

# Jan P Buchmann

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5670286/publications.pdf>

Version: 2024-02-01

26  
papers

4,256  
citations

535685

17  
h-index

651938

25  
g-index

32  
all docs

32  
docs citations

32  
times ranked

8336  
citing authors

#	ARTICLE	IF	CITATIONS
1	Critical Assessment of Metagenome Interpretation: the second round of challenges. <i>Nature Methods</i> , 2022, 19, 429-440.	9.0	133
2	Collecting and managing taxonomic data with NCBI-taxonomist. <i>Bioinformatics</i> , 2021, 36, 5548-5550.	1.8	1
3	Novel hepaciviruses and pegivirus-like viruses in native Australian wildlife and non-human primates. <i>Virus Evolution</i> , 2020, 6, veaa064.	2.2	21
4	NCBI's Virus Discovery Codeathon: Building "The Federated Index of Viral Experiments API Index". <i>Viruses</i> , 2020, 12, 1424.	1.5	3
5	Coding-Complete Genome Sequence of Yada Yada Virus, a Novel Alphavirus Detected in Australian Mosquitoes. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	10
6	CCMetagen: comprehensive and accurate identification of eukaryotes and prokaryotes in metagenomic data. <i>Genome Biology</i> , 2020, 21, 103.	3.8	91
7	NCBI's Virus Discovery Hackathon: Engaging Research Communities to Identify Cloud Infrastructure Requirements. <i>Genes</i> , 2019, 10, 714.	1.0	13
8	Entrezpy: a Python library to dynamically interact with the NCBI Entrez databases. <i>Bioinformatics</i> , 2019, 35, 4511-4514.	1.8	11
9	A Simple Method to Detect Candidate Overlapping Genes in Viruses Using Single Genome Sequences. <i>Molecular Biology and Evolution</i> , 2018, 35, 2572-2581.	3.5	27
10	Virological Sampling of Inaccessible Wildlife with Drones. <i>Viruses</i> , 2018, 10, 300.	1.5	49
11	The Biological Object Notation (BON): a structured file format for biological data. <i>Scientific Reports</i> , 2018, 8, 9644.	1.6	1
12	17th Century Variola Virus Reveals the Recent History of Smallpox. <i>Current Biology</i> , 2016, 26, 3407-3412.	1.8	197
13	Fire blight disease reactome: RNA-seq transcriptional profile of apple host plant defense responses to <i>Erwinia amylovora</i> pathogen infection. <i>Scientific Reports</i> , 2016, 6, 21600.	1.6	38
14	Redefining the invertebrate RNA virosphere. <i>Nature</i> , 2016, 540, 539-543.	13.7	1,328
15	Distinct lineages of Ebola virus in Guinea during the 2014 West African epidemic. <i>Nature</i> , 2015, 524, 102-104.	13.7	96
16	Cell Walls and the Convergent Evolution of the Viral Envelope. <i>Microbiology and Molecular Biology Reviews</i> , 2015, 79, 403-418.	2.9	29
17	Analysis of CACTA transposases reveals intron loss as major factor influencing their exon/intron structure in monocotyledonous and eudicotyledonous hosts. <i>Mobile DNA</i> , 2014, 5, 24.	1.3	10
18	The Ttv1 retrotransposon family is conserved between plant genomes separated by over 100 million years. <i>Theoretical and Applied Genetics</i> , 2014, 127, 1223-1235.	1.8	21

#	ARTICLE	IF	CITATIONS
19	The wheat powdery mildew genome shows the unique evolution of an obligate biotroph. <i>Nature Genetics</i> , 2013, 45, 1092-1096.	9.4	236
20	Genotype-specific SNP map based on whole chromosome 3B sequence information from wheat cultivars Arina and Forno. <i>Plant Biotechnology Journal</i> , 2013, 11, 23-32.	4.1	22
21	Transposons in Cereals: Shaping Genomes and Driving Their Evolution. , 2013, , 127-154.		1
22	Inter-species sequence comparison of <i>Brachypodium</i> reveals how transposon activity corrodes genome colinearity. <i>Plant Journal</i> , 2012, 71, 550-563.	2.8	26
23	Comparative sequence analysis of wheat and barley powdery mildew fungi reveals gene colinearity, dates divergence and indicates host-pathogen co-evolution. <i>Fungal Genetics and Biology</i> , 2011, 48, 327-334.	0.9	33
24	Fine mapping and syntenic integration of the semi-dwarfing gene <i>sdw3</i> of barley. <i>Functional and Integrative Genomics</i> , 2010, 10, 509-521.	1.4	19
25	Genome sequencing and analysis of the model grass <i>Brachypodium distachyon</i> . <i>Nature</i> , 2010, 463, 763-768.	13.7	1,685
26	Patching gaps in plant genomes results in gene movement and erosion of colinearity. <i>Genome Research</i> , 2010, 20, 1229-1237.	2.4	139