

# Florian Breitwieser

## List of Publications by Year in descending order

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Version: 2024-02-01

29  
papers

4,046  
citations

361045

20  
h-index

525886

27  
g-index

32  
all docs

32  
docs citations

32  
times ranked

6839  
citing authors

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

#	ARTICLE	IF	CITATIONS
19	Presence of Human Hepegivirus-1 in a Cohort of People Who Inject Drugs. <i>Annals of Internal Medicine</i> , 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. <i>Journal of Proteome Research</i> , 2009, 8, 4753-4765.	1.8	27
21	Trait-based analysis of the human skin microbiome. <i>Microbiome</i> , 2019, 7, 101.	4.9	25
22	A Computational Approach to Analyze the Mechanism of Action of the Kinase Inhibitor Bafetinib. <i>PLoS Computational Biology</i> , 2010, 6, e1001001.	1.5	23
23	Identification of Kinase Inhibitor Targets in the Lung Cancer Microenvironment by Chemical and Phosphoproteomics. <i>Molecular Cancer Therapeutics</i> , 2014, 13, 2751-2762.	1.9	21
24	MASPECTRAS 2: An integration and analysis platform for proteomic data. <i>Proteomics</i> , 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. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2021, 40, 95-102.	1.3	16
26	Deconvoluting virome-wide antibody epitope reactivity profiles. <i>EBioMedicine</i> , 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. <i>Journal of Proteome Research</i> , 2014, 13, 2830-2845.	1.8	15
28	Re-analysis of metagenomic sequences from acute flaccid myelitis patients reveals alternatives to enterovirus D68 infection. <i>F1000Research</i> , 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. <i>Analytical Chemistry</i> , 2013, 85, 1454-1461.	3.2	2