

Anne Kupczok

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

870
citations

623734

14
h-index

526287

27
g-index

38
all docs

38
docs citations

38
times ranked

1725
citing authors

#	ARTICLE	IF	CITATIONS
1	A Consistent Phylogenetic Backbone for the Fungi. <i>Molecular Biology and Evolution</i> , 2012, 29, 1319-1334.	8.9	129
2	A Phage Protein Aids Bacterial Symbionts in Eukaryote Immune Evasion. <i>Cell Host and Microbe</i> , 2019, 26, 542-550.e5.	11.0	94
3	Functional diversity enables multiple symbiont strains to coexist in deep-sea mussels. <i>Nature Microbiology</i> , 2019, 4, 2487-2497.	13.3	76
4	Rates of Mutation and Recombination in Siphoviridae Phage Genome Evolution over Three Decades. <i>Molecular Biology and Evolution</i> , 2018, 35, 1147-1159.	8.9	61
5	Disentangling the genetic basis of rhizosphere microbiome assembly in tomato. <i>Nature Communications</i> , 2022, 13, .	12.8	53
6	Accuracy of phylogeny reconstruction methods combining overlapping gene data sets. <i>Algorithms for Molecular Biology</i> , 2010, 5, 37.	1.2	50
7	Segregational Drift and the Interplay between Plasmid Copy Number and Evolvability. <i>Molecular Biology and Evolution</i> , 2019, 36, 472-486.	8.9	46
8	Horizontally transmitted symbiont populations in deep-sea mussels are genetically isolated. <i>ISME Journal</i> , 2019, 13, 2954-2968.	9.8	42
9	Methanosarcina Spherical Virus, a Novel Archaeal Lytic Virus Targeting Methanosarcina Strains. <i>Journal of Virology</i> , 2017, 91, .	3.4	35
10	The Contribution of Genetic Recombination to CRISPR Array Evolution. <i>Genome Biology and Evolution</i> , 2015, 7, 1925-1939.	2.5	31
11	Recombination Signal in Mycobacterium tuberculosis Stems from Reference-guided Assemblies and Alignment Artefacts. <i>Genome Biology and Evolution</i> , 2018, 10, 1920-1926.	2.5	27
12	Insertion and deletion evolution reflects antibiotics selection pressure in a Mycobacterium tuberculosis outbreak. <i>PLoS Pathogens</i> , 2020, 16, e1008357.	4.7	22
13	Plasticity first: molecular signatures of a complex morphological trait in filamentous cyanobacteria. <i>BMC Evolutionary Biology</i> , 2017, 17, 209.	3.2	19
14	An Exact Algorithm for the Geodesic Distance between Phylogenetic Trees. <i>Journal of Computational Biology</i> , 2008, 15, 577-591.	1.6	18
15	Characterization of the lytic archaeal virus Drs3 infecting Methanobacterium formicicum. <i>Archives of Virology</i> , 2019, 164, 667-674.	2.1	18
16	Probabilistic models for CRISPR spacer content evolution. <i>BMC Evolutionary Biology</i> , 2013, 13, 54.	3.2	13
17	Complete Genome Sequence of the Novel Phage MG-B1 Infecting Bacillus weihenstephanensis. <i>Genome Announcements</i> , 2013, 1, .	0.8	12
18	Marine genomics: News and views. <i>Marine Genomics</i> , 2017, 31, 1-8.	1.1	12

#	ARTICLE	IF	CITATIONS
19	Rates of Molecular Evolution in a Marine <i>Synechococcus</i> Phage Lineage. <i>Viruses</i> , 2019, 11, 720.	3.3	12
20	Determinants of simulated RNA evolution. <i>Journal of Theoretical Biology</i> , 2006, 238, 726-735.	1.7	11
21	Split-based computation of majority-rule supertrees. <i>BMC Evolutionary Biology</i> , 2011, 11, 205.	3.2	11
22	A SAGE based approach to human glomerular endothelium: defining the transcriptome, finding a novel molecule and highlighting endothelial diversity. <i>BMC Genomics</i> , 2014, 15, 725.	2.8	11
23	Motif depletion in bacteriophages infecting hosts with CRISPR systems. <i>BMC Genomics</i> , 2014, 15, 663.	2.8	9
24	Mass burial genomics reveals outbreak of enteric paratyphoid fever in the Late Medieval trade city Lüneburg. <i>IScience</i> , 2021, 24, 102419.	4.1	9
25	Characterization of Blf4, an Archaeal Lytic Virus Targeting a Member of the Methanomicrobiales. <i>Viruses</i> , 2021, 13, 1934.	3.3	8
26	A stable backbone for the fungi. <i>Nature Precedings</i> , 2009, , .	0.1	6
27	Comment on "A congruence index for testing topological similarity between trees". <i>Bioinformatics</i> , 2009, 25, 147-149.	4.1	6
28	Bioinformatics Meets Virology: The European Virus Bioinformatics Center's Second Annual Meeting. <i>Viruses</i> , 2018, 10, 256.	3.3	6
29	Consequences of Different Null Models on the Tree Shape Bias of Supertree Methods. <i>Systematic Biology</i> , 2011, 60, 218-225.	5.6	5
30	Pangenome Evolution in Environmentally Transmitted Symbionts of Deep-Sea Mussels Is Governed by Vertical Inheritance. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	5