

# Lawrence A Kelley

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3932720/publications.pdf>

Version: 2024-02-01

23  
papers

14,530  
citations

516710

16  
h-index

677142

22  
g-index

24  
all docs

24  
docs citations

24  
times ranked

29756  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome3D: integrating a collaborative data pipeline to expand the depth and breadth of consensus protein structure annotation. <i>Nucleic Acids Research</i> , 2020, 48, D314-D319.	14.5	13
2	The Genome3D Consortium for Structural Annotations of Selected Model Organisms. <i>Methods in Molecular Biology</i> , 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. <i>Journal of Molecular Biology</i> , 2019, 431, 2460-2466.	4.2	21
4	ePlant: Visualizing and Exploring Multiple Levels of Data for Hypothesis Generation in Plant Biology. <i>Plant Cell</i> , 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 $\beta^2$ -Helical Passenger. <i>Frontiers in Microbiology</i> , 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. <i>Journal of Molecular Biology</i> , 2016, 428, 702-708.	4.2	15
8	Genome3D: exploiting structure to help users understand their sequences. <i>Nucleic Acids Research</i> , 2015, 43, D382-D386.	14.5	42
9	Partial protein domains: evolutionary insights and bioinformatics challenges. <i>Genome Biology</i> , 2015, 16, 100.	8.8	10
10	The Phyre2 web portal for protein modeling, prediction and analysis. <i>Nature Protocols</i> , 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. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1725-1735.	2.5	30
12	SuSPect: Enhanced Prediction of Single Amino Acid Variant (SAV) Phenotype Using Network Features. <i>Journal of Molecular Biology</i> , 2014, 426, 2692-2701.	4.2	189
13	Functional assignment of Mycobacterium tuberculosis proteome revealed by genome-scale fold-recognition. <i>Tuberculosis</i> , 2013, 93, 40-46.	1.9	18
14	High-quality protein backbone reconstruction from alpha carbons using Gaussian mixture models. <i>Journal of Computational Chemistry</i> , 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. <i>Nucleic Acids Research</i> , 2012, 41, D499-D507.	14.5	53
16	Functional significance of mutations in the Snf2 domain of ATRX. <i>Human Molecular Genetics</i> , 2011, 20, 2603-2610.	2.9	46
17	ePlant and the 3D Data Display Initiative: Integrative Systems Biology on the World Wide Web. <i>PLoS ONE</i> , 2011, 6, e15237.	2.5	43
18	3DLigandSite: predicting ligand-binding sites using similar structures. <i>Nucleic Acids Research</i> , 2010, 38, W469-W473.	14.5	549

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