

Gali Prag

List of Publications by Year in descending order

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29
papers

1,801
citations

516710

16
h-index

501196

28
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34
all docs

34
docs citations

34
times ranked

2368
citing authors

#	ARTICLE	IF	CITATIONS
1	Split chloramphenicol acetyl-transferase assay reveals self-ubiquitylation-dependent regulation of UBE3B. <i>Journal of Molecular Biology</i> , 2021, 433, 167276.	4.2	3
2	Deubiquitylating enzymes in neuronal health and disease. <i>Cell Death and Disease</i> , 2021, 12, 120.	6.3	13
3	HK022 bacteriophage Integrase mediated RMCE as a potential tool for human gene therapy. <i>Nucleic Acids Research</i> , 2020, 48, 12804-12816.	14.5	6
4	An Integrative Synthetic Biology Approach to Interrogating Cellular Ubiquitin and Ufm Signaling. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4231.	4.1	19
5	Remodeling Membrane Binding by Mono-Ubiquitylation. <i>Biomolecules</i> , 2019, 9, 325.	4.0	7
6	Regulation of the anaphase promoting complex/cyclosome by the degradation of its unassembled catalytic subunit, Apc11. <i>FASEB Journal</i> , 2019, 33, 9752-9761.	0.5	5
7	Ubiquitin Signaling and Degradation of Aggregate-Prone Proteins. <i>Trends in Biochemical Sciences</i> , 2019, 44, 872-884.	7.5	57
8	A mutagenesis analysis of Tim50, the major receptor of the TIM23 complex, identifies regions that affect its interaction with Tim23. <i>Scientific Reports</i> , 2019, 9, 2012.	3.3	13
9	E. coli-Based Selection and Expression Systems for Discovery, Characterization, and Purification of Ubiquitylated Proteins. <i>Methods in Molecular Biology</i> , 2018, 1844, 155-166.	0.9	1
10	Anti-cancer binary system activated by bacteriophage HK022 integrase. <i>Oncotarget</i> , 2018, 9, 27487-27501.	1.8	7
11	Ubiquitylation-dependent oligomerization regulates activity of Nedd4 ligases. <i>EMBO Journal</i> , 2017, 36, 425-440.	7.8	51
12	A bacterial genetic selection system for ubiquitylation cascade discovery. <i>Nature Methods</i> , 2016, 13, 945-952.	19.0	21
13	Structure of ubiquitylated-Rpn10 provides insight into its autoregulation mechanism. <i>Nature Communications</i> , 2016, 7, 12960.	12.8	34
14	Tetrameric Assembly of Monoubiquitin Accurately Mimics the Lys11 Polyubiquitin Chain Structure. <i>Biochemistry</i> , 2015, 54, 4704-4710.	2.5	6
15	A Multilaboratory Comparison of Calibration Accuracy and the Performance of External References in Analytical Ultracentrifugation. <i>PLoS ONE</i> , 2015, 10, e0126420.	2.5	71
16	Structure-based in silico identification of ubiquitin-binding domains provides insights into the ALIX-V:ubiquitin complex and retrovirus budding. <i>EMBO Journal</i> , 2013, 32, 538-551.	7.8	59
17	Synthetic biology approach to reconstituting the ubiquitylation cascade in bacteria. <i>EMBO Journal</i> , 2012, 31, 378-390.	7.8	47
18	Purification and crystallization of mono-ubiquitylated ubiquitin receptor Rpn10. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1120-1123.	0.7	10

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19	Purification and crystallization of yeast Ent1 ENTH domain. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 820-823.	0.7	3
20	The Hetero-Hexameric Nature of a Chloroplast AAA+ FtsH Protease Contributes to Its Thermodynamic Stability. <i>PLoS ONE</i> , 2012, 7, e36008.	2.5	33
21	A phage display system designed to detect and study protein-protein interactions. <i>Molecular Microbiology</i> , 2008, 67, 719-728.	2.5	19
22	The Vps27/Hse1 Complex Is a GAT Domain-Based Scaffold for Ubiquitin-Dependent Sorting. <i>Developmental Cell</i> , 2007, 12, 973-986.	7.0	67
23	Ubiquitin-binding domains. <i>Biochemical Journal</i> , 2006, 399, 361-372.	3.7	544
24	Structural mechanism for ubiquitinated-cargo recognition by the Golgi-localized, Arp-containing, ADP-ribosylation-factor-binding proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 2334-2339.	7.1	66
25	A ubiquitin-binding motif required for intramolecular monoubiquitylation, the CUE domain. <i>EMBO Journal</i> , 2003, 22, 1273-1281.	7.8	260
26	Mechanism of Ubiquitin Recognition by the CUE Domain of Vps9p. <i>Cell</i> , 2003, 113, 609-620.	28.9	215
27	High Resolution Structural Analyses of Mutant Chitinase A Complexes with Substrates Provide New Insight into the Mechanism of Catalysis. <i>Biochemistry</i> , 2001, 40, 11338-11343.	2.5	156
28	Structural principles of prokaryotic gene regulatory proteins and the evolution of repressors and gene activators. <i>Molecular Microbiology</i> , 1997, 26, 619-620.	2.5	8
29	Structural Insight into Regulation of the Proteasome Ub-Receptor Rpn10. , 0, , .		0