

# Jan P Buchmann

## 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.

27  
papers

2,996  
citations

16  
h-index

32  
g-index

32  
ext. papers

3,798  
ext. citations

13.3  
avg, IF

5.95  
L-index

#	Paper	IF	Citations
27	Critical Assessment of Metagenome Interpretation: the second round of challenges.. <i>Nature Methods</i> , <b>2022</b> ,	21.6	14
26	NCBI/Virus Discovery Codeathon: Building "FIVE" -The Federated Index of Viral Experiments API Index. <i>Viruses</i> , <b>2020</b> , 12,	6.2	1
25	Coding-Complete Genome Sequence of Yada Yada Virus, a Novel Alphavirus Detected in Australian Mosquitoes. <i>Microbiology Resource Announcements</i> , <b>2020</b> , 9,	1.3	7
24	CCMetagen: comprehensive and accurate identification of eukaryotes and prokaryotes in metagenomic data. <i>Genome Biology</i> , <b>2020</b> , 21, 103	18.3	35
23	Novel hepaci- and pegi-like viruses in native Australian wildlife and non-human primates. <i>Virus Evolution</i> , <b>2020</b> , 6, veaa064	3.7	6
22	NCBI/Virus Discovery Hackathon: Engaging Research Communities to Identify Cloud Infrastructure Requirements. <i>Genes</i> , <b>2019</b> , 10,	4.2	8
21	Entrezpy: a Python library to dynamically interact with the NCBI Entrez databases. <i>Bioinformatics</i> , <b>2019</b> , 35, 4511-4514	7.2	5
20	Virological Sampling of Inaccessible Wildlife with Drones. <i>Viruses</i> , <b>2018</b> , 10,	6.2	31
19	The Biological Object Notation (BON): a structured file format for biological data. <i>Scientific Reports</i> , <b>2018</b> , 8, 9644	4.9	
18	A Simple Method to Detect Candidate Overlapping Genes in Viruses Using Single Genome Sequences. <i>Molecular Biology and Evolution</i> , <b>2018</b> , 35, 2572-2581	8.3	20
17	Redefining the invertebrate RNA virosphere. <i>Nature</i> , <b>2016</b> , 540, 539-543	50.4	821
16	17 Century Variola Virus Reveals the Recent History of Smallpox. <i>Current Biology</i> , <b>2016</b> , 26, 3407-3412	6.3	118
15	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> , <b>2016</b> , 6, 21600	4.9	26
14	Distinct lineages of Ebola virus in Guinea during the 2014 West African epidemic. <i>Nature</i> , <b>2015</b> , 524, 102-104	36.4	78
13	Cell Walls and the Convergent Evolution of the Viral Envelope. <i>Microbiology and Molecular Biology Reviews</i> , <b>2015</b> , 79, 403-18	13.2	21
12	The Tvv1 retrotransposon family is conserved between plant genomes separated by over 100 million years. <i>Theoretical and Applied Genetics</i> , <b>2014</b> , 127, 1223-35	6	18
11	Analysis of CACTA transposases reveals intron loss as major factor influencing their exon/intron structure in monocotyledonous and eudicotyledonous hosts. <i>Mobile DNA</i> , <b>2014</b> , 5, 24	4.4	8

10	The wheat powdery mildew genome shows the unique evolution of an obligate biotroph. <i>Nature Genetics</i> , <b>2013</b> , 45, 1092-6	36.3	169
9	Genotype-specific SNP map based on whole chromosome 3B sequence information from wheat cultivars Arina and Forno. <i>Plant Biotechnology Journal</i> , <b>2013</b> , 11, 23-32	11.6	16
8	Transposons in Cereals: Shaping Genomes and Driving Their Evolution <b>2013</b> , 127-154		1
7	Inter-species sequence comparison of Brachypodium reveals how transposon activity corrodes genome colinearity. <i>Plant Journal</i> , <b>2012</b> , 71, 550-63	6.9	22
6	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> , <b>2011</b> , 48, 327-349	3.9	32
5	Genome sequencing and analysis of the model grass Brachypodium distachyon. <i>Nature</i> , <b>2010</b> , 463, 763-850.4	50.4	1399
4	Patching gaps in plant genomes results in gene movement and erosion of colinearity. <i>Genome Research</i> , <b>2010</b> , 20, 1229-37	9.7	117
3	Fine mapping and syntenic integration of the semi-dwarfing gene sdw3 of barley. <i>Functional and Integrative Genomics</i> , <b>2010</b> , 10, 509-21	3.8	18
2	Metagenomic identification of diverse animal hepaciviruses and pegiviruses		1
1	CCMetagen: comprehensive and accurate identification of eukaryotes and prokaryotes in metagenomic data		2