

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	BRAKER1: Unsupervised RNA-Seq-Based Genome Annotation with GeneMark-ET and AUGUSTUS. <i>Bioinformatics</i> , 2016, 32, 767-769.	4.1	918
2	BRAKER2: automatic eukaryotic genome annotation with GeneMark-EP+ and AUGUSTUS supported by a protein database. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqaa108.	3.2	803
3	Whole-Genome Annotation with BRAKER. <i>Methods in Molecular Biology</i> , 2019, 1962, 65-95.	0.9	461
4	The genomes of two key bumblebee species with primitive eusocial organization. <i>Genome Biology</i> , 2015, 16, 76.	8.8	330
5	WebAUGUSTUS--a web service for training AUGUSTUS and predicting genes in eukaryotes. <i>Nucleic Acids Research</i> , 2013, 41, W123-W128.	14.5	253
6	Predicting Genes in Single Genomes with AUGUSTUS. <i>Current Protocols in Bioinformatics</i> , 2019, 65, e57.	25.8	225
7	Mitigating Anticipated Effects of Systematic Errors Supports Sister-Group Relationship between Xenacoelomorpha and Ambulacraria. <i>Current Biology</i> , 2019, 29, 1818-1826.e6.	3.9	120
8	TSEBRA: transcript selector for BRAKER. <i>BMC Bioinformatics</i> , 2021, 22, 566.	2.6	91
9	The nervous system of Xenacoelomorpha: a genomic perspective. <i>Journal of Experimental Biology</i> , 2015, 218, 618-628.	1.7	36
10	Chromosome-level reference genome of the European wasp spider <i>Argiope bruennichi</i> : a resource for studies on range expansion and evolutionary adaptation. <i>GigaScience</i> , 2021, 10, .	6.4	35
11	Standards recommendations for the Earth BioGenome Project. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	33
12	An initial comparative genomic autopsy of wasting disease in sea stars. <i>Molecular Ecology</i> , 2020, 29, 1087-1102.	3.9	22
13	Transposable elements and introgression introduce genetic variation in the invasive ant <i>Cardiocondyla obscurior</i> . <i>Molecular Ecology</i> , 2021, 30, 6211-6228.	3.9	20
14	The genomic basis of evolutionary differentiation among honey bees. <i>Genome Research</i> , 2021, 31, 1203-1215.	5.5	17
15	The draft chromosome-level genome assembly of tetraploid ground cherry (<i>Prunus fruticosa</i> Pall.) from long reads. <i>Genomics</i> , 2021, 113, 4173-4183.	2.9	14
16	VARUS: sampling complementary RNA reads from the sequence read archive. <i>BMC Bioinformatics</i> , 2019, 20, 558.	2.6	10
17	Non-invasive and label-free 3D-visualization shows in vivo oligomerization of the staphylococcal alkaline shock protein 23 (Asp23). <i>Scientific Reports</i> , 2020, 10, 125.	3.3	8
18	<i>Pseudomonas</i> Strains Induce Transcriptional and Morphological Changes and Reduce Root Colonization of <i>Verticillium</i> spp.. <i>Frontiers in Microbiology</i> , 2021, 12, 652468.	3.5	6

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19	A 20â€kb lineageâ€specific genomic region tames virulence in pathogenic amphidiploid <i>Verticillium longisporum</i> . <i>Molecular Plant Pathology</i> , 2021, 22, 939-953.	4.2	6
20	Full Genome Sequence of a <i>Methanomassiliicoccales</i> Representative Enriched from Peat Soil. <i>Microbiology Resource Announcements</i> , 2021, 10, e0044321.	0.6	4