

Alexander Keller

List of Publications by Year in descending order

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Version: 2024-02-01

84
papers

4,299
citations

147801

31
h-index

123424

61
g-index

92
all docs

92
docs citations

92
times ranked

5426
citing authors

#	ARTICLE	IF	CITATIONS
1	5.8S-28S rRNA interaction and HMM-based ITS2 annotation. <i>Gene</i> , 2009, 430, 50-57.	2.2	394
2	Climate–land-use interactions shape tropical mountain biodiversity and ecosystem functions. <i>Nature</i> , 2019, 568, 88-92.	27.8	313
3	ITS2 Database V: Twice as Much: Table 1.. <i>Molecular Biology and Evolution</i> , 2015, 32, 3030-3032.	8.9	231
4	The ITS2 Database III—sequences and structures for phylogeny. <i>Nucleic Acids Research</i> , 2010, 38, D275-D279.	14.5	223
5	Evaluating multiplexed next-generation sequencing as a method in palynology for mixed pollen samples. <i>Plant Biology</i> , 2015, 17, 558-566.	3.8	182
6	Increased efficiency in identifying mixed pollen samples by meta-barcoding with a dual-indexing approach. <i>BMC Ecology</i> , 2015, 15, 20.	3.0	167
7	Pollen DNA barcoding: current applications and future prospects. <i>Genome</i> , 2016, 59, 629-640.	2.0	166
8	Composition of epiphytic bacterial communities differs on petals and leaves. <i>Plant Biology</i> , 2011, 13, 918-924.	3.8	160
9	Including RNA secondary structures improves accuracy and robustness in reconstruction of phylogenetic trees. <i>Biology Direct</i> , 2010, 5, 4.	4.6	154
10	bcgTree: automatized phylogenetic tree building from bacterial core genomes. <i>Genome</i> , 2016, 59, 783-791.	2.0	151
11	Open Science principles for accelerating trait-based science across the Tree of Life. <i>Nature Ecology and Evolution</i> , 2020, 4, 294-303.	7.8	144
12	Honey bee foraging ecology: Season but not landscape diversity shapes the amount and diversity of collected pollen. <i>PLoS ONE</i> , 2017, 12, e0183716.	2.5	101
13	Microhabitat heterogeneity across leaves and flower organs promotes bacterial diversity. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv097.	2.7	97
14	Internal Transcribed Spacer 2 (nu ITS2 rRNA) Sequence-Structure Phylogenetics: Towards an Automated Reconstruction of the Green Algal Tree of Life. <i>PLoS ONE</i> , 2011, 6, e16931.	2.5	80
15	The importance of environmental heterogeneity for species diversity and assemblage structure in Bornean stream frogs. <i>Journal of Animal Ecology</i> , 2009, 78, 305-314.	2.8	78
16	ITS2 sequence-structure phylogeny in the Scenedesmaceae with special reference to <i>Coelastrum</i> (Chlorophyta, Chlorophyceae), including the new genera <i>Comasiella</i> and <i>Pectinodesmus</i> . <i>Phycologia</i> , 2010, 49, 325-335.	1.4	77
17	ITS2 secondary structure improves phylogeny estimation in a radiation of blue butterflies of the subgenus <i>Agrodiaetus</i> (Lepidoptera: Lycaenidae: <i>Polyommatus</i>). <i>BMC Evolutionary Biology</i> , 2009, 9, 300.	3.2	69
18	Density-dependent negative responses by bumblebees to bacteria isolated from flowers. <i>Apidologie</i> , 2014, 45, 467-477.	2.0	62

