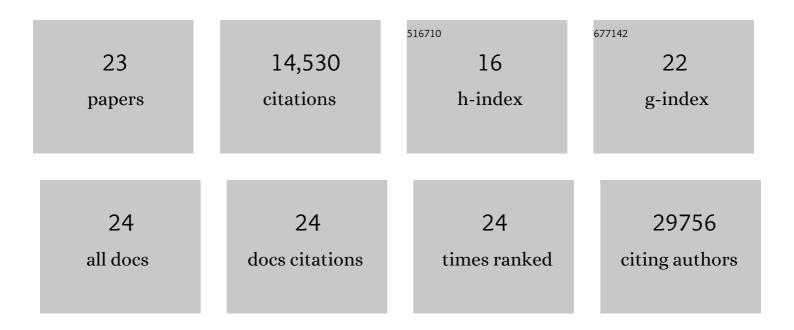
Lawrence A Kelley

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3932720/publications.pdf Version: 2024-02-01



LAWDENCE & KELLEY

#	Article	IF	CITATIONS
1	Genome3D: integrating a collaborative data pipeline to expand the depth and breadth of consensus protein structure annotation. Nucleic Acids Research, 2020, 48, D314-D319.	14.5	13
2	The Genome3D Consortium for Structural Annotations of Selected Model Organisms. Methods in Molecular Biology, 2020, 2165, 27-67.	0.9	3
3	PhyreRisk: A Dynamic Web Application to Bridge Genomics, Proteomics and 3D Structural Data to Guide Interpretation of Human Genetic Variants. Journal of Molecular Biology, 2019, 431, 2460-2466.	4.2	21
4	ePlant: Visualizing and Exploring Multiple Levels of Data for Hypothesis Generation in Plant Biology. Plant Cell, 2017, 29, 1806-1821.	6.6	316
5	Identification of the Autochaperone Domain in the Type Va Secretion System (T5aSS): Prevalent Feature of Autotransporters with a Î ² -Helical Passenger. Frontiers in Microbiology, 2017, 8, 2607.	3.5	17
6	Fold Recognition. , 2017, , 59-90.		0
7	PhyreStorm: A Web Server for Fast Structural Searches Against the PDB. Journal of Molecular Biology, 2016, 428, 702-708.	4.2	15
8	Genome3D: exploiting structure to help users understand their sequences. Nucleic Acids Research, 2015, 43, D382-D386.	14.5	42
9	Partial protein domains: evolutionary insights and bioinformatics challenges. Genome Biology, 2015, 16, 100.	8.8	10
10	The Phyre2 web portal for protein modeling, prediction and analysis. Nature Protocols, 2015, 10, 845-858.	12.0	8,366
11	Three-dimensional structure of the human breast cancer resistance protein (BCRP/ABCG2) in an inward-facing conformation. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1725-1735.	2.5	30
12	SuSPect: Enhanced Prediction of Single Amino Acid Variant (SAV) Phenotype Using Network Features. Journal of Molecular Biology, 2014, 426, 2692-2701.	4.2	189
13	Functional assignment of Mycobacterium tuberculosis proteome revealed byÂgenome-scale fold-recognition. Tuberculosis, 2013, 93, 40-46.	1.9	18
14	High–quality protein backbone reconstruction from alpha carbons using Gaussian mixture models. Journal of Computational Chemistry, 2013, 34, 1881-1889.	3.3	52
15	Genome3D: a UK collaborative project to annotate genomic sequences with predicted 3D structures based on SCOP and CATH domains. Nucleic Acids Research, 2012, 41, D499-D507.	14.5	53
16	Functional significance of mutations in the Snf2 domain of ATRX. Human Molecular Genetics, 2011, 20, 2603-2610.	2.9	46
17	ePlant and the 3D Data Display Initiative: Integrative Systems Biology on the World Wide Web. PLoS ONE, 2011, 6, e15237.	2.5	43
18	3DLigandSite: predicting ligand-binding sites using similar structures. Nucleic Acids Research, 2010, 38, W469-W473.	14.5	549

LAWRENCE A KELLEY

#	Article	IF	CITATIONS
19	Protein Folding Requires Crowd Control in a Simulated Cell. Journal of Molecular Biology, 2010, 397, 1329-1338.	4.2	76
20	Protein structure prediction on the Web: a case study using the Phyre server. Nature Protocols, 2009, 4, 363-371.	12.0	3,815
21	OLDERADO: On-line database of ensemble representatives and domains. Protein Science, 2008, 6, 2628-2630.	7.6	53
22	Exploring the extremes of sequence/structure space with ensemble fold recognition in the program Phyre. Proteins: Structure, Function and Bioinformatics, 2008, 70, 611-625.	2.6	377
23	An automated approach for clustering an ensemble of NMR-derived protein structures into conformationally related subfamilies. Protein Engineering, Design and Selection, 1996, 9, 1063-1065.	2.1	426