

Sebastian A Wagner

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

3,932
citations

304743

22
h-index

434195

31
g-index

33
all docs

33
docs citations

33
times ranked

8013
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	The proteogenomic subtypes of acute myeloid leukemia. <i>Cancer Cell</i> , 2022, 40, 301-317.e12.	16.8	43
3	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
4	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
5	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
6	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
7	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
8	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
9	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
10	LSD1 inhibition by tranlycypromine 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
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	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
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	Mass Spectrometry-Based Proteomics for Quantifying DNA Damage-Induced Phosphorylation. <i>Methods in Molecular Biology</i> , 2017, 1599, 215-227.	0.9	14
16	The experience of physicians in pharmacogenomic clinical decision support within eight German university hospitals. <i>Pharmacogenomics</i> , 2017, 18, 773-785.	1.3	7
17	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
18	Mass Spectrometry-Based Proteomics for Investigating DNA Damage-Associated Protein Ubiquitylation. <i>Frontiers in Genetics</i> , 2016, 7, 109.	2.3	5

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19	<scp>SPATA</scp> 2 links <scp>CYLD</scp> to the <scp>TNF</scp> $\hat{=}$ receptor signaling complex and modulates the receptor signaling outcomes. EMBO Journal, 2016, 35, 1868-1884.	7.8	129
20	Phosphorylation of OPTN by TBK1 enhances its binding to Ub chains and promotes selective autophagy of damaged mitochondria. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 4039-4044.	7.1	554
21	ATR inhibition rewires cellular signaling networks induced by replication stress. Proteomics, 2016, 16, 402-416.	2.2	29
22	Systems-wide analysis of <scp>BCR</scp> signalosomes and downstream phosphorylation and ubiquitylation. Molecular Systems Biology, 2015, 11, 810.	7.2	119
23	Illuminating Spatial and Temporal Organization of Protein Interaction Networks by Mass Spectrometry-Based Proteomics. Frontiers in Genetics, 2015, 6, 344.	2.3	16
24	p38- and MK2-dependent signalling promotes stress-induced centriolar satellite remodelling via 14-3-3-dependent sequestration of CEP131/AZI1. Nature Communications, 2015, 6, 10075.	12.8	40
25	Acetylation site specificities of lysine deacetylase inhibitors in human cells. Nature Biotechnology, 2015, 33, 415-423.	17.5	237
26	A quantitative 14-3-3 interaction screen connects the nuclear exosome targeting complex to the DNA damage response. Genes and Development, 2014, 28, 1977-1982.	5.9	50
27	Lysine Succinylation Is a Frequently Occurring Modification in Prokaryotes and Eukaryotes and Extensively Overlaps with Acetylation. Cell Reports, 2013, 4, 842-851.	6.4	619
28	Proteomic Analyses Reveal Divergent Ubiquitylation Site Patterns in Murine Tissues. Molecular and Cellular Proteomics, 2012, 11, 1578-1585.	3.8	244
29	Proteomic Investigations Reveal a Role for RNA Processing Factor THRAP3 in the DNA Damage Response. Molecular Cell, 2012, 46, 212-225.	9.7	298
30	A phospho-proteomic screen identifies substrates of the checkpoint kinase Chk1. Genome Biology, 2011, 12, R78.	9.6	123
31	A Proteome-wide, Quantitative Survey of In Vivo Ubiquitylation Sites Reveals Widespread Regulatory Roles. Molecular and Cellular Proteomics, 2011, 10, M111.013284.	3.8	754