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19	Grapevine (<i>Vitis vinifera</i>) Crown Galls Host Distinct Microbiota. <i>Applied and Environmental Microbiology</i> , 2016, 82, 5542-5552.	3.1	62
20	Novel form of X-linked nonsyndromic hearing loss with cochlear malformation caused by a mutation in the type IV collagen gene COL4A6. <i>European Journal of Human Genetics</i> , 2014, 22, 208-215.	2.8	60
21	Drivers, Diversity, and Functions of the Solitary-Bee Microbiota. <i>Trends in Microbiology</i> , 2019, 27, 1034-1044.	7.7	57
22	ITS2 data corroborate a monophyletic chlorophycean DO-group (Sphaeropleales). <i>BMC Evolutionary Biology</i> , 2008, 8, 218.	3.2	56
23	(More than) Hitchhikers through the network: the shared microbiome of bees and flowers. <i>Current Opinion in Insect Science</i> , 2021, 44, 8-15.	4.4	55
24	Hawaiian ant-flower networks: nectar-thieving ants prefer undefended native over introduced plants with floral defenses. <i>Ecological Monographs</i> , 2011, 81, 295-311.	5.4	52
25	Critical links between biodiversity and health in wild bee conservation. <i>Trends in Ecology and Evolution</i> , 2022, 37, 309-321.	8.7	48
26	Functional and phylogenetic diversity of plant communities differently affect the structure of flower-visitor interactions and reveal convergences in floral traits. <i>Evolutionary Ecology</i> , 2015, 29, 437-450.	1.2	47
27	Microbial Community Structure in a Malaysian Tropical Peat Swamp Forest: The Influence of Tree Species and Depth. <i>Frontiers in Microbiology</i> , 2018, 9, 2859.	3.5	43
28	Generalist social bees maximize diversity intake in plant species-rich and resource-abundant environments. <i>Ecosphere</i> , 2017, 8, e01758.	2.2	42
29	Bacterial community structure and succession in nests of two megachilid bee genera. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	2.7	40
30	Only distance matters – non-choosy females in a poison frog population. <i>Frontiers in Zoology</i> , 2013, 10, 29.	2.0	39
31	Diverse Microbiota Identified in Whole Intact Nest Chambers of the Red Mason Bee <i>Osmia bicornis</i> (Linnaeus 1758). <i>PLoS ONE</i> , 2013, 8, e78296.	2.5	39
32	Honey bee waggle dance communication increases diversity of pollen diets in intensively managed agricultural landscapes. <i>Molecular Ecology</i> , 2019, 28, 3602-3611.	3.9	38
33	Osmotic Adaptation and Compatible Solute Biosynthesis of Phototrophic Bacteria as Revealed from Genome Analyses. <i>Microorganisms</i> , 2021, 9, 46.	3.6	37
34	Linking pollen foraging of megachilid bees to their nest bacterial microbiota. <i>Ecology and Evolution</i> , 2019, 9, 10788-10800.	1.9	36
35	Species richness is more important for ecosystem functioning than species turnover along an elevational gradient. <i>Nature Ecology and Evolution</i> , 2021, 5, 1582-1593.	7.8	35
36	Common ancestry or environmental trait filters: cross-continental comparisons of trait-habitat relationships in tropical anuran amphibian assemblages. <i>Global Ecology and Biogeography</i> , 2012, 21, 704-715.	5.8	30

