

# Markus Ankenbrand

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5564101/publications.pdf>

Version: 2024-02-01

32  
papers

1,562  
citations

567247

15  
h-index

454934

30  
g-index

44  
all docs

44  
docs citations

44  
times ranked

2722  
citing authors

#	ARTICLE	IF	CITATIONS
1	ITS2 Database V: Twice as Much: Table 1.. Molecular Biology and Evolution, 2015, 32, 3030-3032.	8.9	231
2	Evaluating multiplexed next-generation sequencing as a method in palynology for mixed pollen samples. Plant Biology, 2015, 17, 558-566.	3.8	182
3	Increased efficiency in identifying mixed pollen samples by meta-barcoding with a dual-indexing approach. BMC Ecology, 2015, 15, 20.	3.0	167
4	bcgTree: automatized phylogenetic tree building from bacterial core genomes. Genome, 2016, 59, 783-791.	2.0	151
5	Open Science principles for accelerating trait-based science across the Tree of Life. Nature Ecology and Evolution, 2020, 4, 294-303.	7.8	144
6	Compensatory Base Changes in ITS2 Secondary Structures Correlate with the Biological Species Concept Despite Intragenomic Variability in ITS2 Sequences – A Proof of Concept. PLoS ONE, 2013, 8, e66726.	2.5	115
7	Venus flytrap carnivorous lifestyle builds on herbivore defense strategies. Genome Research, 2016, 26, 812-825.	5.5	88
8	AliTV – interactive visualization of whole genome comparisons. PeerJ Computer Science, 0, 3, e116.	4.5	80
9	Genomes of the Venus Flytrap and Close Relatives Unveil the Roots of Plant Carnivory. Current Biology, 2020, 30, 2312-2320.e5.	3.9	60
10	A systematic comparison of chloroplast genome assembly tools. Genome Biology, 2020, 21, 254.	8.8	42
11	Chronic exposure to the pesticide flupyradifurone can lead to premature onset of foraging in honeybees <i>Apis mellifera</i> . Journal of Applied Ecology, 2020, 57, 609-618.	4.0	37
12	Linking pollen foraging of megachilid bees to their nest bacterial microbiota. Ecology and Evolution, 2019, 9, 10788-10800.	1.9	36
13	BCdatabaser: on-the-fly reference database creation for (meta-)barcoding. Bioinformatics, 2020, 36, 2630-2631.	4.1	30
14	Standard methods for pollen research. Journal of Apicultural Research, 2021, 60, 1-109.	1.5	25
15	chloroExtractor: extraction and assembly of the chloroplast genome from whole genome shotgun data. Journal of Open Source Software, 2018, 3, 464.	4.6	24
16	Wild bees and their nests host Paenibacillus bacteria with functional potential of avail. Microbiome, 2018, 6, 229.	11.1	23
17	Sensitivity analysis for interpretation of machine learning based segmentation models in cardiac MRI. BMC Medical Imaging, 2021, 21, 27.	2.7	16
18	Deep learning-based cardiac cine segmentation: Transfer learning application to 7T ultrahigh-field MRI. Magnetic Resonance in Medicine, 2021, 86, 2179-2191.	3.0	14

#	ARTICLE	IF	CITATIONS
19	B <sub>0</sub> shimming of the human heart at 7T. <i>Magnetic Resonance in Medicine</i> , 2021, 85, 182-196.	3.0	13
20	On the way to routine cardiac MRI at 7 Tesla - a pilot study on consecutive 84 examinations. <i>PLoS ONE</i> , 2021, 16, e0252797.	2.5	11
21	Self-configuring nnU-net pipeline enables fully automatic infarct segmentation in late enhancement MRI after myocardial infarction. <i>European Journal of Radiology</i> , 2021, 141, 109817.	2.6	10
22	Dealing with software complexity in individual-based models. <i>Methods in Ecology and Evolution</i> , 2021, 12, 2324-2333.	5.2	6
23	Functional exploration of natural networks and ecological communities. <i>Methods in Ecology and Evolution</i> , 2018, 9, 2028-2033.	5.2	5
24	Exploring Ensemble Applications for Multi-sequence Myocardial Pathology Segmentation. <i>Lecture Notes in Computer Science</i> , 2020, , 60-67.	1.3	3
25	TBro: visualization and management of de novo transcriptomes. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw146.	3.0	3
26	In Vitro Rearing Changes Social Task Performance and Physiology in Honeybees. <i>Insects</i> , 2022, 13, 4.	2.2	3
27	Inferring Core Genome Phylogenies for Bacteria. <i>Methods in Molecular Biology</i> , 2021, 2242, 59-68.	0.9	2
28	biojs-io-biom, a BioJS component for handling data in Biological Observation Matrix (BIOM) format. <i>F1000Research</i> , 2016, 5, 2348.	1.6	2
29	A data-driven semantic segmentation model for direct cardiac functional analysis based on undersampled radial MR cine series. <i>Magnetic Resonance in Medicine</i> , 2022, 87, 972-983.	3.0	2
30	Draft Genome Sequence of <i>Klebsiella</i> sp. Strain C31 Isolated from a Malaysian Tropical Peat Swamp Forest. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
31	Draft Genome Sequence of <i>Paraburkholderia</i> sp. Strain C35, Isolated from a Malaysian Tropical Peat Swamp Forest. <i>Genome Announcements</i> , 2018, 6, .	0.8	0
32	biojs-io-biom, a BioJS component for handling data in Biological Observation Matrix (BIOM) format. <i>F1000Research</i> , 2016, 5, 2348.	1.6	0