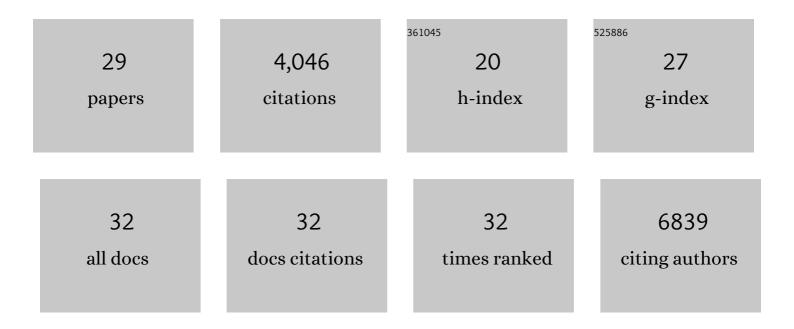
## Florian Breitwieser

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/570516/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Centrifuge: rapid and sensitive classification of metagenomic sequences. Genome Research, 2016, 26, 1721-1729.	2.4	1,025
2	Bracken: estimating species abundance in metagenomics data. PeerJ Computer Science, 0, 3, e104.	2.7	928
3	A review of methods and databases for metagenomic classification and assembly. Briefings in Bioinformatics, 2019, 20, 1125-1136.	3.2	368
4	CHESS: a new human gene catalog curated from thousands of large-scale RNA sequencing experiments reveals extensive transcriptional noise. Genome Biology, 2018, 19, 208.	3.8	263
5	Pavian: interactive analysis of metagenomics data for microbiome studies and pathogen identification. Bioinformatics, 2020, 36, 1303-1304.	1.8	255
6	Next-generation sequencing in neuropathologic diagnosis of infections of the nervous system. Neurology: Neuroimmunology and NeuroInflammation, 2016, 3, e251.	3.1	142
7	Human contamination in bacterial genomes has created thousands of spurious proteins. Genome Research, 2019, 29, 954-960.	2.4	111
8	Fast and sensitive taxonomic assignment to metagenomic contigs. Bioinformatics, 2021, 37, 3029-3031.	1.8	110
9	Systems-pharmacology dissection of a drug synergy in imatinib-resistant CML. Nature Chemical Biology, 2012, 8, 905-912.	3.9	96
10	CD4+ T cell lineage integrity is controlled by the histone deacetylases HDAC1 and HDAC2. Nature Immunology, 2014, 15, 439-448.	7.0	70
11	Initial characterization of the human central proteome. BMC Systems Biology, 2011, 5, 17.	3.0	66
12	Development and Optimization of Metagenomic Next-Generation Sequencing Methods for Cerebrospinal Fluid Diagnostics. Journal of Clinical Microbiology, 2018, 56, .	1.8	65
13	CMPK2 and BCL-G are associated with type 1 interferon–induced HIV restriction in humans. Science Advances, 2018, 4, eaat0843.	4.7	64
14	Quantitative proteomics of aqueous and vitreous fluid from patients with idiopathic epiretinal membranes. Experimental Eye Research, 2013, 108, 48-58.	1.2	58
15	Identifying Corneal Infections in Formalin-Fixed Specimens Using Next Generation Sequencing. , 2018, 59, 280.		51
16	Germline RBBP6 mutations in familial myeloproliferative neoplasms. Blood, 2016, 127, 362-365.	0.6	49
17	Using iTRAQ Combined with Tandem Affinity Purification to Enhance Low-Abundance Proteins Associated with Somatically Mutated EGFR Core Complexes in Lung Cancer. Journal of Proteome Research, 2011, 10, 182-190.	1.8	29
18	Statistical analysis of co-occurrence patterns in microbial presence-absence datasets. PLoS ONE, 2017, 12, e0187132.	1.1	29

#	Article	IF	CITATIONS
19	Presence of Human Hepegivirus-1 in a Cohort of People Who Inject Drugs. Annals of Internal Medicine, 2017, 167, 1.	2.0	28
20	Acid Elution and One-Dimensional Shotgun Analysis on an Orbitrap Mass Spectrometer: An Application to Drug Affinity Chromatography. Journal of Proteome Research, 2009, 8, 4753-4765.	1.8	27
21	Trait-based analysis of the human skin microbiome. Microbiome, 2019, 7, 101.	4.9	25
22	A Computational Approach to Analyze the Mechanism of Action of the Kinase Inhibitor Bafetinib. PLoS Computational Biology, 2010, 6, e1001001.	1.5	23
23	Identification of Kinase Inhibitor Targets in the Lung Cancer Microenvironment by Chemical and Phosphoproteomics. Molecular Cancer Therapeutics, 2014, 13, 2751-2762.	1.9	21
24	MASPECTRAS 2: An integration and analysis platform for proteomic data. Proteomics, 2010, 10, 2719-2722.	1.3	20
25	Metagenomic next-generation sequencing of rectal swabs for the surveillance of antimicrobial-resistant organisms on the Illumina Miseq and Oxford MinION platforms. European Journal of Clinical Microbiology and Infectious Diseases, 2021, 40, 95-102.	1.3	16
26	Deconvoluting virome-wide antibody epitope reactivity profiles. EBioMedicine, 2022, 75, 103747.	2.7	16
27	Comprehensive Comparative and Semiquantitative Proteome of a Very Low Number of Native and Matched Epstein–Barr-Virus-Transformed B Lymphocytes Infiltrating Human Melanoma. Journal of Proteome Research, 2014, 13, 2830-2845.	1.8	15
28	Re-analysis of metagenomic sequences from acute flaccid myelitis patients reveals alternatives to enterovirus D68 infection. F1000Research, 2015, 4, 180.	0.8	9
29	Multiple and Sequential Data Acquisition Method: An Improved Method for Fragmentation and Detection of Cross-Linked Peptides on a Hybrid Linear Trap Quadrupole Orbitrap Velos Mass Spectrometer. Analytical Chemistry, 2013, 85, 1454-1461.	3.2	2