

# Petra Beli

## List of Publications by Year in descending order

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Version: 2024-02-01

43  
papers

4,768  
citations

230014

27  
h-index

286692

43  
g-index

49  
all docs

49  
docs citations

49  
times ranked

9790  
citing authors

#	ARTICLE	IF	CITATIONS
1	Linkage reprogramming by tailor-made E3s reveals polyubiquitin chain requirements in DNA-damage bypass. <i>Molecular Cell</i> , 2022, 82, 1589-1602.e5.	4.5	4
2	Ubiquitylation of MYC couples transcription elongation with double-strand break repair at active promoters. <i>Molecular Cell</i> , 2021, 81, 830-844.e13.	4.5	28
3	Combined inhibition of Aurora-A and ATR kinases results in regression of MYCN-amplified neuroblastoma. <i>Nature Cancer</i> , 2021, 2, 312-326.	5.7	50
4	Proteomic analysis of tyrosine phosphorylation induced by exogenous expression of oncogenic kinase fusions identified in lung adenocarcinoma. <i>Proteomics</i> , 2021, 21, e2000283.	1.3	1
5	Hakai is required for stabilization of core components of the m6A mRNA methylation machinery. <i>Nature Communications</i> , 2021, 12, 3778.	5.8	77
6	Localization matters: nuclear-trapped Survivin sensitizes glioblastoma cells to temozolomide by elevating cellular senescence and impairing homologous recombination. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 5587-5604.	2.4	9
7	Causes and consequences of DNA damage-induced autophagy. <i>Matrix Biology</i> , 2021, 100-101, 39-53.	1.5	18
8	Wnt signaling recruits KIF2A to the spindle to ensure chromosome congression and alignment during mitosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	10
9	USP22 controls necroptosis by regulating receptor-interacting protein kinase 3 ubiquitination. <i>EMBO Reports</i> , 2021, 22, e50163.	2.0	48
10	R-loop proximity proteomics identifies a role of DDX41 in transcription-associated genomic instability. <i>Nature Communications</i> , 2021, 12, 7314.	5.8	64
11	Makorin 1 controls embryonic patterning by alleviating Bruno1-mediated repression of oskar translation. <i>PLoS Genetics</i> , 2020, 16, e1008581.	1.5	11
12	Chronic irradiation of human cells reduces histone levels and deregulates gene expression. <i>Scientific Reports</i> , 2020, 10, 2200.	1.6	18
13	The RNA-binding ubiquitin ligase MKRN1 functions in ribosome-associated quality control of poly(A) translation. <i>Genome Biology</i> , 2019, 20, 216.	3.8	29
14	NCAM1 (CD56) promotes leukemogenesis and confers drug resistance in AML. <i>Blood</i> , 2019, 133, 2305-2319.	0.6	49
15	Quantitative Phosphoproteomics of Selective Autophagy Receptors. <i>Methods in Molecular Biology</i> , 2019, 1880, 691-701.	0.4	3
16	ATM orchestrates the DNA-damage response to counter toxic non-homologous end-joining at broken replication forks. <i>Nature Communications</i> , 2019, 10, 87.	5.8	133
17	Proteomic profiling of VCP substrates links VCP to K6-linked ubiquitylation and c-Myc function. <i>EMBO Reports</i> , 2018, 19, .	2.0	82
18	p38-MK2 signaling axis regulates RNA metabolism after UV-light-induced DNA damage. <i>Nature Communications</i> , 2018, 9, 1017.	5.8	61

