

# David Lee

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8040071/publications.pdf>

Version: 2024-02-01

11  
papers

1,938  
citations

840776

11  
h-index

1281871

11  
g-index

11  
all docs

11  
docs citations

11  
times ranked

3163  
citing authors

#	ARTICLE	IF	CITATIONS
1	CATH: an expanded resource to predict protein function through structure and sequence. <i>Nucleic Acids Research</i> , 2017, 45, D289-D295.	14.5	344
2	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016, 17, 184.	8.8	308
3	Gene3D: expanding the utility of domain assignments. <i>Nucleic Acids Research</i> , 2016, 44, D404-D409.	14.5	64
4	Novel Computational Protocols for Functionally Classifying and Characterising Serine Beta-Lactamases. <i>PLoS Computational Biology</i> , 2016, 12, e1004926.	3.2	24
5	CATH FunFHMMer web server: protein functional annotations using functional family assignments. <i>Nucleic Acids Research</i> , 2015, 43, W148-W153.	14.5	59
6	CATH: comprehensive structural and functional annotations for genome sequences. <i>Nucleic Acids Research</i> , 2015, 43, D376-D381.	14.5	399
7	Functional classification of CATH superfamilies: a domain-based approach for protein function annotation. <i>Bioinformatics</i> , 2015, 31, 3460-3467.	4.1	93
8	Gene3D: Multi-domain annotations for protein sequence and comparative genome analysis. <i>Nucleic Acids Research</i> , 2014, 42, D240-D245.	14.5	50
9	1,000 structures and more from the MCSG. <i>BMC Structural Biology</i> , 2011, 11, 2.	2.3	14
10	Domain-Based and Family-Specific Sequence Identity Thresholds Increase the Levels of Reliable Protein Function Transfer. <i>Journal of Molecular Biology</i> , 2009, 387, 416-430.	4.2	98
11	Predicting protein function from sequence and structure. <i>Nature Reviews Molecular Cell Biology</i> , 2007, 8, 995-1005.	37.0	485