Hai Rao

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4423665/publications.pdf

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394421 302126 6,383 39 19 citations h-index papers

g-index 40 40 40 15316 docs citations citing authors all docs times ranked

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#	Article	IF	Citations
1	Positive feedback of SuFu negating protein 1 on Hedgehog signaling promotes colorectal tumor growth. Cell Death and Disease, 2021, 12, 199.	6.3	7
2	Autophagy regulator Atg9 is degraded by the proteasome. Biochemical and Biophysical Research Communications, 2020, 522, 254-258.	2.1	16
3	The N-terminal domain of the non-receptor tyrosine kinase ABL confers protein instability and suppresses tumorigenesis. Journal of Biological Chemistry, 2020, 295, 9069-9075.	3.4	4
4	A modular PROTAC design for target destruction using a degradation signal based on a single amino acid. Journal of Biological Chemistry, 2019, 294, 15172-15175.	3.4	21
5	A Simple PCR-based Strategy for the Introduction of Point Mutations in the Yeast Saccharomyces cerevisiae via CRISPR/Cas9. Biochemistry & Molecular Biology Journal, 2018, 04, .	0.3	9
6	Nek2A/SuFu feedback loop regulates Gli-mediated Hedgehog signaling pathway. International Journal of Oncology, 2017, 50, 373-380.	3.3	15
7	Arl13b Promotes Gastric Tumorigenesis by Regulating Smo Trafficking and Activation of the Hedgehog Signaling Pathway. Cancer Research, 2017, 77, 4000-4013.	0.9	33
8	Ubiquitylation of p62/sequestosome1 activates its autophagy receptor function and controls selective autophagy upon ubiquitin stress. Cell Research, 2017, 27, 657-674.	12.0	143
9	Multiple E3s promote the degradation of histone H3 variant Cse4. Scientific Reports, 2017, 7, 8565.	3.3	33
10	Nek2A phosphorylates and stabilizes SuFu: A new strategy of Gli2/Hedgehog signaling regulatory mechanism. Cellular Signalling, 2016, 28, 1304-1313.	3.6	15
11	The F-box Protein Rcy1 Is Involved in the Degradation of Histone H3 Variant Cse4 and Genome Maintenance. Journal of Biological Chemistry, 2016, 291, 10372-10377.	3.4	28
12	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). Autophagy, 2016, 12, 1-222.	9.1	4,701
13	Inhibition of Hedgehog signaling pathway impedes cancer cell proliferation by promotion of autophagy. European Journal of Cell Biology, 2015, 94, 223-233.	3.6	17
14	Rad25 Protein Is Targeted for Degradation by the Ubc4-Ufd4 Pathway. Journal of Biological Chemistry, 2015, 290, 8606-8612.	3.4	4
15	Ubiquitin Ligase gp78 Targets Unglycosylated Prion Protein PrP for Ubiquitylation and Degradation. PLoS ONE, 2014, 9, e92290.	2.5	14
16	XPC promotes MDM2-mediated degradation of the p53 tumor suppressor. Molecular Biology of the Cell, 2014, 25, 213-221.	2.1	20
17	Heat shock protein $90\hat{1}^2$ stabilizes focal adhesion kinase and enhances cell migration and invasion in breast cancer cells. Experimental Cell Research, 2014, 326, 78-89.	2.6	26
18	Down-Regulation of Gli Transcription Factor Leads to the Inhibition of Migration and Invasion of Ovarian Cancer Cells via Integrin \hat{l}^2 4-Mediated FAK Signaling. PLoS ONE, 2014, 9, e88386.	2.5	70

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19	Cdc48: A Swiss Army Knife of Cell Biology. Journal of Amino Acids, 2013, 2013, 1-12.	5.8	79
20	The Cdc48 Protein and Its Cofactor Vms1 Are Involved in Cdc13 Protein Degradation. Journal of Biological Chemistry, 2012, 287, 26788-26795.	3.4	14
21	Ubiquitin Ligase Ufd2 Is Required for Efficient Degradation of Mps1 Kinase. Journal of Biological Chemistry, 2011, 286, 43660-43667.	3.4	22
22	The Cdc48 ATPase modulates the interaction between two proteolytic factors Ufd2 and Rad23. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 13558-13563.	7.1	60
23	Genome-wide approaches to systematically identify substrates of the ubiquitin–proteasome pathway. Trends in Biotechnology, 2010, 28, 461-467.	9.3	5
24	A newly identified Pirh2 substrate SCYL1â€BP1 can bind to MDM2 and accelerate MDM2 selfâ€ubiquitination. FEBS Letters, 2010, 584, 3275-3278.	2.8	15
25	Overexpression of SCYL1â€BP1 stabilizes functional p53 by suppressing MDM2â€mediated ubiquitination. FEBS Letters, 2010, 584, 4319-4324.	2.8	13
26	Rad4 Regulates Protein Turnover at a Postubiquitylation Step. Molecular Biology of the Cell, 2010, 21, 177-185.	2.1	17
27	Identification of an Htm1 (EDEM)-dependent, Mns1-independent Endoplasmic Reticulum-associated Degradation (ERAD) Pathway in Saccharomyces cerevisiae. Journal of Biological Chemistry, 2010, 285, 24324-24334.	3.4	38
28	Ubiquitin Chain Elongation Enzyme Ufd2 Regulates a Subset of Doa10 Substrates. Journal of Biological Chemistry, 2010, 285, 10265-10272.	3.4	20
29	A genome-wide synthetic dosage lethality screen reveals multiple pathways that require the functioning of ubiquitin-binding proteins Rad23 and Dsk2. BMC Biology, 2009, 7, 75.	3.8	30
30	Usa 1 Protein Facilitates Substrate Ubiquitylation through Two Separate Domains. PLoS ONE, 2009, 4, e7604.	2.5	13
31	Proteasome inhibition in wild-type yeast <i>Saccharomyces cerevisiae</i> cells. BioTechniques, 2007, 42, 158-162.	1.8	102
32	Cellular tolerance of prion protein PrP in yeast involves proteolysis and the unfolded protein response. Biochemical and Biophysical Research Communications, 2006, 347, 319-326.	2.1	42
33	What's Ub Chain Linkage Got to Do with It?. Science Signaling, 2006, 2006, pe18-pe18.	3.6	19
34	The Png1–Rad23 complex regulates glycoprotein turnover. Journal of Cell Biology, 2006, 172, 211-219.	5.2	117
35	Analysis of Ubiquitin Chainâ€Binding Proteins by Twoâ€Hybrid Methods. Methods in Enzymology, 2005, 399, 157-164.	1.0	1
36	Multiple Interactions of Rad23 Suggest a Mechanism for Ubiquitylated Substrate Delivery Important in Proteolysis. Molecular Biology of the Cell, 2004, 15, 3357-3365.	2.1	145

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37	Recognition of Specific Ubiquitin Conjugates Is Important for the Proteolytic Functions of the Ubiquitin-associated Domain Proteins Dsk2 and Rad23. Journal of Biological Chemistry, 2002, 277, 11691-11695.	3.4	182
38	Degradation of a cohesin subunit by the N-end rule pathway is essential for chromosome stability. Nature, 2001, 410, 955-959.	27.8	264
39	Synthesis and characterization of a 29-amino acid residue DNA-binding peptide derived from $\hat{l}\pm\hat{l}^2$ -type small, acid-soluble spore proteins (SASP) of bacteria. FEBS Letters, 1992, 305, 115-120.	2.8	9