

David Lee

List of Publications by Year in descending order

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

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