

Markus Ankenbrand

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.

34
papers

877
citations

13
h-index

29
g-index

44
ext. papers

1,289
ext. citations

5.4
avg, IF

4.27
L-index

#	Paper	IF	Citations
34	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	4.4	1
33	Deep learning-based cardiac cine segmentation: Transfer learning application to 7T ultrahigh-field MRI. <i>Magnetic Resonance in Medicine</i> , 2021 , 86, 2179-2191	4.4	2
32	On the way to routine cardiac MRI at 7 Tesla - a pilot study on consecutive 84 examinations. <i>PLoS ONE</i> , 2021 , 16, e0252797	3.7	2
31	B shimming of the human heart at 7T. <i>Magnetic Resonance in Medicine</i> , 2021 , 85, 182-196	4.4	5
30	Sensitivity analysis for interpretation of machine learning based segmentation models in cardiac MRI. <i>BMC Medical Imaging</i> , 2021 , 21, 27	2.9	7
29	Standard methods for pollen research. <i>Journal of Apicultural Research</i> , 2021 , 60, 1-109	2	9
28	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	4.7	2
27	Inferring Core Genome Phylogenies for Bacteria. <i>Methods in Molecular Biology</i> , 2021 , 2242, 59-68	1.4	1
26	Genomes of the Venus Flytrap and Close Relatives Unveil the Roots of Plant Carnivory. <i>Current Biology</i> , 2020 , 30, 2312-2320.e5	6.3	25
25	Open Science principles for accelerating trait-based science across the Tree of Life. <i>Nature Ecology and Evolution</i> , 2020 , 4, 294-303	12.3	54
24	Exploring Ensemble Applications for Multi-sequence Myocardial Pathology Segmentation. <i>Lecture Notes in Computer Science</i> , 2020 , 60-67	0.9	2
23	BCdatabaser: on-the-fly reference database creation for (meta-)barcoding. <i>Bioinformatics</i> , 2020 , 36, 2630-2631	11	11
22	Chronic exposure to the pesticide flupyradifurone can lead to premature onset of foraging in honeybees <i>Apis mellifera</i> . <i>Journal of Applied Ecology</i> , 2020 , 57, 609-618	5.8	19
21	A systematic comparison of chloroplast genome assembly tools. <i>Genome Biology</i> , 2020 , 21, 254	18.3	7
20	Linking pollen foraging of megachilid bees to their nest bacterial microbiota. <i>Ecology and Evolution</i> , 2019 , 9, 10788-10800	2.8	15
19	Functional exploration of natural networks and ecological communities. <i>Methods in Ecology and Evolution</i> , 2018 , 9, 2028-2033	7.7	5
18	chloroExtractor: extraction and assembly of the chloroplast genome from whole genome shotgun data. <i>Journal of Open Source Software</i> , 2018 , 3, 464	5.2	13

17	Wild bees and their nests host Paenibacillus bacteria with functional potential of avail. <i>Microbiome</i> , 2018 , 6, 229	16.6	14
16	biojs-io-biom, a BioJS component for handling data in Biological Observation Matrix (BIOM) format. <i>F1000Research</i> , 2016 , 5, 2348	3.6	1
15	TBro: visualization and management of de novo transcriptomes. <i>Database: the Journal of Biological Databases and Curation</i> , 2016 , 2016,	5	2
14	biojs-io-biom, a BioJS component for handling data in Biological Observation Matrix (BIOM) format. <i>F1000Research</i> , 2016 , 5, 2348	3.6	
13	DNA-Metabarcoding – ein neuer Blick auf organismische Diversität. <i>BioSpektrum</i> , 2016 , 22, 147-150	0.1	
12	Venus flytrap carnivorous lifestyle builds on herbivore defense strategies. <i>Genome Research</i> , 2016 , 26, 812-25	9.7	60
11	bcgTree: automatized phylogenetic tree building from bacterial core genomes. <i>Genome</i> , 2016 , 59, 783-794	2.1	77
10	ITS2 Database V: Twice as Much. <i>Molecular Biology and Evolution</i> , 2015 , 32, 3030-2	8.3	158
9	Evaluating multiplexed next-generation sequencing as a method in palynology for mixed pollen samples. <i>Plant Biology</i> , 2015 , 17, 558-66	3.7	121
8	Increased efficiency in identifying mixed pollen samples by meta-barcoding with a dual-indexing approach. <i>BMC Ecology</i> , 2015 , 15, 20	2.7	122
7	Compensatory base changes in ITS2 secondary structures correlate with the biological species concept despite intragenomic variability in ITS2 sequences—a proof of concept. <i>PLoS ONE</i> , 2013 , 8, e66728	3.7	91
6	AliTV—interactive visualization of whole genome comparisons. <i>PeerJ Computer Science</i> , 2013 , 3, e116	2.7	30
5	A Deep Learning Based Cardiac Cine Segmentation Framework for Clinicians – Transfer Learning Application to 7T		2
4	Novel integrative elements and genomic plasticity in ocean ecosystems		7
3	A systematic comparison of chloroplast genome assembly tools		3
2	GWAS-Flow: A GPU accelerated framework for efficient permutation based genome-wide association studies		5
1	Dealing with software complexity in individual-based models. <i>Methods in Ecology and Evolution</i> ,	7.7	2