

# Douglas L Theobald

## List of Publications by Year in descending order

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34  
papers

2,899  
citations

257450

24  
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377865

34  
g-index

42  
all docs

42  
docs citations

42  
times ranked

4178  
citing authors

#	ARTICLE	IF	CITATIONS
1	Nucleic Acid Recognition by OB-Fold Proteins. Annual Review of Biophysics and Biomolecular Structure, 2003, 32, 115-133.	18.3	448
2	Analysis of Drosophila TRPA1 reveals an ancient origin for human chemical nociception. Nature, 2010, 464, 597-600.	27.8	299
3	Likelihood-based classification of cryo-EM images using FREALIGN. Journal of Structural Biology, 2013, 183, 377-388.	2.8	241
4	A gustatory receptor paralogue controls rapid warmth avoidance in Drosophila. Nature, 2013, 500, 580-584.	27.8	200
5	THESEUS: maximum likelihood superpositioning and analysis of macromolecular structures. Bioinformatics, 2006, 22, 2171-2172.	4.1	188
6	A formal test of the theory of universal common ancestry. Nature, 2010, 465, 219-222.	27.8	187
7	Rapid calculation of RMSDs using a quaternion-based characteristic polynomial. Acta Crystallographica Section A: Foundations and Advances, 2005, 61, 478-480.	0.3	164
8	Evolutionary drivers of thermoadaptation in enzyme catalysis. Science, 2017, 355, 289-294.	12.6	147
9	Fast determination of the optimal rotational matrix for macromolecular superpositions. Journal of Computational Chemistry, 2010, 31, 1561-1563.	3.3	104
10	Structural Basis for Telomeric Single-stranded DNA Recognition by Yeast Cdc13. Journal of Molecular Biology, 2004, 338, 241-255.	4.2	91
11	Accurate Structural Correlations from Maximum Likelihood Superpositions. PLoS Computational Biology, 2008, 4, e43.	3.2	85
12	Optimal simultaneous superpositioning of multiple structures with missing data. Bioinformatics, 2012, 28, 1972-1979.	4.1	78
13	An atomic-resolution view of neofunctionalization in the evolution of apicomplexan lactate dehydrogenases. ELife, 2014, 3, .	6.0	70
14	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
15	An Empirical Test of Convergent Evolution in Rhodopsins. Molecular Biology and Evolution, 2014, 31, 85-95.	8.9	53
16	Prediction of Multiple Tandem OB-Fold Domains in Telomere End-Binding Proteins Pot1 and Cdc13. Structure, 2004, 12, 1877-1879.	3.3	52
17	Potassium-selective block of barium permeation through single KcsA channels. Journal of General Physiology, 2011, 138, 421-436.	1.9	51
18	Structure determination of high-energy states in a dynamic protein ensemble. Nature, 2022, 603, 528-535.	27.8	51

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19	Nucleotide shuffling and ssDNA recognition in <i>Oxytricha nova</i> telomere end-binding protein complexes. <i>EMBO Journal</i> , 2003, 22, 4314-4324.	7.8	41
20	Divergent Evolution Within Protein Superfolds Inferred from Profile-based Phylogenetics. <i>Journal of Molecular Biology</i> , 2005, 354, 722-737.	4.2	40
21	Homology Among Telomeric End-Protection Proteins. <i>Structure</i> , 2003, 11, 1049-1050.	3.3	33
22	Purification and Characterization of RhoPDE, a Retinylidene/Phosphodiesterase Fusion Protein and Potential Optogenetic Tool from the Choanoflagellate <i>Salpingoeca rosetta</i> . <i>Biochemistry</i> , 2017, 56, 5812-5822.	2.5	32
23	Relocating the active-site lysine in rhodopsin and implications for evolution of retinylidene proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 13351-13355.	7.1	29
24	Membrane transport proteins: surprises in structural sameness. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 2-3.	8.2	27
25	Gradual neofunctionalization in the convergent evolution of trichomonad lactate and malate dehydrogenases. <i>Protein Science</i> , 2016, 25, 1319-1331.	7.6	27
26	Expression, purification, and spectral tuning of RhoGC, a retinylidene/guanylyl cyclase fusion protein and optogenetics tool from the aquatic fungus <i>Blastocladiella emersonii</i> . <i>Journal of Biological Chemistry</i> , 2017, 292, 10379-10389.	3.4	20
27	On universal common ancestry, sequence similarity, and phylogenetic structure: the sins of P-values and the virtues of Bayesian evidence. <i>Biology Direct</i> , 2011, 6, 60.	4.6	17
28	A thermodynamic model of protein structure evolution explains empirical amino acid substitution matrices. <i>Protein Science</i> , 2021, 30, 2057-2068.	7.6	13
29	Functional and Structural Resilience of the Active Site Loop in the Evolution of <i>Plasmodium</i> Lactate Dehydrogenase. <i>Biochemistry</i> , 2018, 57, 6434-6442.	2.5	11
30	Bayesian alignment of similarity shapes. <i>Annals of Applied Statistics</i> , 2013, 7, 989-1009.	1.1	9
31	Rapid communication reply to comment on: "Fast determination of the optimal rotational matrix for macromolecular superpositions". <i>Journal of Computational Chemistry</i> , 2011, 32, 185-186.	3.3	7
32	Presenilin adopts the $\beta$ -barrel channel fold. <i>Protein Science</i> , 2016, 25, 1363-1365.	7.6	6
33	Relocating the Active-Site Lysine in Rhodopsin: 2. Evolutionary Intermediates. <i>Biochemistry</i> , 2016, 55, 4864-4870.	2.5	3
34	Bayesian machine learning analysis of single-molecule fluorescence colocalization images. <i>ELife</i> , 2022, 11, .	6.0	3