Douglas L Theobald

List of Publications by Year
in descending order

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34	2,899	257450 24	377865 34
papers	citations	h-index	g-index
42	42	42	4178
all docs	docs citations	times ranked	citing authors

#	ARTICLE	IF	CITATIONS
1	Structure determination of high-energy states in a dynamic protein ensemble. Nature, 2022, 603, 528-535.	27.8	51
2	Bayesian machine learning analysis of single-molecule fluorescence colocalization images. ELife, 2022, 11, .	6.0	3
3	A thermodynamic model of protein structure evolution explains empirical amino acid substitution matrices. Protein Science, 2021, 30, 2057-2068.	7.6	13
4	Functional and Structural Resilience of the Active Site Loop in the Evolution of <i>Plasmodium</i> Lactate Dehydrogenase. Biochemistry, 2018, 57, 6434-6442.	2.5	11
5	Expression, purification, and spectral tuning of RhoGC, a retinylidene/guanylyl cyclase fusion protein and optogenetics tool from the aquatic fungus Blastocladiella emersonii. Journal of Biological Chemistry, 2017, 292, 10379-10389.	3.4	20
6	Evolutionary drivers of thermoadaptation in enzyme catalysis. Science, 2017, 355, 289-294.	12.6	147
7	Purification and Characterization of RhoPDE, a Retinylidene/Phosphodiesterase Fusion Protein and Potential Optogenetic Tool from the Choanoflagellate <i>Salpingoeca rosetta</i>. Biochemistry, 2017, 56, 5812-5822.	2.5	32
8	Presenilin adopts the <scp>C</scp>l<scp>C</scp> channel fold. Protein Science, 2016, 25, 1363-1365.	7.6	6
9	Gradual neofunctionalization in the convergent evolution of trichomonad lactate and malate dehydrogenases. Protein Science, 2016, 25, 1319-1331.	7.6	27
10	Relocating the Active-Site Lysine in Rhodopsin: 2. Evolutionary Intermediates. Biochemistry, 2016, 55, 4864-4870.	2.5	3
11	An Empirical Test of Convergent Evolution in Rhodopsins. Molecular Biology and Evolution, 2014, 31, 85-95.	8.9	53
12	An atomic-resolution view of neofunctionalization in the evolution of apicomplexan lactate dehydrogenases. ELife, 2014, 3, .	6.0	70
13	A gustatory receptor paralogue controls rapid warmth avoidance in Drosophila. Nature, 2013, 500, 580-584.	27.8	200
14	Likelihood-based classification of cryo-EM images using FREALIGN. Journal of Structural Biology, 2013, 183, 377-388.	2.8	241
15	Relocating the active-site lysine in rhodopsin and implications for evolution of retinylidene proteins. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 13351-13355.	7.1	29
16	Bayesian alignment of similarity shapes. Annals of Applied Statistics, 2013, 7, 989-1009.	1.1	9
17	Optimal simultaneous superpositioning of multiple structures with missing data. Bioinformatics, 2012, 28, 1972-1979.	4.1	78
18	On universal common ancestry, sequence similarity, and phylogenetic structure: the sins of P-values and the virtues of Bayesian evidence. Biology Direct, 2011, 6, 60.	4.6	17

#	ARTICLE	IF	CITATIONS
19	Rapid communication reply to comment on: â€œFast determination of the optimal rotational matrix for macromolecular superpositionsâ€: Journal of Computational Chemistry, 2011, 32, 185-186.	3.3	7
20	Potassium-selective block of barium permeation through single KcsA channels. Journal of General Physiology, 2011, 138, 421-436.	1.9	51
21	Fast determination of the optimal rotational matrix for macromolecular superpositions. Journal of Computational Chemistry, 2010, 31, 1561-1563.	3.3	104
22	Membrane transport proteins: surprises in structural sameness. Nature Structural and Molecular Biology, 2010, 17, 2-3.	8.2	27
23	Analysis of Drosophila TRPA1 reveals an ancient origin for human chemical nociception. Nature, 2010, 464, 597-600.	27.8	299
24	A formal test of the theory of universal common ancestry. Nature, 2010, 465, 219-222.	27.8	187
25	Accurate Structural Correlations from Maximum Likelihood Superpositions. PLoS Computational Biology, 2008, 4, e43.	3.2	85
26	Empirical Bayes hierarchical models for regularizing maximum likelihood estimation in the matrix Gaussian Procrustes problem. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 18521-18527.	7.1	66
27	THESEUS: maximum likelihood superpositioning and analysis of macromolecular structures. Bioinformatics, 2006, 22, 2171-2172.	4.1	188
28	Rapid calculation of RMSDs using a quaternion-based characteristic polynomial. Acta Crystallographica Section A: Foundations and Advances, 2005, 61, 478-480.	0.3	164
29	Divergent Evolution Within Protein Superfolds Inferred from Profile-based Phylogenetics. Journal of Molecular Biology, 2005, 354, 722-737.	4.2	40
30	Prediction of Multiple Tandem OB-Fold Domains in Telomere End-Binding Proteins Pot1 and Cdc13. Structure, 2004, 12, 1877-1879.	3.3	52
31	Structural Basis for Telomeric Single-stranded DNA Recognition by Yeast Cdc13. Journal of Molecular Biology, 2004, 338, 241-255.	4.2	91
32	Nucleotide shuffling and ssDNA recognition in Oxytricha nova telomere end-binding protein complexes. EMBO Journal, 2003, 22, 4314-4324.	7.8	41
33	Homology Among Telomeric End-Protection Proteins. Structure, 2003, 11, 1049-1050.	3.3	33
34	Nucleic Acid Recognition by OB-Fold Proteins. Annual Review of Biophysics and Biomolecular Structure, 2003, 32, 115-133.	18.3	448