

Shaofeng Lin

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

1,377
citations

567281

15
h-index

752698

20
g-index

21
all docs

21
docs citations

21
times ranked

2119
citing authors

#	ARTICLE	IF	CITATIONS
1	PLMD: An updated data resource of protein lysine modifications. <i>Journal of Genetics and Genomics</i> , 2017, 44, 243-250.	3.9	198
2	GPS 5.0: An Update on the Prediction of Kinase-specific Phosphorylation Sites in Proteins. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 72-80.	6.9	197
3	Database Resources of the National Genomics Data Center in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D24-D33.	14.5	165
4	Database Resources of the BIG Data Center in 2019. <i>Nucleic Acids Research</i> , 2019, 47, D8-D14.	14.5	157
5	PTMD: A Database of Human Disease-associated Post-translational Modifications. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 244-251.	6.9	129
6	DrLLPS: a data resource of liquid-liquid phase separation in eukaryotes. <i>Nucleic Acids Research</i> , 2020, 48, D288-D295.	14.5	112
7	dbPAF: an integrative database of protein phosphorylation in animals and fungi. <i>Scientific Reports</i> , 2016, 6, 23534.	3.3	78
8	OUP accepted manuscript. <i>Nucleic Acids Research</i> , 2017, 45, D264-D270.	14.5	62
9	iLUUCD 2.0: an update with rich annotations for ubiquitin and ubiquitin-like conjugations. <i>Nucleic Acids Research</i> , 2018, 46, D447-D453.	14.5	57
10	EPSPD: a well-annotated data resource of protein phosphorylation sites in eukaryotes. <i>Briefings in Bioinformatics</i> , 2021, 22, 298-307.	6.5	49
11	Posttranscriptional regulation of de novo lipogenesis by glucose-induced O-GlcNAcylation. <i>Molecular Cell</i> , 2021, 81, 1890-1904.e7.	9.7	39
12	Integrated omics in <i>Drosophila</i> uncover a circadian kinome. <i>Nature Communications</i> , 2020, 11, 2710.	12.8	23
13	iEKPD 2.0: an update with rich annotations for eukaryotic protein kinases, protein phosphatases and proteins containing phosphoprotein-binding domains. <i>Nucleic Acids Research</i> , 2019, 47, D344-D350.	14.5	22
14	dbPSP 2.0, an updated database of protein phosphorylation sites in prokaryotes. <i>Scientific Data</i> , 2020, 7, 164.	5.3	20
15	CPLM 4.0: an updated database with rich annotations for protein lysine modifications. <i>Nucleic Acids Research</i> , 2022, 50, D451-D459.	14.5	20
16	WocEA: The visualization of functional enrichment results in word clouds. <i>Journal of Genetics and Genomics</i> , 2018, 45, 415-417.	3.9	16
17	GPS-PBS: A Deep Learning Framework to Predict Phosphorylation Sites that Specifically Interact with Phosphoprotein-Binding Domains. <i>Cells</i> , 2020, 9, 1266.	4.1	10
18	GPS-Uber: a hybrid-learning framework for prediction of general and E3-specific lysine ubiquitination sites. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	10

#	ARTICLE	IF	CITATIONS
19	PTMsnp: A Web Server for the Identification of Driver Mutations That Affect Protein Post-translational Modification. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 593661.	3.7	7
20	Atg9-centered multi-omics integration reveals new autophagy regulators in <i>Saccharomyces cerevisiae</i> . <i>Autophagy</i> , 2021, 17, 4453-4476.	9.1	6
21	iPCD: A Comprehensive Data Resource of Regulatory Proteins in Programmed Cell Death. <i>Cells</i> , 2022, 11, 2018.	4.1	0