## Hans-Jörg Warnatz

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2551530/publications.pdf

Version: 2024-02-01

27 papers 6,070 citations

20 h-index 26 g-index

27 all docs

27 docs citations

times ranked

27

12213 citing authors

#	Article	IF	CITATIONS
1	Molecular Classification of Ependymal Tumors across All CNS Compartments, Histopathological Grades, and Age Groups. Cancer Cell, 2015, 27, 728-743.	16.8	933
2	The whole-genome landscape of medulloblastoma subtypes. Nature, 2017, 547, 311-317.	27.8	787
3	Dissecting the genomic complexity underlying medulloblastoma. Nature, 2012, 488, 100-105.	27.8	765
4	Recurrent somatic alterations of FGFR1 and NTRK2 in pilocytic astrocytoma. Nature Genetics, 2013, 45, 927-932.	21.4	674
5	Enhancer hijacking activates GFI1 family oncogenes in medulloblastoma. Nature, 2014, 511, 428-434.	27.8	520
6	Decoding the regulatory landscape of medulloblastoma using DNA methylation sequencing. Nature, 2014, 510, 537-541.	27.8	378
7	Active medulloblastoma enhancers reveal subgroup-specific cellular origins. Nature, 2016, 530, 57-62.	27.8	318
8	Integrative Genomic Analyses Reveal an Androgen-Driven Somatic Alteration Landscape in Early-Onset Prostate Cancer. Cancer Cell, 2013, 23, 159-170.	16.8	292
9	Molecular dissection of colorectal cancer in pre-clinical models identifies biomarkers predicting sensitivity to EGFR inhibitors. Nature Communications, 2017, 8, 14262.	12.8	260
10	Genomics and drug profiling of fatal TCF3-HLFâ^positive acute lymphoblastic leukemia identifies recurrent mutation patterns and therapeutic options. Nature Genetics, 2015, 47, 1020-1029.	21.4	190
11	Molecular Evolution of Early-Onset Prostate Cancer Identifies Molecular Risk Markers and Clinical Trajectories. Cancer Cell, 2018, 34, 996-1011.e8.	16.8	190
12	An efficient and economic enhancer mix for PCR. Biochemical and Biophysical Research Communications, 2006, 347, 747-751.	2.1	177
13	The BTB and CNC Homology 1 (BACH1) Target Genes Are Involved in the Oxidative Stress Response and in Control of the Cell Cycle. Journal of Biological Chemistry, 2011, 286, 23521-23532.	3.4	136
14	Analysis of the DNA-Binding Profile and Function of TALE Homeoproteins Reveals Their Specialization and Specific Interactions with Hox Genes/Proteins. Cell Reports, 2013, 3, 1321-1333.	6.4	125
15	Medulloblastoma-associated DDX3 variant selectively alters the translational response to stress. Oncotarget, 2016, 7, 28169-28182.	1.8	62
16	Xenogeneic Graft-Versus-Host Disease in Humanized NSG and NSG-HLA-A2/HHD Mice. Frontiers in Immunology, 2018, 9, 1943.	4.8	58
17	Parallel Profiling of the Transcriptome, Cistrome, and Epigenome in the Cellular Response to Ionizing Radiation. Science Signaling, 2014, 7, rs3.	3.6	51
18	The Leukemogenic TCF3-HLF Complex Rewires Enhancers Driving Cellular Identity and Self-Renewal Conferring EP300 Vulnerability. Cancer Cell, 2019, 36, 630-644.e9.	16.8	35

#	Article	IF	CITATIONS
19	Cell array-based intracellular localization screening reveals novel functional features of human chromosome 21 proteins. BMC Genomics, 2006, 7, 155.	2.8	31
20	ChIP-Seq and RNA-Seq Analyses Identify Components of the Wnt and Fgf Signaling Pathways as Prep1 Target Genes in Mouse Embryonic Stem Cells. PLoS ONE, 2015, 10, e0122518.	2.5	24
21	Human Lineage-Specific Transcriptional Regulation through GA-Binding Protein Transcription Factor Alpha (GABPa). Molecular Biology and Evolution, 2016, 33, 1231-1244.	8.9	21
22	Functional analysis and identification of cis-regulatory elements of human chromosome 21 gene promoters. Nucleic Acids Research, 2010, 38, 6112-6123.	14.5	19
23	Simple paired heavy- and light-chain antibody repertoire sequencing using endoplasmic reticulum microsomes. Genome Medicine, 2018, 10, 34.	8.2	13
24	Impact of congenital cytomegalovirus infection on transcriptomes from archived dried blood spots in relation to long-term clinical outcome. PLoS ONE, 2018, 13, e0200652.	2.5	5
25	The hematopoietic stem cell marker VNN2 is associated with chemoresistance in pediatric B-cell precursor ALL. Blood Advances, 2020, 4, 4052-4064.	<b>5.</b> 2	5
26	ICGC PedBrain - dissecting the genomic complexity underlying medulloblastoma using whole-genome sequencing. BMC Proceedings, 2012, 6, .	1.6	1
27	Profiling T Cell Receptor Repertoires in Phase I/II Clinical Trials of Donor Treg Infusion for the Treatment of Chronic Graft-Versus-Host Disease. Blood, 2018, 132, 4563-4563.	1.4	0