

Alexey M Kozlov

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

6,788
citations

394421

19
h-index

610901

24
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44
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44
docs citations

44
times ranked

10067
citing authors

#	ARTICLE	IF	CITATIONS
1	RAxML-NG: a fast, scalable and user-friendly tool for maximum likelihood phylogenetic inference. <i>Bioinformatics</i> , 2019, 35, 4453-4455.	4.1	2,287
2	ModelTest-NG: A New and Scalable Tool for the Selection of DNA and Protein Evolutionary Models. <i>Molecular Biology and Evolution</i> , 2020, 37, 291-294.	8.9	1,021
3	Eleven grand challenges in single-cell data science. <i>Genome Biology</i> , 2020, 21, 31.	8.8	742
4	Evolutionary History of the Hymenoptera. <i>Current Biology</i> , 2017, 27, 1013-1018.	3.9	611
5	EPA-ng: Massively Parallel Evolutionary Placement of Genetic Sequences. <i>Systematic Biology</i> , 2019, 68, 365-369.	5.6	400
6	Phylogenomics and the evolution of hemipteroid insects. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 12775-12780.	7.1	275
7	Parasites dominate hyperdiverse soil protist communities in Neotropical rainforests. <i>Nature Ecology and Evolution</i> , 2017, 1, 91.	7.8	262
8	ExaML version 3: a tool for phylogenomic analyses on supercomputers. <i>Bioinformatics</i> , 2015, 31, 2577-2579.	4.1	209
9	Phylogenetic Analysis of SARS-CoV-2 Data Is Difficult. <i>Molecular Biology and Evolution</i> , 2021, 38, 1777-1791.	8.9	119
10	Phylogeny-aware identification and correction of taxonomically mislabeled sequences. <i>Nucleic Acids Research</i> , 2016, 44, 5022-5033.	14.5	97
11	Transcriptome and target DNA enrichment sequence data provide new insights into the phylogeny of vespid wasps (Hymenoptera: Aculeata: Vespidae). <i>Molecular Phylogenetics and Evolution</i> , 2017, 116, 213-226.	2.7	87
12	GeneRax: A Tool for Species-Tree-Aware Maximum Likelihood-Based Gene Family Tree Inference under Gene Duplication, Transfer, and Loss. <i>Molecular Biology and Evolution</i> , 2020, 37, 2763-2774.	8.9	87
13	Transcriptome sequence-based phylogeny of chalcidoid wasps (Hymenoptera: Chalcidoidea) reveals a history of rapid radiations, convergence, and evolutionary success. <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 286-296.	2.7	83
14	Long-read metabarcoding of the eukaryotic rDNA operon to phylogenetically and taxonomically resolve environmental diversity. <i>Molecular Ecology Resources</i> , 2020, 20, 429-443.	4.8	68
15	New data, same story: phylogenomics does not support Syrphoidea (Diptera: Syrphidae, Pipunculidae). <i>Systematic Entomology</i> , 2018, 43, 447-459.	3.9	53
16	ParGenes: a tool for massively parallel model selection and phylogenetic tree inference on thousands of genes. <i>Bioinformatics</i> , 2019, 35, 1771-1773.	4.1	51
17	A roadmap for global synthesis of the plant tree of life. <i>American Journal of Botany</i> , 2018, 105, 614-622.	1.7	38
18	Resolving complex phylogeographic patterns in the Balkan Peninsula using closely related wall-lizard species as a model system. <i>Molecular Phylogenetics and Evolution</i> , 2018, 125, 100-115.	2.7	29

#	ARTICLE	IF	CITATIONS
19	CellPhy: accurate and fast probabilistic inference of single-cell phylogenies from scDNA-seq data. <i>Genome Biology</i> , 2022, 23, 37.	8.8	28
20	HIV-1 Full-Genome Phylogenetics of Generalized Epidemics in Sub-Saharan Africa: Impact of Missing Nucleotide Characters in Next-Generation Sequences. <i>AIDS Research and Human Retroviruses</i> , 2017, 33, 1083-1098.	1.1	18
21	A fast and memory-efficient implementation of the transfer bootstrap. <i>Bioinformatics</i> , 2020, 36, 2280-2281.	4.1	15
22	NetRAX: accurate and fast maximum likelihood phylogenetic network inference. <i>Bioinformatics</i> , 2022, 38, 3725-3733.	4.1	13
23	Modeling Structural Constraints on Protein Evolution via Side-Chain Conformational States. <i>Molecular Biology and Evolution</i> , 2019, 36, 2086-2103.	8.9	10
24	Exploring parallel MPI fault tolerance mechanisms for phylogenetic inference with RAxML-NG. <i>Bioinformatics</i> , 2021, 37, 4056-4063.	4.1	4