

Thomas E Ferrin

List of Publications by Citations

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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.

58
papers

36,496
citations

31
h-index

70
g-index

70
ext. papers

46,272
ext. citations

7.9
avg, IF

7.03
L-index

#	Paper	IF	Citations
58	UCSF Chimera--a visualization system for exploratory research and analysis. <i>Journal of Computational Chemistry</i> , 2004 , 25, 1605-12	3.5	26500
57	A geometric approach to macromolecule-ligand interactions. <i>Journal of Molecular Biology</i> , 1982 , 161, 269-88	6.5	1790
56	UCSF ChimeraX: Meeting modern challenges in visualization and analysis. <i>Protein Science</i> , 2018 , 27, 14-25	6.3	1519
55	The MIDAS display system. <i>Journal of Molecular Graphics</i> , 1988 , 6, 13-27		852
54	UCSF ChimeraX: Structure visualization for researchers, educators, and developers. <i>Protein Science</i> , 2021 , 30, 70-82	6.3	775
53	Visualizing density maps with UCSF Chimera. <i>Journal of Structural Biology</i> , 2007 , 157, 281-7	3.4	621
52	Tools for integrated sequence-structure analysis with UCSF Chimera. <i>BMC Bioinformatics</i> , 2006 , 7, 339	3.6	376
51	UCSF Chimera, MODELLER, and IMP: an integrated modeling system. <i>Journal of Structural Biology</i> , 2012 , 179, 269-78	3.4	373
50	Designed divergent evolution of enzyme function. <i>Nature</i> , 2006 , 440, 1078-82	50.4	345
49	clusterMaker: a multi-algorithm clustering plugin for Cytoscape. <i>BMC Bioinformatics</i> , 2011 , 12, 436	3.6	337
48	Using sequence similarity networks for visualization of relationships across diverse protein superfamilies. <i>PLoS ONE</i> , 2009 , 4, e4345	3.7	287
47	ModBase, a database of annotated comparative protein structure models, and associated resources. <i>Nucleic Acids Research</i> , 2011 , 39, D465-74	20.1	252
46	Evolutionary conservation predicts function of variants of the human organic cation transporter, OCT1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 5902-7	11.5	241
45	MODBASE, a database of annotated comparative protein structure models, and associated resources. <i>Nucleic Acids Research</i> , 2004 , 32, D217-22	20.1	233
44	Natural variation in human membrane transporter genes reveals evolutionary and functional constraints. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 5896-901	11.5	208
43	The Structure-Function Linkage Database. <i>Nucleic Acids Research</i> , 2014 , 42, D521-30	20.1	169
42	Software extensions to UCSF chimera for interactive visualization of large molecular assemblies. <i>Structure</i> , 2005 , 13, 473-82	5.2	152

