# Thomas E Ferrin

List of Publications by Year
in descending order



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|---|---|---|---|
| 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 | UCSF Chimera?A visualization system for exploratory research and analysis. Journal of Computational Chemistry, 2004, 25, 1605-1612. | 1.5 | 37,095 |
| 2 | <scp>UCSF ChimeraX</scp>: Structure visualization for researchers, educators, and developers. Protein Science, 2021, 30, 70-82. | 3.1 | 4,478 |
| 3 | UCSF ChimeraX: Meeting modern challenges in visualization and analysis. Protein Science, 2018, 27, 14-25. | 3.1 | 3,377 |
| 4 | A geometric approach to macromolecule-ligand interactions. Journal of Molecular Biology, 1982, 161, 269-288. | 2.0 | 2,043 |
| 5 | The MIDAS display system. Journal of Molecular Graphics, 1988, 6, 13-27. | 1.7 | 914 |
| 6 | Visualizing density maps with UCSF Chimera. Journal of Structural Biology, 2007, 157, 281-287. | 1.3 | 802 |
| 7 | clusterMaker: a multi-algorithm clustering plugin for Cytoscape. BMC Bioinformatics, 2011, 12, 436. | 1.2 | 541 |
| 8 | Tools for integrated sequence-structure analysis with UCSF Chimera. BMC Bioinformatics, 2006, 7, 339. | 1.2 | 524 |
| 9 | ModBase, a database of annotated comparative protein structure models, and associated resources. Nucleic Acids Research, 2011, 39, D465-D474. | 6.5 | 506 |
| 10 | UCSF Chimera, MODELLER, and IMP: An integrated modeling system. Journal of Structural Biology, 2012, 179, 269-278. | 1.3 | 506 |
| 11 | Designed divergent evolution of enzyme function. Nature, 2006, 440, 1078-1082. | 13.7 | 414 |
| 12 | Using Sequence Similarity Networks for Visualization of Relationships Across Diverse Protein Superfamilies. PLoS ONE, 2009, 4, e4345. | 1.1 | 385 |
| 13 | 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 |
| 14 | MODBASE, a database of annotated comparative protein structure models, and associated resources. Nucleic Acids Research, 2004, 32, 217D-222. | 6.5 | 256 |
| 15 | 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 |
| 16 | The Structureâ€“Function Linkage Database. Nucleic Acids Research, 2014, 42, D521-D530. | 6.5 | 210 |
| 17 | Software Extensions to UCSF Chimera for Interactive Visualization of Large Molecular Assemblies. Structure, 2005, 13, 473-482. | 1.6 | 204 |
| 18 | Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. Structure, 2015, 23, 1156-1167. | 1.6 | 159 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | 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 |
| 20 | Conic: A fast renderer for spacefilling molecules with shadows. Journal of Molecular Graphics, 1991, 9, 230-236. | 1.7 | 134 |
| 21 | Enhancing UCSF Chimera through web services. Nucleic Acids Research, 2014, 42, W478-W484. | 6.5 | 116 |
| 22 | Actin-based protrusions of migrating neutrophils are intrinsically lamellar and facilitate direction changes. ELife, 2017, 6, . | 2.8 | 107 |
| 23 | Comparison of human solute carriers. Protein Science, 2010, 19, 412-428. | 3.1 | 99 |
| 24 | Van der Waals Surfaces in Molecular Modeling: Implementation with Real-Time Computer Graphics. Science, 1983, 222, 1325-1327. | 6.0 | 96 |
| 25 | Automated site-directed drug design using molecular lattices. Journal of Molecular Graphics, 1992, 10, 66-78. | 1.7 | 95 |
| 26 | Computer graphics in drug design: molecular modeling of thyroid hormone-prealbumin interactions. Journal of Medicinal Chemistry, 1982, 25, 785-790. | 2.9 | 93 |
| 27 | Engineering Cotton (+)-Î´-Cadinene Synthase to an Altered Function: Germacrene D-4-ol Synthase. Chemistry and Biology, 2006, 13, 91-98. | 6.2 | 83 |
| 28 | structureViz: linking Cytoscape and UCSF Chimera. Bioinformatics, 2007, 23, 2345-2347. | 1.8 | 71 |
| 29 | Molecular Visualization on the Holodeck. Journal of Molecular Biology, 2018, 430, 3982-3996. | 2.0 | 70 |
| 30 | Nucleic acid visualization with UCSF Chimera. Nucleic Acids Research, 2006, 34, e29-e29. | 6.5 | 69 |
| 31 | RRDistMaps: a UCSF Chimera tool for viewing and comparing protein distance maps. Bioinformatics, 2015, 31, 1484-1486. | 1.8 | 52 |
| 32 | enhancedGraphics: a Cytoscape app for enhanced node graphics. F1000Research, 2014, 3, 147. | 0.8 | 45 |
| 33 | Visualization software for molecular assemblies. Current Opinion in Structural Biology, 2007, 17, 587-595. | 2.6 | 40 |
| 34 | Improving the quality of protein similarity network clustering algorithms using the network edge weight distribution. Bioinformatics, 2011, 27, 326-333. | 1.8 | 36 |
| 35 | The MIDAS database system. Journal of Molecular Graphics, 1988, 6, 2-12. | 1.7 | 27 |
| 36 | Interactive computer graphics with the UNIX time-sharing system. Computer Graphics, 1980, 13, 320-331. | 0.1 | 23 |

