Ronghui You

List of Publications by Year
in descending order

13 papers	**940** citations	933447 **10** h-index	1281871 **11** g-index
13 all docs	**13** docs citations	**13** times ranked	**797** citing authors

#	Article	IF	Citations
1	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244.	8.8	261
2	GOLabeler: improving sequence-based large-scale protein function prediction by learning to rank. Bioinformatics, 2018, 34, 2465-2473.	4.1	136
3	Critical Assessment of Metagenome Interpretation: the second round of challenges. Nature Methods, 2022, 19, 429-440.	19.0	133
4	DeepMeSH: deep semantic representation for improving large-scale MeSH indexing. Bioinformatics, 2016, 32, i70-i79.	4.1	93
5	NetGO: improving large-scale protein function prediction with massive network information. Nucleic Acids Research, 2019, 47, W379-W387.	14.5	86
6	DeepText2GO: Improving large-scale protein function prediction with deep semantic text representation. Methods, 2018, 145, 82-90.	3.8	58
7	NetGO 2.0: improving large-scale protein function prediction with massive sequence, text, domain, family and network information. Nucleic Acids Research, 2021, 49, W469-W475.	14.5	53
8	DeepGraphGO: graph neural network for large-scale, multispecies protein function prediction. Bioinformatics, 2021, 37, i262-i271.	4.1	50
9	FullMeSH: improving large-scale MeSH indexing with full text. Bioinformatics, 2020, 36, 1533-1541.	4.1	26
10	BERTMeSH: deep contextual representation learning for large-scale high-performance MeSH indexing with full text. Bioinformatics, 2021, 37, 684-692.	4.1	19
11	DeepDock: Enhancing Ligand-protein Interaction Prediction by a Combination of Ligand and Structure Information. , 2019, , .		15
12	ARG-SHINE: improve antibiotic resistance class prediction by integrating sequence homology, functional information and deep convolutional neural network. NAR Genomics and Bioinformatics, 2021, 3, lqab066.	3.2	6
13	DeepText2Go: Improving large-scale protein function prediction with deep semantic text representation. , 2017, , .		4