Thomas E Ferrin

List of Publications by Year
in descending order

64 papers	54,571 citations	117453 34 h-index	143772 57 g-index
70 all docs	70 docs citations	70 times ranked	67910 citing authors

#	Article	IF	Citations
1	<scp>UCSF ChimeraX</scp>: Structure visualization for researchers, educators, and developers. Protein Science, 2021, 30, 70-82.	3.1	4,478
2	Clinical Persistence of Chlamydia trachomatis Sexually Transmitted Strains Involves Novel Mutations in the Functional Î±Î²Î²Î± Tetramer of the Tryptophan Synthase Operon. MBio, 2019, 10, .	1.8	20
3	Reply to Rockey et al., â€œGenomics and Chlamydial Persistence In Vivo â€. MBio, 2019, 10, .	1.8	0
4	UCSF ChimeraX: Meeting modern challenges in visualization and analysis. Protein Science, 2018, 27, 14-25.	3.1	3,377
5	Molecular Visualization on the Holodeck. Journal of Molecular Biology, 2018, 430, 3982-3996.	2.0	70
6	An approach to functionally relevant clustering of the protein universe: Active site profileâ€based clustering of protein structures and sequences. Protein Science, 2017, 26, 677-699.	3.1	13
7	Biocuration in the structureâ€“function linkage database: the anatomy of a superfamily. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	6
8	Biocuration in the structureâ€“function linkage database: the anatomy of a superfamily. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	2
9	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
10	Actin-based protrusions of migrating neutrophils are intrinsically lamellar and facilitate direction changes. ELife, 2017, 6, .	2.8	107
11	DASP3: identification of protein sequences belonging to functionally relevant groups. BMC Bioinformatics, 2016, 17, 458.	1.2	6
12	RRDistMaps: a UCSF Chimera tool for viewing and comparing protein distance maps. Bioinformatics, 2015, 31, 1484-1486.	1.8	52
13	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. Structure, 2015, 23, 1156-1167.	1.6	159
14	Multidomain Assembler (MDA) Generates Models of Large Multidomain Proteins. Biophysical Journal, 2015, 108, 2097-2102.	0.2	18
15	cddApp: a Cytoscape app for accessing the NCBI conserved domain database. Bioinformatics, 2015, 31, 134-136.	1.8	4
16	CyAnimator: Simple Animations of Cytoscape Networks. F1000Research, 2015, 4, 482.	0.8	11
17	CyAnimator: Simple Animations of Cytoscape Networks. F1000Research, 2015, 4, 482.	0.8	10
18	The Structureâ€“Function Linkage Database. Nucleic Acids Research, 2014, 42, D521-D530.	6.5	210

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19	Enhancing UCSF Chimera through web services. Nucleic Acids Research, 2014, 42, W478-W484.	6.5	116
20	setsApp: Set operations for Cytoscape Nodes and Edges. F1000Research, 2014, 3, 149.	0.8	14
21	enhancedGraphics: a Cytoscape app for enhanced node graphics. F1000Research, 2014, 3, 147.	0.8	45
22	setsApp for Cytoscape: Set operations for Cytoscape Nodes and Edges. F1000Research, 2014, 3, 149.	0.8	8
23	UCSF Chimera, MODELLER, and IMP: An integrated modeling system. Journal of Structural Biology, 2012, 179, 269-278.	1.3	506
24	Macromolecular Assembly Structures by Comparative Modeling and Electron Microscopy. Methods in Molecular Biology, 2011, 857, 331-350.	0.4	4
25	clusterMaker: a multi-algorithm clustering plugin for Cytoscape. BMC Bioinformatics, 2011, 12, 436.	1.2	541
26	Improving the quality of protein similarity network clustering algorithms using the network edge weight distribution. Bioinformatics, 2011, 27, 326-333.	1.8	36
27	ModBase, a database of annotated comparative protein structure models, and associated resources. Nucleic Acids Research, 2011, 39, D465-D474.	6.5	506
28	Comparison of human solute carriers. Protein Science, 2010, 19, 412-428.	3.1	99
29	Computational Tools for the Interactive Exploration of Proteomic and Structural Data. Molecular and Cellular Proteomics, 2010, 9, 1703-1715.	2.5	9
30	Using Sequence Similarity Networks for Visualization of Relationships Across Diverse Protein Superfamilies. PLoS ONE, 2009, 4, e4345.	1.1	385
31	structureViz: linking Cytoscape and UCSF Chimera. Bioinformatics, 2007, 23, 2345-2347.	1.8	71
32	Visualizing density maps with UCSF Chimera. Journal of Structural Biology, 2007, 157, 281-287.	1.3	802
33	Visualization software for molecular assemblies. Current Opinion in Structural Biology, 2007, 17, 587-595.	2.6	40
34	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
35	Designed divergent evolution of enzyme function. Nature, 2006, 440, 1078-1082.	13.7	414
36	Engineering Cotton (+)-Î´-Cadinene Synthase to an Altered Function: Germacrene D-4-ol Synthase. Chemistry and Biology, 2006, 13, 91-98.	6.2	83