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37	BCdatabaser: on-the-fly reference database creation for (meta-)barcoding. <i>Bioinformatics</i> , 2020, 36, 2630-2631.	4.1	30
38	Pollen diets and niche overlap of honey bees and native bees in protected areas. <i>Basic and Applied Ecology</i> , 2021, 50, 169-180.	2.7	30
39	The genus <i>Micromonospora</i> as a model microorganism for bioactive natural product discovery. <i>RSC Advances</i> , 2020, 10, 20939-20959.	3.6	29
40	Many small rather than few large sources identified in long-term bee pollen diets in agroecosystems. <i>Agriculture, Ecosystems and Environment</i> , 2021, 310, 107296.	5.3	29
41	Floral Species Richness Correlates with Changes in the Nutritional Quality of Larval Diets in a Stingless Bee. <i>Insects</i> , 2020, 11, 125.	2.2	28
42	Standard methods for pollen research. <i>Journal of Apicultural Research</i> , 2021, 60, 1-109.	1.5	25
43	CRISPR/Cas 9-Mediated Mutations as a New Tool for Studying Taste in Honeybees. <i>Chemical Senses</i> , 2020, 45, 655-666.	2.0	24
44	Wild bees and their nests host <i>Paenibacillus</i> bacteria with functional potential of avail. <i>Microbiome</i> , 2018, 6, 229.	11.1	23
45	Susceptibility of Red Mason Bee Larvae to Bacterial Threats Due to Microbiome Exchange with Imported Pollen Provisions. <i>Insects</i> , 2020, 11, 373.	2.2	23
46	Changes amid constancy: Flower and leaf microbiomes along land use gradients and between bioregions. <i>Basic and Applied Ecology</i> , 2021, 50, 1-15.	2.7	22
47	Reptiles as Reservoirs of Bacterial Infections: Real Threat or Methodological Bias?. <i>Microbial Ecology</i> , 2015, 70, 579-584.	2.8	21
48	Introduced bees (<i>Osmia cornifrons</i>) collect pollen from both coevolved and novel host-plant species within their family-level phylogenetic preferences. <i>Royal Society Open Science</i> , 2020, 7, 200225.	2.4	20
49	Computational integration of genomic traits into 16S rDNA microbiota sequencing studies. <i>Gene</i> , 2014, 549, 186-191.	2.2	19
50	Employing DNA metabarcoding to determine the geographical origin of honey. <i>Heliyon</i> , 2020, 6, e05596.	3.2	19
51	How wild bees find a way in European cities: Pollen metabarcoding unravels multiple feeding strategies and their effects on distribution patterns in four wild bee species. <i>Journal of Applied Ecology</i> , 2022, 59, 457-470.	4.0	19
52	WISP 1 is an important survival factor in human mesenchymal stromal cells. <i>Gene</i> , 2014, 551, 243-254.	2.2	18
53	Contact of myeloma cells induces a characteristic transcriptome signature in skeletal precursor cells – Implications for myeloma bone disease. <i>Bone</i> , 2016, 93, 155-166.	2.9	18
54	Silent listeners: can preferences of eavesdropping midges predict their hosts' parasitism risk?. <i>Behavioral Ecology</i> , 2016, 27, 995-1003.	2.2	18

