

Florian Breitwieser

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

32
papers

2,128
citations

20
h-index

32
g-index

32
ext. papers

3,257
ext. citations

7.9
avg, IF

5.46
L-index

#	Paper	IF	Citations
32	Deconvoluting virome-wide antibody epitope reactivity profiles.. <i>EBioMedicine</i> , 2021 , 75, 103747	8.8	3
31	Fast and sensitive taxonomic assignment to metagenomic contigs. <i>Bioinformatics</i> , 2021 ,	7.2	17
30	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	5.3	5
29	Pavian: interactive analysis of metagenomics data for microbiome studies and pathogen identification. <i>Bioinformatics</i> , 2020 , 36, 1303-1304	7.2	95
28	Human contamination in bacterial genomes has created thousands of spurious proteins. <i>Genome Research</i> , 2019 , 29, 954-960	9.7	51
27	Trait-based analysis of the human skin microbiome. <i>Microbiome</i> , 2019 , 7, 101	16.6	13
26	A review of methods and databases for metagenomic classification and assembly. <i>Briefings in Bioinformatics</i> , 2019 , 20, 1125-1136	13.4	209
25	CMPK2 and BCL-G are associated with type 1 interferon-induced HIV restriction in humans. <i>Science Advances</i> , 2018 , 4, eaat0843	14.3	30
24	Development and Optimization of Metagenomic Next-Generation Sequencing Methods for Cerebrospinal Fluid Diagnostics. <i>Journal of Clinical Microbiology</i> , 2018 , 56,	9.7	41
23	Identifying Corneal Infections in Formalin-Fixed Specimens Using Next Generation Sequencing 2018 , 59, 280-288		36
22	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	18.3	158
21	Statistical analysis of co-occurrence patterns in microbial presence-absence datasets. <i>PLoS ONE</i> , 2017 , 12, e0187132	3.7	20
20	Presence of Human Hepatitis B Virus in a Cohort of People Who Inject Drugs. <i>Annals of Internal Medicine</i> , 2017 , 167, 1-7	8	21
19	Centrifuge: rapid and sensitive classification of metagenomic sequences. <i>Genome Research</i> , 2016 , 26, 1721-1729	9.7	537
18	Next-generation sequencing in neuropathologic diagnosis of infections of the nervous system. <i>Neurology: Neuroimmunology and NeuroInflammation</i> , 2016 , 3, e251	9.1	103
17	Germline RBBP6 mutations in familial myeloproliferative neoplasms. <i>Blood</i> , 2016 , 127, 362-5	2.2	41
16	Re-analysis of metagenomic sequences from acute flaccid myelitis patients reveals alternatives to enterovirus D68 infection. <i>F1000Research</i> , 2015 , 4, 180	3.6	6

15	CD4(+) T cell lineage integrity is controlled by the histone deacetylases HDAC1 and HDAC2. <i>Nature Immunology</i> , 2014 , 15, 439-448	19.1	56
14	Identification of kinase inhibitor targets in the lung cancer microenvironment by chemical and phosphoproteomics. <i>Molecular Cancer Therapeutics</i> , 2014 , 13, 2751-62	6.1	18
13	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, 2830-45	5.6	12
12	Quantitative proteomics of aqueous and vitreous fluid from patients with idiopathic epiretinal membranes. <i>Experimental Eye Research</i> , 2013 , 108, 48-58	3.7	48
11	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, 1454-61	7.8	2
10	Systems-pharmacology dissection of a drug synergy in imatinib-resistant CML. <i>Nature Chemical Biology</i> , 2012 , 8, 905-912	11.7	84
9	Initial characterization of the human central proteome. <i>BMC Systems Biology</i> , 2011 , 5, 17	3.5	56
8	Using iTRAQ combined with tandem affinity purification to enhance low-abundance proteins associated with somatically mutated EGFR core complexes in lung cancer. <i>Journal of Proteome Research</i> , 2011 , 10, 182-90	5.6	28
7	A computational approach to analyze the mechanism of action of the kinase inhibitor bafetinib. <i>PLoS Computational Biology</i> , 2010 , 6, e1001001	5	18
6	MASPECTRAS 2: An integration and analysis platform for proteomic data. <i>Proteomics</i> , 2010 , 10, 2719-22	4.8	20
5	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, 4753-65	5.6	24
4	Bracken: estimating species abundance in metagenomics data. <i>PeerJ Computer Science</i> , 3 , e104	2.7	337
3	Pavian: Interactive analysis of metagenomics data for microbiomics and pathogen identification		30
2	Fast and sensitive taxonomic assignment to metagenomic contigs		4
1	KrakenHLL: Confident and fast metagenomics classification using unique k-mer counts		5