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	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. <i>Structure</i> , 2015 , 23, 1156-67	5.2	131
39	Conic: a fast renderer for space-filling molecules with shadows. <i>Journal of Molecular Graphics</i> , 1991 , 9, 230-6, 242		123
38	Van der waals surfaces in molecular modeling: implementation with real-time computer graphics. <i>Science</i> , 1983 , 222, 1325-7	33.3	84
37	Comparison of human solute carriers. <i>Protein Science</i> , 2010 , 19, 412-28	6.3	83
36	Automated site-directed drug design using molecular lattices. <i>Journal of Molecular Graphics</i> , 1992 , 10, 66-78, 106		83
35	Computer graphics in drug design: molecular modeling of thyroid hormone-prealbumin interactions. <i>Journal of Medicinal Chemistry</i> , 1982 , 25, 785-90	8.3	83
34	Enhancing UCSF Chimera through web services. <i>Nucleic Acids Research</i> , 2014 , 42, W478-84	20.1	80
33	Engineering cotton (+)-delta-cadinene synthase to an altered function: germacrene D-4-ol synthase. <i>Chemistry and Biology</i> , 2006 , 13, 91-8		72
32	Actin-based protrusions of migrating neutrophils are intrinsically lamellar and facilitate direction changes. <i>ELife</i> , 2017 , 6,	8.9	70
31	Nucleic acid visualization with UCSF Chimera. <i>Nucleic Acids Research</i> , 2006 , 34, e29	20.1	60
30	structureViz: linking Cytoscape and UCSF Chimera. <i>Bioinformatics</i> , 2007 , 23, 2345-7	7.2	60
29	Molecular Visualization on the Holodeck. <i>Journal of Molecular Biology</i> , 2018 , 430, 3982-3996	6.5	46
28	Visualization software for molecular assemblies. <i>Current Opinion in Structural Biology</i> , 2007 , 17, 587-95	8.1	32
27	RRDistMaps: a UCSF Chimera tool for viewing and comparing protein distance maps. <i>Bioinformatics</i> , 2015 , 31, 1484-6	7.2	30
26	enhancedGraphics: a Cytoscape app for enhanced node graphics. <i>F1000Research</i> , 2014 , 3, 147	3.6	30
25	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
24	The MIDAS database system. <i>Journal of Molecular Graphics</i> , 1988 , 6, 2-12		24

23	Interactive computer graphics with the UNIX time-sharing system. <i>Computer Graphics</i> , 1980 , 13, 320-331		17
22	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
21	A real-time malleable molecular surface. <i>Journal of Molecular Graphics</i> , 1990 , 8, 16-24, 26		15
20	Representing structure-function relationships in mechanistically diverse enzyme superfamilies. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2005 , 358-69	1.3	14
19	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
18	Multidomain Assembler (MDA) Generates Models of Large Multidomain Proteins. <i>Biophysical Journal</i> , 2015 , 108, 2097-102	2.9	11
17	setsApp: Set operations for Cytoscape Nodes and Edges. <i>F1000Research</i> , 2014 , 3, 149	3.6	11
16	Clinical Persistence of Chlamydia trachomatis Sexually Transmitted Strains Involves Novel Mutations in the Functional Tetramer of the Tryptophan Synthase Operon. <i>MBio</i> , 2019 , 10,	7.8	8
15	CyAnimator: Simple Animations of Cytoscape Networks. <i>F1000Research</i> , 2015 , 4, 482	3.6	8
14	CyAnimator: Simple Animations of Cytoscape Networks. <i>F1000Research</i> , 2015 , 4, 482	3.6	8
13	Computational tools for the interactive exploration of proteomic and structural data. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 1703-15	7.6	7
12	Annotating PDB files with scene information. <i>Journal of Molecular Graphics</i> , 1995 , 13, 153-8, 193		7
11	Computer-Assisted Drug Receptor Mapping Analysis. <i>ACS Symposium Series</i> , 1986 , 147-158	0.4	7
10	The Structure Superposition Database. <i>Nucleic Acids Research</i> , 2003 , 31, 505-10	20.1	6
9	Integrated tools for structural and sequence alignment and analysis. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2000 , 230-41	1.3	6
8	setsApp for Cytoscape: Set operations for Cytoscape Nodes and Edges. <i>F1000Research</i> , 2014 , 3, 149	3.6	6
7	DASP3: identification of protein sequences belonging to functionally relevant groups. <i>BMC Bioinformatics</i> , 2016 , 17, 458	3.6	6
6	Macromolecular assembly structures by comparative modeling and electron microscopy. <i>Methods in Molecular Biology</i> , 2012 , 857, 331-50	1.4	4

5	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
4	cddApp: a Cytoscape app for accessing the NCBI conserved domain database. <i>Bioinformatics</i> , 2015 , 31, 134-6	7.2	3
3	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
2	The Structure-Function Linkage Database. <i>FASEB Journal</i> , 2006 , 20, A899	0.9	
1	Enhancing data sharing in collaborative research projects with DASH. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2005 , 260-71	1.3	