrices via Cytoscape Automation. F1000Research, 2018, 7, 823.	0.8	5

#	ARTICLE	IF	CITATIONS
19	The Cytoscape Automation app article collection. F1000Research, 2018, 7, 800.	0.8	17
20	aMatReader: Importing adjacency matrices via Cytoscape Automation. F1000Research, 2018, 7, 823.	0.8	6
21	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
22	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
23	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
24	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
25	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
26	DASP3: identification of protein sequences belonging to functionally relevant groups. BMC Bioinformatics, 2016, 17, 458.	1.2	6
27	cddApp: a Cytoscape app for accessing the NCBI conserved domain database. Bioinformatics, 2015, 31, 134-136.	1.8	4
28	CyAnimator: Simple Animations of Cytoscape Networks. F1000Research, 2015, 4, 482.	0.8	11
29	CyAnimator: Simple Animations of Cytoscape Networks. F1000Research, 2015, 4, 482.	0.8	10
30	The Structure-Function Linkage Database. Nucleic Acids Research, 2014, 42, D521-D530.	6.5	210
31	Affinity purification-mass spectrometry and network analysis to understand protein-protein interactions. Nature Protocols, 2014, 9, 2539-2554.	5.5	169
32	Enhancing UCSF Chimera through web services. Nucleic Acids Research, 2014, 42, W478-W484.	6.5	116
33	Integrative visual analysis of protein sequence mutations. BMC Proceedings, 2014, 8, S2.	1.8	13
34	Biological Network Exploration with Cytoscape 3. Current Protocols in Bioinformatics, 2014, 47, 8.13.1-24.	25.8	780
35	setsApp: Set operations for Cytoscape Nodes and Edges. F1000Research, 2014, 3, 149.	0.8	14
36	enhancedGraphics: a Cytoscape app for enhanced node graphics. F1000Research, 2014, 3, 147.	0.8	45

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37	The Cytoscape app article collection. F1000Research, 2014, 3, 138.	0.8	10
38	setsApp for Cytoscape: Set operations for Cytoscape Nodes and Edges. F1000Research, 2014, 3, 149.	0.8	8
39	From Structure to Systems: High-Resolution, Quantitative Genetic Analysis of RNA Polymerase II. Cell, 2013, 154, 775-788.	13.5	132
40	Global landscape of HIVâ€‘human protein complexes. Nature, 2012, 481, 365-370.	13.7	651
41	clusterMaker: a multi-algorithm clustering plugin for Cytoscape. BMC Bioinformatics, 2011, 12, 436.	1.2	541
42	Improving the quality of protein similarity network clustering algorithms using the network edge weight distribution. Bioinformatics, 2011, 27, 326-333.	1.8	36
43	Protein network prediction and topological analysis in Leishmania major as a tool for drug target selection. BMC Bioinformatics, 2010, 11, 484.	1.2	81
44	Partitioning biological data with transitivity clustering. Nature Methods, 2010, 7, 419-420.	9.0	84
45	Computational Tools for the Interactive Exploration of Proteomic and Structural Data. Molecular and Cellular Proteomics, 2010, 9, 1703-1715.	2.5	9
46	GWay: community structure analysis of biological networks. Bioinformatics, 2010, 26, 3135-3137.	1.8	241
47	Using Sequence Similarity Networks for Visualization of Relationships Across Diverse Protein Superfamilies. PLoS ONE, 2009, 4, e4345.	1.1	385
48	structureViz: linking Cytoscape and UCSF Chimera. Bioinformatics, 2007, 23, 2345-2347.	1.8	71
49	Integration of biological networks and gene expression data using Cytoscape. Nature Protocols, 2007, 2, 2366-2382.	5.5	2,275
50	Leveraging Enzyme Structureâ€™Function Relationships for Functional Inference and Experimental Design:â€‘ The Structureâ€™Function Linkage Database. Biochemistry, 2006, 45, 2545-2555.	1.2	157
51	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
52	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
53	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
54	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data. F1000Research, 0, 8, 296.	0.8	2