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37	Tools for integrated sequence-structure analysis with UCSF Chimera. BMC Bioinformatics, 2006, 7, 339.	1.2	524
38	Nucleic acid visualization with UCSF Chimera. Nucleic Acids Research, 2006, 34, e29-e29.	6.5	69
39	The Structureâ€Function Linkage Database. FASEB Journal, 2006, 20, A899.	0.2	0
40	Software Extensions to UCSF Chimera for Interactive Visualization of Large Molecular Assemblies. Structure, 2005, 13, 473-482.	1.6	204
41	Enhancing data sharing in collaborative research projects with DASH. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2005, , 260-71.	0.7	0
42	Representing structure-function relationships in mechanistically diverse enzyme superfamilies. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2005, , 358-69.	0.7	14
43	UCSF Chimera?A visualization system for exploratory research and analysis. Journal of Computational Chemistry, 2004, 25, 1605-1612.	1.5	37,095
44	MODBASE, a database of annotated comparative protein structure models, and associated resources. Nucleic Acids Research, 2004, 32, 217D-222.	6.5	256
45	Evolutionary conservation predicts function of variants of the human organic cation transporter, OCT1. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 5902-5907.	3.3	265
46	Natural variation in human membrane transporter genes reveals evolutionary and functional constraints. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 5896-5901.	3.3	224
47	The Structure Superposition Database. Nucleic Acids Research, 2003, 31, 505-510.	6.5	7
48	SNP ANALYSIS AND PRESENTATION IN THE PHARMACOGENETICS OF MEMBRANE TRANSPORTERS PROJECT. , 2002, , .		2
49	High-Performance Computing for Computational Biology. , 2000, , .		0
50	MOLECULES TO MAPS: TOOLS FOR VISUALIZATION AND INTERACTION IN COMPUTATIONAL BIOLOGY. , 1999, , .		0
51	Integrated Tools for Structural and Sequence Alignment and Analysis. , 1999, , 230-41.		9
52	MOLECULES TO MAPS: TOOLS FOR VISUALIZATION AND INTERACTION IN COMPUTATIONAL BIOLOGY. , 1998, , .		0
53	Annotating PDB files with scene information. Journal of Molecular Graphics, 1995, 13, 153-158.	1.7	8
54	Molecular image representations and their uses. Journal of Molecular Graphics, 1992, 10, 47.	1.7	0

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55	Automated site-directed drug design using molecular lattices. Journal of Molecular Graphics, 1992, 10, 66-78.	1.7	95
56	Conic: A fast renderer for spacefilling molecules with shadows. Journal of Molecular Graphics, 1991, 9, 230-236.	1.7	134
57	A real-time malleable molecular surface. Journal of Molecular Graphics, 1990, 8, 16-24.	1.7	16
58	The MIDAS database system. Journal of Molecular Graphics, 1988, 6, 2-12.	1.7	27
59	The MIDAS display system. Journal of Molecular Graphics, 1988, 6, 13-27.	1.7	914
60	Computer-Assisted Drug Receptor Mapping Analysis. ACS Symposium Series, 1986, , 147-158.	0.5	10
61	Van der Waals Surfaces in Molecular Modeling: Implementation with Real-Time Computer Graphics. Science, 1983, 222, 1325-1327.	6.0	96
62	Computer graphics in drug design: molecular modeling of thyroid hormone-prealbumin interactions. Journal of Medicinal Chemistry, 1982, 25, 785-790.	2.9	93
63	A geometric approach to macromolecule-ligand interactions. Journal of Molecular Biology, 1982, 161, 269-288.	2.0	2,043
64	Interactive computer graphics with the UNIX time-sharing system. Computer Graphics, 1980, 13, 320-331.	0.1	23