# Florian Breitwieser

## List of Publications by Citations

| 32 | 2,128 | 20 | 32 |
|----|-------|------|------|
| papers | citations | h-index | g-index |

| 32 | 3,257 | 7.9 | 5.46 |
|----|-------|------|------|
| ext. papers | ext. citations | avg, IF | L-index |

| # | Paper | IF | Citations |
|---|-------|----|-----------|
| 32 | Centrifuge: rapid and sensitive classification of metagenomic sequences. *Genome Research*, **2016**, 26, 1721-1729 | 9.7 | 537 |
| 31 | Bracken: estimating species abundance in metagenomics data. *PeerJ Computer Science*,3, e104 | 2.7 | 337 |
| 30 | A review of methods and databases for metagenomic classification and assembly. *Briefings in Bioinformatics*, **2019**, 20, 1125-1136 | 13.4 | 209 |
| 29 | CHESS: a new human gene catalog curated from thousands of large-scale RNA sequencing experiments reveals extensive transcriptional noise. *Genome Biology*, **2018**, 19, 208 | 18.3 | 158 |
| 28 | Next-generation sequencing in neuropathologic diagnosis of infections of the nervous system. *Neurology: Neuroimmunology and NeuroInflammation*, **2016**, 3, e251 | 9.1 | 103 |
| 27 | Pavian: interactive analysis of metagenomics data for microbiome studies and pathogen identification. *Bioinformatics*, **2020**, 36, 1303-1304 | 7.2 | 95 |
| 26 | Systems-pharmacology dissection of a drug synergy in imatinib-resistant CML. *Nature Chemical Biology*, **2012**, 8, 905-912 | 11.7 | 84 |
| 25 | CD4(+) T cell lineage integrity is controlled by the histone deacetylases HDAC1 and HDAC2. *Nature Immunology*, **2014**, 15, 439-448 | 19.1 | 56 |
| 24 | Initial characterization of the human central proteome. *BMC Systems Biology*, **2011**, 5, 17 | 3.5 | 56 |
| 23 | Human contamination in bacterial genomes has created thousands of spurious proteins. *Genome Research*, **2019**, 29, 954-960 | 9.7 | 51 |
| 22 | Quantitative proteomics of aqueous and vitreous fluid from patients with idiopathic epiretinal membranes. *Experimental Eye Research*, **2013**, 108, 48-58 | 3.7 | 48 |
| 21 | Development and Optimization of Metagenomic Next-Generation Sequencing Methods for Cerebrospinal Fluid Diagnostics. *Journal of Clinical Microbiology*, **2018**, 56, | 9.7 | 41 |
| 20 | Germline RBBP6 mutations in familial myeloproliferative neoplasms. *Blood*, **2016**, 127, 362-5 | 2.2 | 41 |
| 19 | Identifying Corneal Infections in Formalin-Fixed Specimens Using Next Generation Sequencing **2018**, 59, 280-288 | | 36 |
| 18 | CMPK2 and BCL-G are associated with type 1 interferon-induced HIV restriction in humans. *Science Advances*, **2018**, 4, eaat0843 | 14.3 | 30 |
| 17 | Pavian: Interactive analysis of metagenomics data for microbiomics and pathogen identification | | 30 |
| 16 | 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, 182-90 | 5.6 | 28 |

# List of Publications

| # | Publication | IF | Cit |
|---|---|---|---|
| 15 | Acid elution and one-dimensional shotgun analysis on an Orbitrap mass spectrometer: an application to drug affinity chromatography. *Journal of Proteome Research*, **2009**, 8, 4753-65 | 5.6 | 24 |
| 14 | Presence of Human Hepegivirus-1 in a Cohort of People Who Inject Drugs. *Annals of Internal Medicine*, **2017**, 167, 1-7 | 8 | 21 |
| 13 | Statistical analysis of co-occurrence patterns in microbial presence-absence datasets. *PLoS ONE*, **2017**, 12, e0187132 | 3.7 | 20 |
| 12 | MASPECTRAS 2: An integration and analysis platform for proteomic data. *Proteomics*, **2010**, 10, 2719-22 | 4.8 | 20 |
| 11 | Identification of kinase inhibitor targets in the lung cancer microenvironment by chemical and phosphoproteomics. *Molecular Cancer Therapeutics*, **2014**, 13, 2751-62 | 6.1 | 18 |
| 10 | A computational approach to analyze the mechanism of action of the kinase inhibitor bafetinib. *PLoS Computational Biology*, **2010**, 6, e1001001 | 5 | 18 |
| 9 | Fast and sensitive taxonomic assignment to metagenomic contigs. *Bioinformatics*, **2021**, | 7.2 | 17 |
| 8 | Trait-based analysis of the human skin microbiome. *Microbiome*, **2019**, 7, 101 | 16.6 | 13 |
| 7 | 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, 2830-45 | 5.6 | 12 |
| 6 | Re-analysis of metagenomic sequences from acute flaccid myelitis patients reveals alternatives to enterovirus D68 infection. *F1000Research*, **2015**, 4, 180 | 3.6 | 6 |
| 5 | KrakenHLL: Confident and fast metagenomics classification using unique k-mer counts | | 5 |
| 4 | 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 | 5.3 | 5 |
| 3 | Fast and sensitive taxonomic assignment to metagenomic contigs | | 4 |
| 2 | Deconvoluting virome-wide antibody epitope reactivity profiles.. *EBioMedicine*, **2021**, 75, 103747 | 8.8 | 3 |
| 1 | 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, 1454-61 | 7.8 | 2 |