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	Site-specific MCM sumoylation prevents genome rearrangements by controlling origin-bound MCM. PLoS Genetics, 2022, 18, e1010275.	3.5	1
2	Shared and distinct roles of Esc2 and Mms21 in suppressing genome rearrangements and regulating intracellular sumoylation. PLoS ONE, 2021, 16, e0247132.	2.5	3
3	Ctf3/CENP-I provides a docking site for the desumoylase Ulp2 at the kinetochore. Journal of Cell Biology, 2021, 220, .	5.2	4
4	SUMO orchestrates multiple alternative DNA-protein crosslink repair pathways. Cell Reports, 2021, 37, 110034.	6.4	19
5	Recruitment of the Ulp2 protease to the inner kinetochore prevents its hyper-sumoylation to ensure accurate chromosome segregation. PLoS Genetics, 2019, 15, e1008477.	3.5	20
6	Binding to small ubiquitin-like modifier and the nucleolar protein Csm1 regulates substrate specificity of the Ulp2 protease. Journal of Biological Chemistry, 2018, 293, 12105-12119.	3.4	9
7	SUMO E3 ligase Mms21 prevents spontaneous DNA damage induced genome rearrangements. PLoS Genetics, 2018, 14, e1007250.	3.5	16
8	Recruitment of a SUMO isopeptidase to rDNA stabilizes silencing complexes by opposing SUMO targeted ubiquitin ligase activity. Genes and Development, 2017, 31, 802-815.	5.9	31
9	mTORC2 Regulates Amino Acid Metabolism in Cancer by Phosphorylation of the Cystine-Glutamate Antiporter xCT. Molecular Cell, 2017, 67, 128-138.e7.	9.7	147
10	Molecular Circuitry of the SUMO (Small Ubiquitin-like Modifier) Pathway in Controlling Sumoylation Homeostasis and Suppressing Genome Rearrangements. Journal of Biological Chemistry, 2016, 291, 8825-8835.	3.4	28
11	Proteomics studies of the interactome of RNA polymerase II C-terminal repeated domain. BMC Research Notes, 2015, 8, 616.	1.4	13
12	A Chemical and Enzymatic Approach to Study Site-Specific Sumoylation. PLoS ONE, 2015, 10, e0143810.	2.5	10
13	Phosphorylation of Sae2 Mediates Forkhead-associated (FHA) Domain-specific Interaction and Regulates Its DNA Repair Function. Journal of Biological Chemistry, 2015, 290, 10751-10763.	3.4	44
14	Macrophage Migration Inhibitory Factor as a Chaperone Inhibiting Accumulation of Misfolded SOD1. Neuron, 2015, 86, 218-232.	8.1	98
15	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. G3: Genes, Genomes, Genetics, 2014, 4, 2125-2135.	1.8	12
16	Both Decreased and Increased SRPK1 Levels Promote Cancer by Interfering with PHLPP-Mediated Dephosphorylation of Akt. Molecular Cell, 2014, 54, 378-391.	9.7	105
17	A new approach to study siteâ€specific protein sumoylation (925.3). FASEB Journal, 2014, 28, 925.3.	0.5	3
18	Distinct SUMO Ligases Cooperate with Esc2 and Slx5 to Suppress Duplication-Mediated Genome Rearrangements. PLoS Genetics, 2013, 9, e1003670.	3.5	68

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19	Multiple phosphorylation of Rad9 by CDK is required for DNA damage checkpoint activation. Cell Cycle, 2012, 11, 3792-3800.	2.6	27
20	Preserving Yeast Genetic Heritage through DNA Damage Checkpoint Regulation and Telomere Maintenance. Biomolecules, 2012, 2, 505-523.	4.0	3
21	A Proteome-wide Analysis of Kinase-Substrate Network in the DNA Damage Response. Journal of Biological Chemistry, 2010, 285, 12803-12812.	3.4	110
22	Quantitative phosphoproteomics. Cell Cycle, 2010, 9, 3479-3484.	2.6	7
23	Reconstitution of Rad53 Activation by Mec1 through Adaptor Protein Mrc1. Journal of Biological Chemistry, 2009, 284, 18593-18604.	3.4	42
24	Phosphorylation-Specific MS/MS Scoring for Rapid and Accurate Phosphoproteome Analysis. Journal of Proteome Research, 2008, 7, 3373-3381.	3.7	51
25	A Multidimensional Chromatography Technology for In-depth Phosphoproteome Analysis. Molecular and Cellular Proteomics, 2008, 7, 1389-1396.	3.8	472
26	Proteome-wide identification of in vivo targets of DNA damage checkpoint kinases. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 10364-10369.	7.1	378
27	Mechanism of Dun1 Activation by Rad53 Phosphorylation in Saccharomyces cerevisiae. Journal of Biological Chemistry, 2007, 282, 986-995.	3.4	68
28	Quantitative Phosphoproteomic Analysis Identifies Targets of the DNA Damage Checkpoint Kinases in Yeast. FASEB Journal, 2007, 21, A659.	0.5	0
29	An FHA domainâ€“mediated protein interaction network of Rad53 reveals its role in polarized cell growth. Journal of Cell Biology, 2006, 175, 743-753.	5.2	85
30	FHA domain mediated protein interaction network of Dun1 identifies its novel functions in the DNA damage response. FASEB Journal, 2006, 20, A509.	0.5	0
31	Dynamic Changes in Protein-Protein Interaction and Protein Phosphorylation Probed with Amine-reactive Isotope Tag. Molecular and Cellular Proteomics, 2005, 4, 1358-1369.	3.8	71
32	Quantitative Protein Analysis by Solid Phase Isotope Tagging and Mass Spectrometry. , 2004, 261, 511-518.		22
33	Global Analyses of Sumoylated Proteins in Saccharomyces cerevisiae. Journal of Biological Chemistry, 2004, 279, 32262-32268.	3.4	284
34	Quantitative proteome analysis by solid-phase isotope tagging and mass spectrometry. Nature Biotechnology, 2002, 20, 512-515.	17.5	372
35	A systematic approach to the analysis of protein phosphorylation. Nature Biotechnology, 2001, 19, 375-378.	17.5	742
36	Quantitative profiling of differentiation-induced microsomal proteins using isotope-coded affinity tags and mass spectrometry. Nature Biotechnology, 2001, 19, 946-951.	17.5	913