

Sebastian A Wagner

List of Publications by Year in descending order

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31
papers

3,932
citations

304743

22
h-index

434195

31
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33
all docs

33
docs citations

33
times ranked

8013
citing authors

#	ARTICLE	IF	CITATIONS
1	A Proteome-wide, Quantitative Survey of In Vivo Ubiquitylation Sites Reveals Widespread Regulatory Roles. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.013284.	3.8	754
2	Lysine Succinylation Is a Frequently Occurring Modification in Prokaryotes and Eukaryotes and Extensively Overlaps with Acetylation. <i>Cell Reports</i> , 2013, 4, 842-851.	6.4	619
3	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.	7.1	554
4	Proteomic Investigations Reveal a Role for RNA Processing Factor THRAP3 in the DNA Damage Response. <i>Molecular Cell</i> , 2012, 46, 212-225.	9.7	298
5	Proteomic Analyses Reveal Divergent Ubiquitylation Site Patterns in Murine Tissues. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1578-1585.	3.8	244
6	Acetylation site specificities of lysine deacetylase inhibitors in human cells. <i>Nature Biotechnology</i> , 2015, 33, 415-423.	17.5	237
7	Pooled In Vitro and In Vivo CRISPR-Cas9 Screening Identifies Tumor Suppressors in Human Colon Organoids. <i>Cell Stem Cell</i> , 2020, 26, 782-792.e7.	11.1	131
8	<sc>SPATA</sc> 2 links <sc>CYLD</sc> to the <sc>TNF</sc> receptor signaling complex and modulates the receptor signaling outcomes. <i>EMBO Journal</i> , 2016, 35, 1868-1884.	7.8	129
9	A phospho-proteomic screen identifies substrates of the checkpoint kinase Chk1. <i>Genome Biology</i> , 2011, 12, R78.	9.6	123
10	Systems-wide analysis of <sc>BCR</sc> signalosomes and downstream phosphorylation and ubiquitylation. <i>Molecular Systems Biology</i> , 2015, 11, 810.	7.2	119
11	Large scale multifactorial likelihood quantitative analysis of <i>BRCA1</i> and <i>BRCA2</i> variants: An ENIGMA resource to support clinical variant classification. <i>Human Mutation</i> , 2019, 40, 1557-1578.	2.5	102
12	Cancer Risks Associated With <i>BRCA1</i> and <i>BRCA2</i> Pathogenic Variants. <i>Journal of Clinical Oncology</i> , 2022, 40, 1529-1541.	1.6	90
13	Proteomic profiling of VCP substrates links VCP to K6-linked ubiquitylation and c-Myc function. <i>EMBO Reports</i> , 2018, 19, .	4.5	82
14	p38-MK2 signaling axis regulates RNA metabolism after UV-light-induced DNA damage. <i>Nature Communications</i> , 2018, 9, 1017.	12.8	61
15	LSD1 inhibition by tranlylcypromine derivatives interferes with GFI1-mediated repression of PU.1 target genes and induces differentiation in AML. <i>Leukemia</i> , 2019, 33, 1411-1426.	7.2	53
16	A quantitative 14-3-3 interaction screen connects the nuclear exosome targeting complex to the DNA damage response. <i>Genes and Development</i> , 2014, 28, 1977-1982.	5.9	50
17	Functional Dominance of CHIP-Mutated Hematopoietic Stem Cells in Patients Undergoing Autologous Transplantation. <i>Cell Reports</i> , 2019, 27, 2022-2028.e3.	6.4	44
18	Integrating clinical decision support systems for pharmacogenomic testing into clinical routine - a scoping review of designs of user-system interactions in recent system development. <i>BMC Medical Informatics and Decision Making</i> , 2017, 17, 81.	3.0	43

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19	The proteogenomic subtypes of acute myeloid leukemia. <i>Cancer Cell</i> , 2022, 40, 301-317.e12.	16.8	43
20	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.	12.8	40
21	ATR inhibition rewires cellular signaling networks induced by replication stress. <i>Proteomics</i> , 2016, 16, 402-416.	2.2	29
22	Conceptual framework for precision cancer medicine in Germany: Consensus statement of the Deutsche Krebshilfe working group "Molecular Diagnostics and Therapy"™. <i>European Journal of Cancer</i> , 2020, 135, 1-7.	2.8	23
23	Illuminating Spatial and Temporal Organization of Protein Interaction Networks by Mass Spectrometry-Based Proteomics. <i>Frontiers in Genetics</i> , 2015, 6, 344.	2.3	16
24	Mass Spectrometry-Based Proteomics for Quantifying DNA Damage-Induced Phosphorylation. <i>Methods in Molecular Biology</i> , 2017, 1599, 215-227.	0.9	14
25	VCP inhibition induces an unfolded protein response and apoptosis in human acute myeloid leukemia cells. <i>PLoS ONE</i> , 2022, 17, e0266478.	2.5	10
26	The experience of physicians in pharmacogenomic clinical decision support within eight German university hospitals. <i>Pharmacogenomics</i> , 2017, 18, 773-785.	1.3	7
27	Acute kidney injury adversely affects the clinical course of acute myeloid leukemia patients undergoing induction chemotherapy. <i>Annals of Hematology</i> , 2021, 100, 1159-1167.	1.8	6
28	Mass Spectrometry-Based Proteomics for Investigating DNA Damage-Associated Protein Ubiquitylation. <i>Frontiers in Genetics</i> , 2016, 7, 109.	2.3	5
29	Relapse surveillance of acute myeloid leukemia patients in first remission after consolidation chemotherapy: diagnostic value of regular bone marrow aspirations. <i>Annals of Hematology</i> , 2022, 101, 1703-1710.	1.8	3
30	Proteomic analysis of tyrosine phosphorylation induced by exogenous expression of oncogenic kinase fusions identified in lung adenocarcinoma. <i>Proteomics</i> , 2021, 21, e2000283.	2.2	1
31	Fluid overload is associated with increased 90-day mortality in AML patients undergoing induction chemotherapy. <i>Annals of Hematology</i> , 2021, 100, 2603-2611.	1.8	1