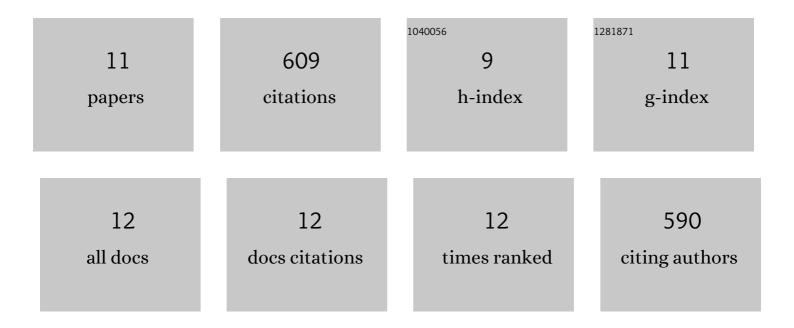
Jinjun Gao

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5932220/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Class I histone deacetylases (HDAC1–3) are histone lysine delactylases. Science Advances, 2022, 8, eabi6696.	10.3	141
2	Quantitative Profiling of Protein Carbonylations in Ferroptosis by an Aniline-Derived Probe. Journal of the American Chemical Society, 2018, 140, 4712-4720.	13.7	139
3	Quantitative Profiling of Protein O-GlcNAcylation Sites by an Isotope-Tagged Cleavable Linker. ACS Chemical Biology, 2018, 13, 1983-1989.	3.4	73
4	RNA-Seq Analysis of Transcriptome and Glucosinolate Metabolism in Seeds and Sprouts of Broccoli (Brassica oleracea var. italic). PLoS ONE, 2014, 9, e88804.	2.5	63
5	Selenium-Encoded Isotopic Signature Targeted Profiling. ACS Central Science, 2018, 4, 960-970.	11.3	56
6	A Dimethyl-Labeling-Based Strategy for Site-Specifically Quantitative Chemical Proteomics. Analytical Chemistry, 2018, 90, 9576-9582.	6.5	50
7	A Quantitative Chemoproteomic Platform to Monitor Selenocysteine Reactivity within a Complex Proteome. Cell Chemical Biology, 2018, 25, 1157-1167.e4.	5.2	41
8	Histone lysine methacrylation is a dynamic post-translational modification regulated by HAT1 and SIRT2. Cell Discovery, 2021, 7, 122.	6.7	19
9	CIMAGE2.0: An Expanded Tool for Quantitative Analysis of Activity-Based Protein Profiling (ABPP) Data. Journal of Proteome Research, 2021, 20, 4893-4900.	3.7	18
10	An accelerated and optimized algorithm of selenium-encoded isotopic signature targeted profiling for global selenoproteome analysis. Methods in Enzymology, 2022, 662, 241-258.	1.0	5
11	Quantifying Turnover Dynamics of Selenoproteome by Isotopic Perturbation. Analytical Chemistry, 2022, 94, 9636-9647.	6.5	3