

Siqi Liang

List of Publications by Year in descending order

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Version: 2024-02-01

10
papers

343
citations

1163117

8
h-index

1372567

10
g-index

13
all docs

13
docs citations

13
times ranked

540
citing authors

#	ARTICLE	IF	CITATIONS
1	Deep learning methods for 3D structural proteome and interactome modeling. <i>Current Opinion in Structural Biology</i> , 2022, 73, 102329.	5.7	19
2	SAAMBE-SEQ: a sequence-based method for predicting mutation effect on protein-protein binding affinity. <i>Bioinformatics</i> , 2021, 37, 992-999.	4.1	17
3	A 3D structural SARS-CoV-2-human interactome to explore genetic and drug perturbations. <i>Nature Methods</i> , 2021, 18, 1477-1488.	19.0	17
4	Revealing new therapeutic opportunities through drug target prediction: a class imbalance-tolerant machine learning approach. <i>Bioinformatics</i> , 2020, 36, 4490-4497.	4.1	9
5	SAAMBE-3D: Predicting Effect of Mutations on Protein-Protein Interactions. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2563.	4.1	66
6	Extensive disruption of protein interactions by genetic variants across the allele frequency spectrum in human populations. <i>Nature Communications</i> , 2019, 10, 4141.	12.8	48
7	Leveraging genetic interactions for adverse drug-drug interaction prediction. <i>PLoS Computational Biology</i> , 2019, 15, e1007068.	3.2	18
8	Interactome INSIDER: a structural interactome browser for genomic studies. <i>Nature Methods</i> , 2018, 15, 107-114.	19.0	133
9	Extracting complementary insights from molecular phenotypes for prioritization of disease-associated mutations. <i>Current Opinion in Systems Biology</i> , 2018, 11, 107-116.	2.6	4
10	iRegNet3D: three-dimensional integrated regulatory network for the genomic analysis of coding and non-coding disease mutations. <i>Genome Biology</i> , 2017, 18, 10.	8.8	9