Alexey M Kozlov

List of Publications by Year
in descending order

24	6,788	394421	610901
papers	citations	19	24
		h-index	g-index

44	44	44	10067
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	CellPhy: accurate and fast probabilistic inference of single-cell phylogenies from scDNA-seq data. Genome Biology, 2022, 23, 37.	8.8	28
2	NetRAX: accurate and fast maximum likelihood phylogenetic network inference. Bioinformatics, 2022, 38, 3725-3733.	4.1	13
3	Phylogenetic Analysis of SARS-CoV-2 Data Is Difficult. Molecular Biology and Evolution, 2021, 38, 1777-1791.	8.9	119
4	Exploring parallel MPI fault tolerance mechanisms for phylogenetic inference with RAxML-NG. Bioinformatics, 2021, 37, 4056-4063.	4.1	4
5	ModelTest-NG: A New and Scalable Tool for the Selection of DNA and Protein Evolutionary Models. Molecular Biology and Evolution, 2020, 37, 291-294.	8.9	1,021
6	Longâ€read metabarcoding of the eukaryotic rDNA operon to phylogenetically and taxonomically resolve environmental diversity. Molecular Ecology Resources, 2020, 20, 429-443.	4.8	68
7	A fast and memory-efficient implementation of the transfer bootstrap. Bioinformatics, 2020, 36, 2280-2281.	4.1	15
8	GeneRax: A Tool for Species-Tree-Aware Maximum Likelihood-Based Gene ÂFamily Tree Inference under Gene Duplication, Transfer, and Loss. Molecular Biology and Evolution, 2020, 37, 2763-2774.	8.9	87
9	Eleven grand challenges in single-cell data science. Genome Biology, 2020, 21, 31.	8.8	742
10	EPA-ng: Massively Parallel Evolutionary Placement of Genetic Sequences. Systematic Biology, 2019, 68, 365-369.	5.6	400
11	Modeling Structural Constraints on Protein Evolution via Side-Chain Conformational States. Molecular Biology and Evolution, 2019, 36, 2086-2103.	8.9	10
12	RAxML-NG: a fast, scalable and user-friendly tool for maximum likelihood phylogenetic inference. Bioinformatics, 2019, 35, 4453-4455.	4.1	2,287
13	ParGenes: a tool for massively parallel model selection and phylogenetic tree inference on thousands of genes. Bioinformatics, 2019, 35, 1771-1773.	4.1	51
14	New data, same story: phylogenomics does not support Syrphoidea (Diptera: Syrphidae, Pipunculidae). Systematic Entomology, 2018, 43, 447-459.	3.9	53
15	A roadmap for global synthesis of the plant tree of life. American Journal of Botany, 2018, 105, 614-622.	1.7	38
16	Transcriptome sequence-based phylogeny of chalcidoid wasps (Hymenoptera: Chalcidoidea) reveals a history of rapid radiations, convergence, and evolutionary success. Molecular Phylogenetics and Evolution, 2018, 120, 286-296.	2.7	83
17	Resolving complex phylogeographic patterns in the Balkan Peninsula using closely related wall-lizard species as a model system. Molecular Phylogenetics and Evolution, 2018, 125, 100-115.	2.7	29
18	Phylogenomics and the evolution of hemipteroid insects. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 12775-12780.	7.1	275

#	Article	IF	Citations
19	HIV-1 Full-Genome Phylogenetics of Generalized Epidemics in Sub-Saharan Africa: Impact of Missing Nucleotide Characters in Next-Generation Sequences. AIDS Research and Human Retroviruses, 2017, 33, 1083-1098.	1.1	18
20	Evolutionary History of the Hymenoptera. Current Biology, 2017, 27, 1013-1018.	3.9	611
21	Parasites dominate hyperdiverse soil protist communities in Neotropical rainforests. Nature Ecology and Evolution, 2017, 1, 91.	7.8	262
22	Transcriptome and target DNA enrichment sequence data provide new insights into the phylogeny of vespid wasps (Hymenoptera: Aculeata: Vespidae). Molecular Phylogenetics and Evolution, 2017, 116, 213-226.	2.7	87
23	Phylogeny-aware identification and correction of taxonomically mislabeled sequences. Nucleic Acids Research, 2016, 44, 5022-5033.	14.5	97
24	ExaML version 3: a tool for phylogenomic analyses on supercomputers. Bioinformatics, 2015, 31, 2577-2579.	4.1	209