

Katharina J Hoff

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

3,447
citations

687363

13
h-index

752698

20
g-index

24
all docs

24
docs citations

24
times ranked

5325
citing authors

#	ARTICLE	IF	CITATIONS
1	Standards recommendations for the Earth BioGenome Project. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	33
2	Pseudomonas Strains Induce Transcriptional and Morphological Changes and Reduce Root Colonization of Verticillium spp.. Frontiers in Microbiology, 2021, 12, 652468.	3.5	6
3	A 20â€kb lineageâ€specific genomic region tames virulence in pathogenic amphidiploid Verticillium longisporum. Molecular Plant Pathology, 2021, 22, 939-953.	4.2	6
4	The genomic basis of evolutionary differentiation among honey bees. Genome Research, 2021, 31, 1203-1215.	5.5	17
5	Transposable elements and introgression introduce genetic variation in the invasive ant <i>Cardiocondyla obscurior</i> . Molecular Ecology, 2021, 30, 6211-6228.	3.9	20
6	Chromosome-level reference genome of the European wasp spider <i>Argiope bruennichi</i> : a resource for studies on range expansion and evolutionary adaptation. GigaScience, 2021, 10, .	6.4	35
7	BRAKER2: automatic eukaryotic genome annotation with GeneMark-EP+ and AUGUSTUS supported by a protein database. NAR Genomics and Bioinformatics, 2021, 3, lqaa108.	3.2	803
8	The draft chromosome-level genome assembly of tetraploid ground cherry (<i>Prunus fruticosa</i> Pall.) from long reads. Genomics, 2021, 113, 4173-4183.	2.9	14
9	TSEBRA: transcript selector for BRAKER. BMC Bioinformatics, 2021, 22, 566.	2.6	91
10	Full Genome Sequence of a <i>Methanomassiliicoccales</i> Representative Enriched from Peat Soil. Microbiology Resource Announcements, 2021, 10, e0044321.	0.6	4
11	An initial comparative genomic autopsy of wasting disease in sea stars. Molecular Ecology, 2020, 29, 1087-1102.	3.9	22
12	Non-invasive and label-free 3D-visualization shows in vivo oligomerization of the staphylococcal alkaline shock protein 23 (Asp23). Scientific Reports, 2020, 10, 125.	3.3	8
13	Predicting Genes in Single Genomes with AUGUSTUS. Current Protocols in Bioinformatics, 2019, 65, e57.	25.8	225
14	Mitigating Anticipated Effects of Systematic Errors Supports Sister-Group Relationship between Xenacoelomorpha and Ambulacraria. Current Biology, 2019, 29, 1818-1826.e6.	3.9	120
15	Whole-Genome Annotation with BRAKER. Methods in Molecular Biology, 2019, 1962, 65-95.	0.9	461
16	VARUS: sampling complementary RNA reads from the sequence read archive. BMC Bioinformatics, 2019, 20, 558.	2.6	10
17	BRAKER1: Unsupervised RNA-Seq-Based Genome Annotation with GeneMark-ET and AUGUSTUS. Bioinformatics, 2016, 32, 767-769.	4.1	918
18	The genomes of two key bumblebee species with primitive eusocial organization. Genome Biology, 2015, 16, 76.	8.8	330

#	ARTICLE	IF	CITATIONS
19	The nervous system of Xenacoelomorpha: a genomic perspective. <i>Journal of Experimental Biology</i> , 2015, 218, 618-628.	1.7	36
20	WebAUGUSTUS--a web service for training AUGUSTUS and predicting genes in eukaryotes. <i>Nucleic Acids Research</i> , 2013, 41, W123-W128.	14.5	253