

Christof Winter

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

1,983
citations

361413
20
h-index

254184
43
g-index

46
all docs

46
docs citations

46
times ranked

4242
citing authors

#	ARTICLE	IF	CITATIONS
1	Dynamics of spike-and nucleocapsid specific immunity during long-term follow-up and vaccination of SARS-CoV-2 convalescents. Nature Communications, 2022, 13, 153.	12.8	45
2	NOTCH1 Intracellular Domain and the Tumor Microenvironment as Prognostic Markers in HNSCC. Cancers, 2022, 14, 1080.	3.7	6
3	Circulating Tumor DNA Profiling of a Diffuse Large B Cell Lymphoma Patient with Secondary Acute Myeloid Leukemia. Cancers, 2022, 14, 1371.	3.7	3
4	Detecting drug resistance in pancreatic cancer organoids guides optimized chemotherapy treatment. Journal of Pathology, 2022, 257, 607-619.	4.5	13
5	CMV seropositivity is a potential novel risk factor for severe COVID-19 in non-geriatric patients. PLoS ONE, 2022, 17, e0268530.	2.5	19
6	Mucosal-Associated Invariant T (MAIT) Cells Are Highly Activated and Functionally Impaired in COVID-19 Patients. Viruses, 2021, 13, 241.	3.3	31
7	Cyclophosphamide plus etoposide is a safe and effective mobilization regimen in patients with multiple myeloma. Transfusion and Apheresis Science, 2021, 60, 103197.	1.0	2
8	Implementing cell-free DNA of pancreatic cancer patientâ€‘derived organoids for personalized oncology. JCI Insight, 2020, 5, .	5.0	30
9	The mutational landscape of the <scp>SCAN</scp> â€‘ realâ€‘world primary breast cancer transcriptome. EMBO Molecular Medicine, 2020, 12, e12118.	6.9	36
10	Defining the mutational landscape of 3,217 primary breast cancer transcriptomes through large-scale RNA-seq within the Sweden Cancerome Analysis Network: Breast Project (SCAN-B; NCT03430492).. Journal of Clinical Oncology, 2020, 38, 518-518.	1.6	2
11	RIG-I activation is critical for responsiveness to checkpoint blockade. Science Immunology, 2019, 4, .	11.9	80
12	Gene editing enables T-cell engineering to redirect antigen specificity for potent tumor rejection. Life Science Alliance, 2019, 2, e201900367.	2.8	18
13	RIG-I Activation Is Critical for Responsiveness to Checkpoint Blockade. Blood, 2019, 134, 624-624.	1.4	1
14	External quality assessment schemes for glucose measurements in Germany: factors for successful participation, analytical performance and medical impact. Clinical Chemistry and Laboratory Medicine, 2018, 56, 1238-1250.	2.3	15
15	No mathematical shortcuts for standardization or harmonization of laboratory measurements. Laboratoriums Medizin, 2018, 42, 59-62.	0.6	0
16	Germline mutations in BRCA1 and BRCA2 incidentally revealed in a biobank research study: experiences from re-contacting mutation carriers and relatives. Journal of Community Genetics, 2018, 9, 201-208.	1.2	5
17	Somatic alterations compromised molecular diagnosis of DOCK8 hyper-IgE syndrome caused by a novel intronic splice site mutation. Scientific Reports, 2018, 8, 16719.	3.3	5
18	Efficacy versus effectiveness of clinical genetic testing criteria for BRCA1 and BRCA2 hereditary mutations in incident breast cancer. Familial Cancer, 2017, 16, 187-193.	1.9	18

