

Huilin Zhou

List of Publications by Year in descending order

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36
papers

4,289
citations

361413

20
h-index

395702

33
g-index

42
all docs

42
docs citations

42
times ranked

4762
citing authors

#	ARTICLE	IF	CITATIONS
1	Quantitative profiling of differentiation-induced microsomal proteins using isotope-coded affinity tags and mass spectrometry. <i>Nature Biotechnology</i> , 2001, 19, 946-951.	17.5	913
2	A systematic approach to the analysis of protein phosphorylation. <i>Nature Biotechnology</i> , 2001, 19, 375-378.	17.5	742
3	A Multidimensional Chromatography Technology for In-depth Phosphoproteome Analysis. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1389-1396.	3.8	472
4	Proteome-wide identification of in vivo targets of DNA damage checkpoint kinases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 10364-10369.	7.1	378
5	Quantitative proteome analysis by solid-phase isotope tagging and mass spectrometry. <i>Nature Biotechnology</i> , 2002, 20, 512-515.	17.5	372
6	Global Analyses of Sumoylated Proteins in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 32262-32268.	3.4	284
7	mTORC2 Regulates Amino Acid Metabolism in Cancer by Phosphorylation of the Cystine-Glutamate Antipporter xCT. <i>Molecular Cell</i> , 2017, 67, 128-138.e7.	9.7	147
8	A Proteome-wide Analysis of Kinase-Substrate Network in the DNA Damage Response. <i>Journal of Biological Chemistry</i> , 2010, 285, 12803-12812.	3.4	110
9	Both Decreased and Increased SRPK1 Levels Promote Cancer by Interfering with PHLPP-Mediated Dephosphorylation of Akt. <i>Molecular Cell</i> , 2014, 54, 378-391.	9.7	105
10	Macrophage Migration Inhibitory Factor as a Chaperone Inhibiting Accumulation of Misfolded SOD1. <i>Neuron</i> , 2015, 86, 218-232.	8.1	98
11	An FHA domain-mediated protein interaction network of Rad53 reveals its role in polarized cell growth. <i>Journal of Cell Biology</i> , 2006, 175, 743-753.	5.2	85
12	Dynamic Changes in Protein-Protein Interaction and Protein Phosphorylation Probed with Amine-reactive Isotope Tag. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1358-1369.	3.8	71
13	Mechanism of Dun1 Activation by Rad53 Phosphorylation in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2007, 282, 986-995.	3.4	68
14	Distinct SUMO Ligases Cooperate with Esc2 and Slx5 to Suppress Duplication-Mediated Genome Rearrangements. <i>PLoS Genetics</i> , 2013, 9, e1003670.	3.5	68
15	Phosphorylation-Specific MS/MS Scoring for Rapid and Accurate Phosphoproteome Analysis. <i>Journal of Proteome Research</i> , 2008, 7, 3373-3381.	3.7	51
16	Phosphorylation of Sae2 Mediates Forkhead-associated (FHA) Domain-specific Interaction and Regulates Its DNA Repair Function. <i>Journal of Biological Chemistry</i> , 2015, 290, 10751-10763.	3.4	44
17	Reconstitution of Rad53 Activation by Mec1 through Adaptor Protein Mrc1. <i>Journal of Biological Chemistry</i> , 2009, 284, 18593-18604.	3.4	42
18	Recruitment of a SUMO isopeptidase to rDNA stabilizes silencing complexes by opposing SUMO targeted ubiquitin ligase activity. <i>Genes and Development</i> , 2017, 31, 802-815.	5.9	31

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19	Molecular Circuitry of the SUMO (Small Ubiquitin-like Modifier) Pathway in Controlling Sumoylation Homeostasis and Suppressing Genome Rearrangements. <i>Journal of Biological Chemistry</i> , 2016, 291, 8825-8835.	3.4	28
20	Multiple phosphorylation of Rad9 by CDK is required for DNA damage checkpoint activation. <i>Cell Cycle</i> , 2012, 11, 3792-3800.	2.6	27
21	Quantitative Protein Analysis by Solid Phase Isotope Tagging and Mass Spectrometry. , 2004, 261, 511-518.		22
22	Recruitment of the Ulp2 protease to the inner kinetochore prevents its hyper-sumoylation to ensure accurate chromosome segregation. <i>PLoS Genetics</i> , 2019, 15, e1008477.	3.5	20
23	SUMO orchestrates multiple alternative DNA-protein crosslink repair pathways. <i>Cell Reports</i> , 2021, 37, 110034.	6.4	19
24	SUMO E3 ligase Mms21 prevents spontaneous DNA damage induced genome rearrangements. <i>PLoS Genetics</i> , 2018, 14, e1007250.	3.5	16
25	Proteomics studies of the interactome of RNA polymerase II C-terminal repeated domain. <i>BMC Research Notes</i> , 2015, 8, 616.	1.4	13
26	A Method for Sporulating Budding Yeast Cells That Allows for Unbiased Identification of Kinase Substrates Using Stable Isotope Labeling by Amino Acids in Cell Culture. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2125-2135.	1.8	12
27	A Chemical and Enzymatic Approach to Study Site-Specific Sumoylation. <i>PLoS ONE</i> , 2015, 10, e0143810.	2.5	10
28	Binding to small ubiquitin-like modifier and the nucleolar protein Csm1 regulates substrate specificity of the Ulp2 protease. <i>Journal of Biological Chemistry</i> , 2018, 293, 12105-12119.	3.4	9
29	Quantitative phosphoproteomics. <i>Cell Cycle</i> , 2010, 9, 3479-3484.	2.6	7
30	Ctf3/CENP-I provides a docking site for the desumoylase Ulp2 at the kinetochore. <i>Journal of Cell Biology</i> , 2021, 220, .	5.2	4
31	Preserving Yeast Genetic Heritage through DNA Damage Checkpoint Regulation and Telomere Maintenance. <i>Biomolecules</i> , 2012, 2, 505-523.	4.0	3
32	Shared and distinct roles of Esc2 and Mms21 in suppressing genome rearrangements and regulating intracellular sumoylation. <i>PLoS ONE</i> , 2021, 16, e0247132.	2.5	3
33	A new approach to study site-specific protein sumoylation (925.3). <i>FASEB Journal</i> , 2014, 28, 925.3.	0.5	3
34	Site-specific MCM sumoylation prevents genome rearrangements by controlling origin-bound MCM. <i>PLoS Genetics</i> , 2022, 18, e1010275.	3.5	1
35	FHA domain mediated protein interaction network of Dun1 identifies its novel functions in the DNA damage response. <i>FASEB Journal</i> , 2006, 20, A509.	0.5	0
36	Quantitative Phosphoproteomic Analysis Identifies Targets of the DNA Damage Checkpoint Kinases in Yeast. <i>FASEB Journal</i> , 2007, 21, A659.	0.5	0