

# Christof Winter

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2516249/publications.pdf>

Version: 2024-02-01

45  
papers

1,983  
citations

361045

20  
h-index

253896

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. <i>Nature Communications</i> , 2022, 13, 153.	5.8	45
2	NOTCH1 Intracellular Domain and the Tumor Microenvironment as Prognostic Markers in HNSCC. <i>Cancers</i> , 2022, 14, 1080.	1.7	6
3	Circulating Tumor DNA Profiling of a Diffuse Large B Cell Lymphoma Patient with Secondary Acute Myeloid Leukemia. <i>Cancers</i> , 2022, 14, 1371.	1.7	3
4	Detecting drug resistance in pancreatic cancer organoids guides optimized chemotherapy treatment. <i>Journal of Pathology</i> , 2022, 257, 607-619.	2.1	13
5	CMV seropositivity is a potential novel risk factor for severe COVID-19 in non-geriatric patients. <i>PLoS ONE</i> , 2022, 17, e0268530.	1.1	19
6	Mucosal-Associated Invariant T (MAIT) Cells Are Highly Activated and Functionally Impaired in COVID-19 Patients. <i>Viruses</i> , 2021, 13, 241.	1.5	31
7	Cyclophosphamide plus etoposide is a safe and effective mobilization regimen in patients with multiple myeloma. <i>Transfusion and Apheresis Science</i> , 2021, 60, 103197.	0.5	2
8	Implementing cell-free DNA of pancreatic cancer patientâ€derived organoids for personalized oncology. <i>JCI Insight</i> , 2020, 5, .	2.3	30
9	The mutational landscape of the <scp>SCAN</scp> â€ realâ€world primary breast cancer transcriptome. <i>EMBO Molecular Medicine</i> , 2020, 12, e12118.	3.3	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).. <i>Journal of Clinical Oncology</i> , 2020, 38, 518-518.	0.8	2
11	RIG-I activation is critical for responsiveness to checkpoint blockade. <i>Science Immunology</i> , 2019, 4, .	5.6	80
12	Gene editing enables T-cell engineering to redirect antigen specificity for potent tumor rejection. <i>Life Science Alliance</i> , 2019, 2, e201900367.	1.3	18
13	RIG-I Activation Is Critical for Responsiveness to Checkpoint Blockade. <i>Blood</i> , 2019, 134, 624-624.	0.6	1
14	External quality assessment schemes for glucose measurements in Germany: factors for successful participation, analytical performance and medical impact. <i>Clinical Chemistry and Laboratory Medicine</i> , 2018, 56, 1238-1250.	1.4	15
15	No mathematical shortcuts for standardization or harmonization of laboratory measurements. <i>Laboratoriums Medizin</i> , 2018, 42, 59-62.	0.1	0
16	Germline mutations in BRCA1 and BRCA2 incidentally revealed in a biobank research study: experiences from re-contacting mutation carriers and relatives. <i>Journal of Community Genetics</i> , 2018, 9, 201-208.	0.5	5
17	Somatic alterations compromised molecular diagnosis of DOCK8 hyper-IgE syndrome caused by a novel intronic splice site mutation. <i>Scientific Reports</i> , 2018, 8, 16719.	1.6	5
18	Efficacy versus effectiveness of clinical genetic testing criteria for BRCA1 and BRCA2 hereditary mutations in incident breast cancer. <i>Familial Cancer</i> , 2017, 16, 187-193.	0.9	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.	0.9	86
20	PD-1 is a haploinsufficient suppressor of T cell lymphomagenesis. <i>Nature</i> , 2017, 552, 121-125.	13.7	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.	0.6	103
22	Meta-analysis of Cancer Gene Profiling Data. <i>Methods in Molecular Biology</i> , 2016, 1381, 211-222.	0.4	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.	1.1	6
24	Serial monitoring of circulating tumor DNA in patients with primary breast cancer for detection of occult metastatic disease. <i>EMBO Molecular Medicine</i> , 2015, 7, 1034-1047.	3.3	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.	3.6	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.	2.2	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.	0.8	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.	2.1	58
30	Network information improves cancer outcome prediction. <i>Briefings in Bioinformatics</i> , 2014, 15, 612-625.	3.2	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.	1.5	159
33	Protein interactions in 3D: From interface evolution to drug discovery. <i>Journal of Structural Biology</i> , 2012, 179, 347-358.	1.3	28
34	Structural fragment clustering reveals novel structural and functional motifs in $\alpha$ -helical transmembrane proteins. <i>BMC Bioinformatics</i> , 2010, 11, 204.	1.2	13
35	Xenopus Meiotic Microtubule-Associated Interactome. <i>PLoS ONE</i> , 2010, 5, e9248.	1.1	40
36	Examination of Apoptosis Signaling in Pancreatic Cancer by Computational Signal Transduction Analysis. <i>PLoS ONE</i> , 2010, 5, e12243.	1.1	32

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37	MeMotif: a database of linear motifs in $\alpha$ -helical transmembrane proteins. Nucleic Acids Research, 2010, 38, D181-D189.	6.5	18
38	Long-Term Results of Distal-Origin Bypass After Prior Femoro-Popliteal Angioplasty. Annals of Vascular Surgery, 2010, 24, 1024-1033.	0.4	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.	2.5	14
40	Triangle network motifs predict complexes by complementing high-error interactomes with structural information. BMC Bioinformatics, 2009, 10, 196.	1.2	7
41	Structural templates predict novel protein interactions and targets from pancreas tumour gene expression data. Bioinformatics, 2007, 23, i115-i124.	1.8	19
42	Using structural motif descriptors for sequence-based binding site prediction. BMC Bioinformatics, 2007, 8, S5.	1.2	22
43	The Many Faces of Protein-Protein Interactions: A Compendium of Interface Geometry. PLoS Computational Biology, 2006, 2, e124.	1.5	103
44	SCOPPI: a structural classification of protein-protein interfaces. Nucleic Acids Research, 2006, 34, D310-D314.	6.5	142
45	Cognitive Tools for Medical Knowledge Management (Kognitive Werkzeuge für das Medizinische) Tj ETQq1 1 0.784314 rgBT /Over 0.6		