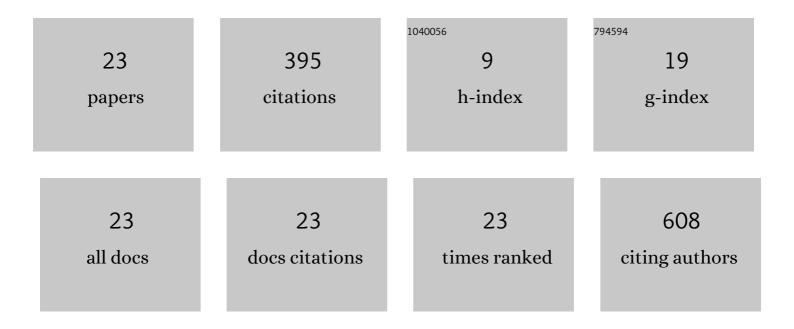
Guijin Zhai

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	TmcA functions as a lysine 2-hydroxyisobutyryltransferase to regulate transcription. Nature Chemical Biology, 2022, 18, 142-151.	8.0	8
2	Serum phosphopeptide profiling for colorectal cancer diagnosis using liquid chromatography–mass spectrometry. Rapid Communications in Mass Spectrometry, 2022, 36, e9316.	1.5	0
3	Systematic Proteome and Lysine Succinylome Analysis Reveals Enhanced Cell Migration by Hyposuccinylation in Esophageal Squamous Cell Carcinoma. Molecular and Cellular Proteomics, 2021, 20, 100053.	3.8	28
4	Identification of Abnormal Proteins in Plasma from Gout Patients by LC-MS/MS. Separations, 2021, 8, 85.	2.4	3
5	DNA-guided photoactivatable probe-based chemical proteomics reveals the reader protein of mRNA methylation. IScience, 2021, 24, 103046.	4.1	3
6	Identification of dual histone modification-binding protein interaction by combining mass spectrometry and isothermal titration calorimetric analysis. Journal of Advanced Research, 2020, 22, 35-46.	9.5	10
7	An Integrated Approach for Combinatorial Readout of Dual Histone Modifications by Epigenetic Tandem Domains. Analytical Chemistry, 2020, 92, 6218-6223.	6.5	3
8	Protein lysine de-2-hydroxyisobutyrylation by CobB in prokaryotes. Science Advances, 2019, 5, eaaw6703.	10.3	51
9	Combinatorial Peptide Ligand Library-Based Photoaffinity Probe for the Identification of Phosphotyrosine-Binding Domain Proteins. Analytical Chemistry, 2019, 91, 3221-3226.	6.5	4
10	An Integrated Approach Based on a DNA Self-Assembly Technique for Characterization of Crosstalk among Combinatorial Histone Modifications. Analytical Chemistry, 2018, 90, 3692-3696.	6.5	12
11	Systematic Identification of Lysine 2-hydroxyisobutyrylated Proteins in Proteus mirabilis. Molecular and Cellular Proteomics, 2018, 17, 482-494.	3.8	43
12	Yes-Associated Protein Promotes Angiogenesis via Signal Transducer and Activator of Transcription 3 in Endothelial Cells. Circulation Research, 2018, 122, 591-605.	4.5	98
13	An Efficient Approach for Selective Enrichment of Histone Modification Readers Using Self-Assembled Multivalent Photoaffinity Peptide Probes. Analytical Chemistry, 2018, 90, 11385-11392.	6.5	12
14	DNA-Templated Aptamer Probe for Identification of Target Proteins. Analytical Chemistry, 2017, 89, 4071-4076.	6.5	22
15	Probing the Binding Interfaces of Histone-Aptamer by Photo Cross-Linking Mass Spectrometry. ACS Chemical Biology, 2017, 12, 57-62.	3.4	6
16	Maleic Anhydride Labeling-Based Approach for Quantitative Proteomics and Successive Derivatization of Peptides. Analytical Chemistry, 2017, 89, 8259-8265.	6.5	9
17	Evaluation of serum phosphopeptides as potential biomarkers of gastric cancer. RSC Advances, 2017, 7, 21630-21637.	3.6	9
18	Development of a DNAâ€Templated Peptide Probe for Photoaffinity Labeling and Enrichment of the Histone Modification Reader Proteins. Angewandte Chemie, 2016, 128, 8125-8129.	2.0	8

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#	Article	IF	CITATIONS
19	The Unexpected and Exceptionally Facile Chemical Modification of the Phenolic Hydroxyl Group of Tyrosine by Polyhalogenated Quinones under Physiological Conditions. Chemical Research in Toxicology, 2016, 29, 1699-1705.	3.3	8
20	Identification of hydroxylation at aromatic amino acid residues in yeast kinase using mass spectrometry with affinity enrichment. Rapid Communications in Mass Spectrometry, 2016, 30, 185-189.	1.5	2
21	Development of a DNAâ€Templated Peptide Probe for Photoaffinity Labeling and Enrichment of the Histone Modification Reader Proteins. Angewandte Chemie - International Edition, 2016, 55, 7993-7997.	13.8	29
22	Profiling post-translational modifications of histones in neural differentiation of embryonic stem cells using liquid chromatography–mass spectrometry. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2016, 1017-1018, 36-44.	2.3	5
23	Evaluation of serum phosphopeptides as potential cancer biomarkers by mass spectrometric absolute quantification. Talanta, 2014, 125, 411-417.	5.5	22