

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	Disentangling the genetic basis of rhizosphere microbiome assembly in tomato. <i>Nature Communications</i> , 2022, 13, .	12.8	53
2	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
3	Mass burial genomics reveals outbreak of enteric paratyphoid fever in the Late Medieval trade city Lübeck. <i>IScience</i> , 2021, 24, 102419.	4.1	9
4	Characterization of Blf4, an Archaeal Lytic Virus Targeting a Member of the Methanomicrobiales. <i>Viruses</i> , 2021, 13, 1934.	3.3	8
5	Insertion and deletion evolution reflects antibiotics selection pressure in a <i>Mycobacterium tuberculosis</i> outbreak. <i>PLoS Pathogens</i> , 2020, 16, e1008357.	4.7	22
6	Rates of Molecular Evolution in a Marine <i>Synechococcus</i> Phage Lineage. <i>Viruses</i> , 2019, 11, 720.	3.3	12
7	Functional diversity enables multiple symbiont strains to coexist in deep-sea mussels. <i>Nature Microbiology</i> , 2019, 4, 2487-2497.	13.3	76
8	Horizontally transmitted symbiont populations in deep-sea mussels are genetically isolated. <i>ISME Journal</i> , 2019, 13, 2954-2968.	9.8	42
9	A Phage Protein Aids Bacterial Symbionts in Eukaryote Immune Evasion. <i>Cell Host and Microbe</i> , 2019, 26, 542-550.e5.	11.0	94
10	Segregational Drift and the Interplay between Plasmid Copy Number and Evolvability. <i>Molecular Biology and Evolution</i> , 2019, 36, 472-486.	8.9	46
11	Characterization of the lytic archaeal virus Drs3 infecting <i>Methanobacterium formicicum</i> . <i>Archives of Virology</i> , 2019, 164, 667-674.	2.1	18
12	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
13	Bioinformatics Meets Virology: The European Virus Bioinformatics Center's Second Annual Meeting. <i>Viruses</i> , 2018, 10, 256.	3.3	6
14	Recombination Signal in <i>Mycobacterium tuberculosis</i> Stems from Reference-guided Assemblies and Alignment Artefacts. <i>Genome Biology and Evolution</i> , 2018, 10, 1920-1926.	2.5	27
15	<i>Methanosarcina</i> Spherical Virus, a Novel Archaeal Lytic Virus Targeting <i>Methanosarcina</i> Strains. <i>Journal of Virology</i> , 2017, 91, .	3.4	35
16	Marine genomics: News and views. <i>Marine Genomics</i> , 2017, 31, 1-8.	1.1	12
17	Plasticity first: molecular signatures of a complex morphological trait in filamentous cyanobacteria. <i>BMC Evolutionary Biology</i> , 2017, 17, 209.	3.2	19
18	The Contribution of Genetic Recombination to CRISPR Array Evolution. <i>Genome Biology and Evolution</i> , 2015, 7, 1925-1939.	2.5	31

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19	Motif depletion in bacteriophages infecting hosts with CRISPR systems. BMC Genomics, 2014, 15, 663.	2.8	9
20	A SAGE based approach to human glomerular endothelium: defining the transcriptome, finding a novel molecule and highlighting endothelial diversity. BMC Genomics, 2014, 15, 725.	2.8	11
21	Probabilistic models for CRISPR spacer content evolution. BMC Evolutionary Biology, 2013, 13, 54.	3.2	13
22	Complete Genome Sequence of the Novel Phage MG-B1 Infecting Bacillus weihenstephanensis. Genome Announcements, 2013, 1, .	0.8	12
23	A Consistent Phylogenetic Backbone for the Fungi. Molecular Biology and Evolution, 2012, 29, 1319-1334.	8.9	129
24	Split-based computation of majority-rule supertrees. BMC Evolutionary Biology, 2011, 11, 205.	3.2	11
25	Consequences of Different Null Models on the Tree Shape Bias of Supertree Methods. Systematic Biology, 2011, 60, 218-225.	5.6	5
26	Accuracy of phylogeny reconstruction methods combining overlapping gene data sets. Algorithms for Molecular Biology, 2010, 5, 37.	1.2	50
27	A stable backbone for the fungi. Nature Precedings, 2009, , .	0.1	6
28	Comment on "A congruence index for testing topological similarity between trees". Bioinformatics, 2009, 25, 147-149.	4.1	6
29	An Exact Algorithm for the Geodesic Distance between Phylogenetic Trees. Journal of Computational Biology, 2008, 15, 577-591.	1.6	18
30	Determinants of simulated RNA evolution. Journal of Theoretical Biology, 2006, 238, 726-735.	1.7	11