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|---|---|---|---|
| 37 | 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 |
| 38 | 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 |
| 39 | Multidomain Assembler (MDA) Generates Models of Large Multidomain Proteins. Biophysical Journal, 2015, 108, 2097-2102. | 0.2 | 18 |
| 40 | A real-time malleable molecular surface. Journal of Molecular Graphics, 1990, 8, 16-24. | 1.7 | 16 |
| 41 | setsApp: Set operations for Cytoscape Nodes and Edges. F1000Research, 2014, 3, 149. | 0.8 | 14 |
| 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 | 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 |
| 44 | CyAnimator: Simple Animations of Cytoscape Networks. F1000Research, 2015, 4, 482. | 0.8 | 11 |
| 45 | Computer-Assisted Drug Receptor Mapping Analysis. ACS Symposium Series, 1986, , 147-158. | 0.5 | 10 |
| 46 | CyAnimator: Simple Animations of Cytoscape Networks. F1000Research, 2015, 4, 482. | 0.8 | 10 |
| 47 | Computational Tools for the Interactive Exploration of Proteomic and Structural Data. Molecular and Cellular Proteomics, 2010, 9, 1703-1715. | 2.5 | 9 |
| 48 | Integrated Tools for Structural and Sequence Alignment and Analysis. , 1999, , 230-41. | | 9 |
| 49 | Annotating PDB files with scene information. Journal of Molecular Graphics, 1995, 13, 153-158. | 1.7 | 8 |
| 50 | setsApp for Cytoscape: Set operations for Cytoscape Nodes and Edges. F1000Research, 2014, 3, 149. | 0.8 | 8 |
| 51 | The Structure Superposition Database. Nucleic Acids Research, 2003, 31, 505-510. | 6.5 | 7 |
| 52 | DASP3: identification of protein sequences belonging to functionally relevant groups. BMC Bioinformatics, 2016, 17, 458. | 1.2 | 6 |
| 53 | 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 |
| 54 | Macromolecular Assembly Structures by Comparative Modeling and Electron Microscopy. Methods in Molecular Biology, 2011, 857, 331-350. | 0.4 | 4 |

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| 55 | cddApp: a Cytoscape app for accessing the NCBI conserved domain database. Bioinformatics, 2015, 31, 134-136. | 1.8 | 4 |
| 56 | 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 |
| 57 | SNP ANALYSIS AND PRESENTATION IN THE PHARMACOGENETICS OF MEMBRANE TRANSPORTERS PROJECT. , 2002, , . | | 2 |
| 58 | Molecular image representations and their uses. Journal of Molecular Graphics, 1992, 10, 47. | 1.7 | 0 |
| 59 | Reply to Rockey et al., â€œGenomics and Chlamydial Persistence In Vivo â€• MBio, 2019, 10, . | 1.8 | 0 |
| 60 | High-Performance Computing for Computational Biology. , 2000, , . | | 0 |
| 61 | The Structureâ€Function Linkage Database. FASEB Journal, 2006, 20, A899. | 0.2 | 0 |
| 62 | MOLECULES TO MAPS: TOOLS FOR VISUALIZATION AND INTERACTION IN COMPUTATIONAL BIOLOGY. , 1998, , . | | 0 |
| 63 | MOLECULES TO MAPS: TOOLS FOR VISUALIZATION AND INTERACTION IN COMPUTATIONAL BIOLOGY. , 1999, , . | | 0 |
| 64 | Enhancing data sharing in collaborative research projects with DASH. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2005, , 260-71. | 0.7 | 0 |