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19	AR-V7 in Peripheral Whole Blood of Patients with Castration-resistant Prostate Cancer: Association with Treatment-specific Outcome Under Abiraterone and Enzalutamide. <i>European Urology</i> , 2017, 72, 828-834.	1.9	86
20	PD-1 is a haploinsufficient suppressor of T cell lymphomagenesis. <i>Nature</i> , 2017, 552, 121-125.	27.8	199
21	Targeted sequencing of BRCA1 and BRCA2 across a large unselected breast cancer cohort suggests that one-third of mutations are somatic. <i>Annals of Oncology</i> , 2016, 27, 1532-1538.	1.2	103
22	Meta-analysis of Cancer Gene Profiling Data. <i>Methods in Molecular Biology</i> , 2016, 1381, 211-222.	0.9	3
23	Mutation Screening of 1,237 Cancer Genes across Six Model Cell Lines of Basal-Like Breast Cancer. <i>PLoS ONE</i> , 2015, 10, e0144528.	2.5	6
24	Serial monitoring of circulating tumor <scp>DNA</scp> in patients with primary breast cancer for detection of occult metastatic disease. <i>EMBO Molecular Medicine</i> , 2015, 7, 1034-1047.	6.9	380
25	The Sweden Cancerome Analysis Network - Breast (SCAN-B) Initiative: a large-scale multicenter infrastructure towards implementation of breast cancer genomic analyses in the clinical routine. <i>Genome Medicine</i> , 2015, 7, 20.	8.2	129
26	Contralateral breast cancer can represent a metastatic spread of the first primary tumor: determination of clonal relationship between contralateral breast cancers using next-generation whole genome sequencing. <i>Breast Cancer Research</i> , 2015, 17, 102.	5.0	30
27	Remarkable similarities of chromosomal rearrangements between primary human breast cancers and matched distant metastases as revealed by whole-genome sequencing. <i>Oncotarget</i> , 2015, 6, 37169-37184.	1.8	25
28	Abstract 4805: Whole genome sequencing of primary breast cancers and matched distant metastases. , 2015, , .		0
29	Molecular and genetic diversity in the metastatic process of melanoma. <i>Journal of Pathology</i> , 2014, 233, 39-50.	4.5	58
30	Network information improves cancer outcome prediction. <i>Briefings in Bioinformatics</i> , 2014, 15, 612-625.	6.5	29
31	Abstract LB-77: Measurement of tumor-specific chromosomal rearrangements in serial blood samples to monitor breast cancer burden and detect occult metastasis.. , 2013, , .		0
32	Google Goes Cancer: Improving Outcome Prediction for Cancer Patients by Network-Based Ranking of Marker Genes. <i>PLoS Computational Biology</i> , 2012, 8, e1002511.	3.2	159
33	Protein interactions in 3D: From interface evolution to drug discovery. <i>Journal of Structural Biology</i> , 2012, 179, 347-358.	2.8	28
34	Structural fragment clustering reveals novel structural and functional motifs in α -helical transmembrane proteins. <i>BMC Bioinformatics</i> , 2010, 11, 204.	2.6	13
35	Xenopus Meiotic Microtubule-Associated Interactome. <i>PLoS ONE</i> , 2010, 5, e9248.	2.5	40
36	Examination of Apoptosis Signaling in Pancreatic Cancer by Computational Signal Transduction Analysis. <i>PLoS ONE</i> , 2010, 5, e12243.	2.5	32

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37	MeMotif: a database of linear motifs in α -helical transmembrane proteins. Nucleic Acids Research, 2010, 38, D181-D189.	14.5	18
38	Long-Term Results of Distal-Origin Bypass After Prior Femoro-Popliteal Angioplasty. Annals of Vascular Surgery, 2010, 24, 1024-1033.	0.9	2
39	Rapid Changes of mRNA-binding Protein Levels following Glucose and 3-Isobutyl-1-methylxanthine Stimulation of Insulinoma INS-1 Cells. Molecular and Cellular Proteomics, 2009, 8, 393-408.	3.8	14
40	Triangle network motifs predict complexes by complementing high-error interactomes with structural information. BMC Bioinformatics, 2009, 10, 196.	2.6	7
41	Structural templates predict novel protein interactions and targets from pancreas tumour gene expression data. Bioinformatics, 2007, 23, i115-i124.	4.1	19
42	Using structural motif descriptors for sequence-based binding site prediction. BMC Bioinformatics, 2007, 8, S5.	2.6	22
43	The Many Faces of Protein-Protein Interactions: A Compendium of Interface Geometry. PLoS Computational Biology, 2006, 2, e124.	3.2	103
44	SCOPPI: a structural classification of protein-protein interfaces. Nucleic Acids Research, 2006, 34, D310-D314.	14.5	142
45	Cognitive Tools for Medical Knowledge Management (Kognitive Werkzeuge für das Medizinische) Tj ETQq1 1 0.784314 rgBT /Over	0.9	1