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19	Shieldin complex promotes DNA end-joining and counters homologous recombination in BRCA1-null cells. <i>Nature Cell Biology</i> , 2018, 20, 954-965.	4.6	291
20	IKK $\beta$ controls ATG16L1 degradation to prevent ER stress during inflammation. <i>Journal of Experimental Medicine</i> , 2017, 214, 423-437.	4.2	55
21	Mass Spectrometry-Based Proteomics for Quantifying DNA Damage-Induced Phosphorylation. <i>Methods in Molecular Biology</i> , 2017, 1599, 215-227.	0.4	14
22	Interaction profiling of RNA-binding ubiquitin ligases reveals a link between posttranscriptional regulation and the ubiquitin system. <i>Scientific Reports</i> , 2017, 7, 16582.	1.6	17
23	Ubiquitylation of the acetyltransferase MOF in <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2017, 12, e0177408.	1.1	11
24	Mass Spectrometry-Based Proteomics for Investigating DNA Damage-Associated Protein Ubiquitylation. <i>Frontiers in Genetics</i> , 2016, 7, 109.	1.1	5
25	SPATA2 links CYLD to the TNF $\alpha$ receptor signaling complex and modulates the receptor signaling outcomes. <i>EMBO Journal</i> , 2016, 35, 1868-1884.	3.5	129
26	Phosphorylation of OPTN by TBK1 enhances its binding to Ub chains and promotes selective autophagy of damaged mitochondria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 4039-4044.	3.3	554
27	ATR inhibition rewires cellular signaling networks induced by replication stress. <i>Proteomics</i> , 2016, 16, 402-416.	1.3	29
28	Systems-wide analysis of BCR signalosomes and downstream phosphorylation and ubiquitylation. <i>Molecular Systems Biology</i> , 2015, 11, 810.	3.2	119
29	Illuminating Spatial and Temporal Organization of Protein Interaction Networks by Mass Spectrometry-Based Proteomics. <i>Frontiers in Genetics</i> , 2015, 6, 344.	1.1	16
30	p38- and MK2-dependent signalling promotes stress-induced centriolar satellite remodelling via 14-3-3-dependent sequestration of CEP131/AZI1. <i>Nature Communications</i> , 2015, 6, 10075.	5.8	40
31	Cmr1/WDR76 defines a nuclear genotoxic stress body linking genome integrity and protein quality control. <i>Nature Communications</i> , 2015, 6, 6533.	5.8	80
32	Acetylation site specificities of lysine deacetylase inhibitors in human cells. <i>Nature Biotechnology</i> , 2015, 33, 415-423.	9.4	237
33	Systematic E2 screening reveals a UBE2D-RNF138-CtIP axis promoting DNA repair. <i>Nature Cell Biology</i> , 2015, 17, 1458-1470.	4.6	90
34	Proteome-wide analysis of SUMO2 targets in response to pathological DNA replication stress in human cells. <i>DNA Repair</i> , 2015, 25, 84-96.	1.3	30
35	UBL5 is essential for pre-mRNA splicing and sister chromatid cohesion in human cells. <i>EMBO Reports</i> , 2014, 15, 956-964.	2.0	41
36	Acetyl-Phosphate Is a Critical Determinant of Lysine Acetylation in <i>E. coli</i> . <i>Molecular Cell</i> , 2013, 51, 265-272.	4.5	407

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37	A new cellular stress response that triggers centriolar satellite reorganization and ciliogenesis. <i>EMBO Journal</i> , 2013, 32, 3029-3040.	3.5	115
38	Proteomic Analyses Reveal Divergent Ubiquitylation Site Patterns in Murine Tissues. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1578-1585.	2.5	244
39	DVC1 (C1orf124) is a DNA damage-targeting p97 adaptor that promotes ubiquitin-dependent responses to replication blocks. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1084-1092.	3.6	153
40	Systems-wide analysis of ubiquitylation dynamics reveals a key role for PAF15 ubiquitylation in DNA-damage bypass. <i>Nature Cell Biology</i> , 2012, 14, 1089-1098.	4.6	234
41	Proteomic Investigations Reveal a Role for RNA Processing Factor THRAP3 in the DNA Damage Response. <i>Molecular Cell</i> , 2012, 46, 212-225.	4.5	298
42	A Proteome-wide, Quantitative Survey of In Vivo Ubiquitylation Sites Reveals Widespread Regulatory Roles. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.013284.	2.5	754
43	WAVE and Arp2/3 jointly inhibit filopodium formation by entering into a complex with mDia2. <i>Nature Cell Biology</i> , 2008, 10, 849-857.	4.6	107