

# Yuxiang Jiang

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9411246/publications.pdf>

Version: 2024-02-01

9  
papers

707  
citations

1307594

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1474206

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989  
citing authors

#	ARTICLE	IF	CITATIONS
1	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016, 17, 184.	8.8	308
2	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019, 20, 244.	8.8	261
3	The impact of incomplete knowledge on the evaluation of protein function prediction: a structured-output learning perspective. <i>Bioinformatics</i> , 2014, 30, i609-i616.	4.1	43
4	Working toward precision medicine: Predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. <i>Human Mutation</i> , 2017, 38, 1182-1192.	2.5	39
5	New <i>Drosophila</i> Long-Term Memory Genes Revealed by Assessing Computational Function Prediction Methods. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 251-267.	1.8	15
6	CAGI SickKids challenges: Assessment of phenotype and variant predictions derived from clinical and genomic data of children with undiagnosed diseases. <i>Human Mutation</i> , 2019, 40, 1373-1391.	2.5	10
7	Predicting venous thromboembolism risk from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. <i>Human Mutation</i> , 2019, 40, 1314-1320.	2.5	10
8	Enumerating consistent sub-graphs of directed acyclic graphs: an insight into biomedical ontologies. <i>Bioinformatics</i> , 2018, 34, i313-i322.	4.1	7
9	Prioritizing de novo autism risk variants with calibrated gene- and variant-scoring models. <i>Human Genetics</i> , 2021, , 1.	3.8	1