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55	Effects of three flower field types on bumblebees and their pollen diets. <i>Basic and Applied Ecology</i> , 2021, 52, 95-108.	2.7	16
56	Cryptic species and hidden ecological interactions of halictine bees along an elevational gradient. <i>Ecology and Evolution</i> , 2021, 11, 7700-7712.	1.9	15
57	Diets maintained in a changing world: Does land-use intensification alter wild bee communities by selecting for flexible generalists?. <i>Ecology and Evolution</i> , 2022, 12, .	1.9	15
58	Do amino and fatty acid profiles of pollen provisions correlate with bacterial microbiomes in the mason bee <i>Osmia bicornis</i> ?. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, 20210171.	4.0	14
59	Confirmation of warfarin resistance of naturally occurring VKORC1 variants by coexpression with coagulation factor IX and in silico protein modelling. <i>BMC Genetics</i> , 2014, 15, 17.	2.7	13
60	The characterization of the circadian clock in the olive fly <i>Bactrocera oleae</i> (Diptera: Tephritidae) reveals a <i>Drosophila</i> -like organization. <i>Scientific Reports</i> , 2018, 8, 816.	3.3	13
61	Functional resin use in solitary bees. <i>Ecological Entomology</i> , 2022, 47, 115-136.	2.2	13
62	Bacterial Diversity and Community Structure in Two Bornean <i>Nepenthes</i> Species with Differences in Nitrogen Acquisition Strategies. <i>Microbial Ecology</i> , 2016, 71, 938-953.	2.8	11
63	An integrative environmental pollen diversity assessment and its importance for the Sustainable Development Goals. <i>Plants People Planet</i> , 2022, 4, 110-121.	3.3	11
64	Draft genome of the <i>Arabidopsis thaliana</i> phyllosphere bacterium, <i>Williamsia</i> sp. ARP1. <i>Standards in Genomic Sciences</i> , 2016, 11, 8.	1.5	10
65	Strong phylogenetic constraint on transition metal incorporation in the mandibles of the hyper-diverse Hymenoptera (Insecta). <i>Organisms Diversity and Evolution</i> , 2020, 20, 511-526.	1.6	10
66	Putative roles of bacteria in the carbon and nitrogen cycles in a tropical peat swamp forest. <i>Basic and Applied Ecology</i> , 2021, 52, 109-123.	2.7	8
67	Ribosomal RNA phylogenetics: the third dimension. <i>Biologia (Poland)</i> , 2010, 65, 388-391.	1.5	6
68	Laboratory rearing of solitary bees and wasps. <i>Insect Science</i> , 2016, 23, 918-923.	3.0	6
69	Forest landscapes increase diversity of honeybee diets in the tropics. <i>Forest Ecology and Management</i> , 2022, 504, 119869.	3.2	6
70	Release from prey preservation behavior via prey switch allowed diversification of cuticular hydrocarbon profiles in digger wasps. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 2562-2571.	2.3	5
71	Functional exploration of natural networks and ecological communities. <i>Methods in Ecology and Evolution</i> , 2018, 9, 2028-2033.	5.2	5
72	Preservation methods of honey bee-collected pollen are not a source of bias in ITS2 metabarcoding. <i>Environmental Monitoring and Assessment</i> , 2021, 193, 785.	2.7	5

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73	Phylogenetic relatedness of food plants reveals highest insect herbivore specialization at intermediate temperatures along a broad climatic gradient. <i>Global Change Biology</i> , 2022, 28, 4027-4040.	9.5	5
74	Systematic Affiliation and Genome Analysis of <i>Subtercola vilae</i> DB165T with Particular Emphasis on Cold Adaptation of an Isolate from a High-Altitude Cold Volcano Lake. <i>Microorganisms</i> , 2019, 7, 107.	3.6	4
75	Draft Genome Sequence of <i>Dyella</i> sp. Strain C9, Isolated from a Malaysian Tropical Peat Swamp Forest. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	3
76	Physical contact between mesenchymal stem cells and endothelial precursors induces distinct signatures with relevance to the very early phase of regeneration. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 9122-9140.	2.6	3
77	Venus flytrap microbiotas withstand harsh conditions during prey digestion. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	2.7	3
78	Monophyletic clades of <i>Macaranga</i> -pollinating thrips show high specificity to taxonomic sections of host plants. <i>Biological Journal of the Linnean Society</i> , 2015, 116, 558-570.	1.6	2
79	Inferring Core Genome Phylogenies for Bacteria. <i>Methods in Molecular Biology</i> , 2021, 2242, 59-68.	0.9	2
80	biojs-io-biom, a BioJS component for handling data in Biological Observation Matrix (BIOM) format. <i>F1000Research</i> , 2016, 5, 2348.	1.6	2
81	Draft Genome Sequence of <i>Klebsiella</i> sp. Strain C31 Isolated from a Malaysian Tropical Peat Swamp Forest. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
82	Draft Genome Sequence of <i>Dyella</i> sp. Strain C11, Isolated from a Malaysian Tropical Peat Swamp Forest. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
83	Wild bee larval food composition in five European cities. <i>Ecology</i> , 2022, , e3740.	3.2	1
84	Draft Genome Sequence of <i>Paraburkholderia</i> sp. Strain C35, Isolated from a Malaysian Tropical Peat Swamp Forest. <i>Genome Announcements</i> , 2018, 6, .	0.8	0