

# Christian Brueffer

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4227826/publications.pdf>

Version: 2024-02-01

22  
papers

1,307  
citations

759233

12  
h-index

839539

18  
g-index

29  
all docs

29  
docs citations

29  
times ranked

3047  
citing authors

#	ARTICLE	IF	CITATIONS
1	Correction for Rando et al., "Pathogenesis, Symptomatology, and Transmission of SARS-CoV-2 through Analysis of Viral Genomics and Structure". <i>MSystems</i> , 2022, , e0144721.	3.8	2
2	Clinical associations of ESR2 (estrogen receptor beta) expression across thousands of primary breast tumors. <i>Scientific Reports</i> , 2022, 12, 4696.	3.3	25
3	PrecisionFDA Truth Challenge V2: Calling variants from short and long reads in difficult-to-map regions. <i>Cell Genomics</i> , 2022, 2, 100129.	6.5	72
4	Preexisting Somatic Mutations of Estrogen Receptor Alpha ( <i>ESR1</i> ) in Early-Stage Primary Breast Cancer. <i>JNCI Cancer Spectrum</i> , 2021, 5, pkab028.	2.9	20
5	Pathogenesis, Symptomatology, and Transmission of SARS-CoV-2 through Analysis of Viral Genomics and Structure. <i>MSystems</i> , 2021, 6, e0009521.	3.8	26
6	Identification and Development of Therapeutics for COVID-19. <i>MSystems</i> , 2021, 6, e0023321.	3.8	20
7	Features of increased malignancy in eosinophilic clear cell renal cell carcinoma. <i>Journal of Pathology</i> , 2020, 252, 384-397.	4.5	13
8	A crowdsourced set of curated structural variants for the human genome. <i>PLoS Computational Biology</i> , 2020, 16, e1007933.	3.2	6
9	The mutational landscape of the <i>SCAN</i> real-world primary breast cancer transcriptome. <i>EMBO Molecular Medicine</i> , 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).. <i>Journal of Clinical Oncology</i> , 2020, 38, 518-518.	1.6	2
11	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
12	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
13	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
14	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
15	Detection of circulating tumor cells and circulating tumor DNA before and after mammographic breast compression in a cohort of breast cancer patients scheduled for neoadjuvant treatment. <i>Breast Cancer Research and Treatment</i> , 2019, 177, 447-455.	2.5	14
16	Clinical Value of RNA Sequencing-Based Classifiers for Prediction of the Five Conventional Breast Cancer Biomarkers: A Report From the Population-Based Multicenter Sweden Cancerome Analysis NetworkBreast Initiative. <i>JCO Precision Oncology</i> , 2018, 2, 1-18.	3.0	101
17	Bioconda: sustainable and comprehensive software distribution for the life sciences. <i>Nature Methods</i> , 2018, 15, 475-476.	19.0	714
18	TopHat-Recondition: a post-processor for TopHat unmapped reads. <i>BMC Bioinformatics</i> , 2016, 17, 199.	2.6	11

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19	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
20	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
21	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
22	Abstract 4805: Whole genome sequencing of primary breast cancers and matched distant metastases. , 2015, , .		0