

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
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123424

61
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92
all docs

92
docs citations

92
times ranked

5426
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | 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 |
| 2 | 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 |
| 3 | Forest landscapes increase diversity of honeybee diets in the tropics. <i>Forest Ecology and Management</i> , 2022, 504, 119869. | 3.2 | 6 |
| 4 | Functional resin use in solitary bees. <i>Ecological Entomology</i> , 2022, 47, 115-136. | 2.2 | 13 |
| 5 | Critical links between biodiversity and health in wild bee conservation. <i>Trends in Ecology and Evolution</i> , 2022, 37, 309-321. | 8.7 | 48 |
| 6 | 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 |
| 7 | Wild bee larval food composition in five European cities. <i>Ecology</i> , 2022, , e3740. | 3.2 | 1 |
| 8 | 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 |
| 9 | 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 |
| 10 | 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 |
| 11 | (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 |
| 12 | 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 |
| 13 | 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 |
| 14 | 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 |
| 15 | 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 |
| 16 | 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 |
| 17 | Standard methods for pollen research. <i>Journal of Apicultural Research</i> , 2021, 60, 1-109. | 1.5 | 25 |
| 18 | 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 |

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|----|--|------|-----------|
| 19 | Inferring Core Genome Phylogenies for Bacteria. <i>Methods in Molecular Biology</i> , 2021, 2242, 59-68. | 0.9 | 2 |
| 20 | Osmotic Adaptation and Compatible Solute Biosynthesis of Phototrophic Bacteria as Revealed from Genome Analyses. <i>Microorganisms</i> , 2021, 9, 46. | 3.6 | 37 |
| 21 | 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 |
| 22 | BCdatabaser: on-the-fly reference database creation for (meta-)barcoding. <i>Bioinformatics</i> , 2020, 36, 2630-2631. | 4.1 | 30 |
| 23 | 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 |
| 24 | 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 |
| 25 | Employing DNA metabarcoding to determine the geographical origin of honey. <i>Heliyon</i> , 2020, 6, e05596. | 3.2 | 19 |
| 26 | 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 |
| 27 | 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 |
| 28 | 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 |
| 29 | 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 |
| 30 | 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 |
| 31 | Linking pollen foraging of megachilid bees to their nest bacterial microbiota. <i>Ecology and Evolution</i> , 2019, 9, 10788-10800. | 1.9 | 36 |
| 32 | Drivers, Diversity, and Functions of the Solitary-Bee Microbiota. <i>Trends in Microbiology</i> , 2019, 27, 1034-1044. | 7.7 | 57 |
| 33 | Venus flytrap microbiotas withstand harsh conditions during prey digestion. <i>FEMS Microbiology Ecology</i> , 2019, 95, . | 2.7 | 3 |
| 34 | 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 |
| 35 | 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 |
| 36 | Climate–land-use interactions shape tropical mountain biodiversity and ecosystem functions. <i>Nature</i> , 2019, 568, 88-92. | 27.8 | 313 |

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|----|--|------|-----------|
| 37 | Bacterial community structure and succession in nests of two megachilid bee genera. <i>FEMS Microbiology Ecology</i> , 2019, 95, . | 2.7 | 40 |
| 38 | 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 |
| 39 | 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 |
| 40 | 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 |
| 41 | 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 |
| 42 | 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 |
| 43 | Wild bees and their nests host <i>Paenibacillus</i> bacteria with functional potential of avail. <i>Microbiome</i> , 2018, 6, 229. | 11.1 | 23 |
| 44 | 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 |
| 45 | Functional exploration of natural networks and ecological communities. <i>Methods in Ecology and Evolution</i> , 2018, 9, 2028-2033. | 5.2 | 5 |
| 46 | 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 |
| 47 | Generalist social bees maximize diversity intake in plant species-rich and resource-abundant environments. <i>Ecosphere</i> , 2017, 8, e01758. | 2.2 | 42 |
| 48 | 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 |
| 49 | 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 |
| 50 | Laboratory rearing of solitary bees and wasps. <i>Insect Science</i> , 2016, 23, 918-923. | 3.0 | 6 |
| 51 | Pollen DNA barcoding: current applications and future prospects. <i>Genome</i> , 2016, 59, 629-640. | 2.0 | 166 |
| 52 | bcgTree: automatized phylogenetic tree building from bacterial core genomes. <i>Genome</i> , 2016, 59, 783-791. | 2.0 | 151 |
| 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 | Grapevine (<i>Vitis vinifera</i>) Crown Galls Host Distinct Microbiota. <i>Applied and Environmental Microbiology</i> , 2016, 82, 5542-5552. | 3.1 | 62 |

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|----|---|-----|-----------|
| 55 | 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 |
| 56 | 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 |
| 57 | Silent listeners: can preferences of eavesdropping midges predict their hosts' parasitism risk?. <i>Behavioral Ecology</i> , 2016, 27, 995-1003. | 2.2 | 18 |
| 58 | biojs-io-biom, a BioJS component for handling data in Biological Observation Matrix (BIOM) format. <i>F1000Research</i> , 2016, 5, 2348. | 1.6 | 2 |
| 59 | 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 |
| 60 | 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 |
| 61 | 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 |
| 62 | ITS2 Database V: Twice as Much: Table 1.. <i>Molecular Biology and Evolution</i> , 2015, 32, 3030-3032. | 8.9 | 231 |
| 63 | Reptiles as Reservoirs of Bacterial Infections: Real Threat or Methodological Bias?. <i>Microbial Ecology</i> , 2015, 70, 579-584. | 2.8 | 21 |
| 64 | Microhabitat heterogeneity across leaves and flower organs promotes bacterial diversity. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv097. | 2.7 | 97 |
| 65 | 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 |
| 66 | Novel form of X-linked nonsyndromic hearing loss with cochlear malformation caused by a mutation in the type IV collagen gene <i>COL4A6</i> . <i>European Journal of Human Genetics</i> , 2014, 22, 208-215. | 2.8 | 60 |
| 67 | Density-dependent negative responses by bumblebees to bacteria isolated from flowers. <i>Apidologie</i> , 2014, 45, 467-477. | 2.0 | 62 |
| 68 | Confirmation of warfarin resistance of naturally occurring <i>VKORC1</i> variants by coexpression with coagulation factor IX and in silico protein modelling. <i>BMC Genetics</i> , 2014, 15, 17. | 2.7 | 13 |
| 69 | Computational integration of genomic traits into 16S rDNA microbiota sequencing studies. <i>Gene</i> , 2014, 549, 186-191. | 2.2 | 19 |
| 70 | WISP 1 is an important survival factor in human mesenchymal stromal cells. <i>Gene</i> , 2014, 551, 243-254. | 2.2 | 18 |
| 71 | Only distance matters – non-choosy females in a poison frog population. <i>Frontiers in Zoology</i> , 2013, 10, 29. | 2.0 | 39 |
| 72 | 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 |

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|----|--|------|-----------|
| 73 | 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 |
| 74 | 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 |
| 75 | 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 |
| 76 | Composition of epiphytic bacterial communities differs on petals and leaves. <i>Plant Biology</i> , 2011, 13, 918-924. | 3.8 | 160 |
| 77 | Ribosomal RNA phylogenetics: the third dimension. <i>Biologia (Poland)</i> , 2010, 65, 388-391. | 1.5 | 6 |
| 78 | Including RNA secondary structures improves accuracy and robustness in reconstruction of phylogenetic trees. <i>Biology Direct</i> , 2010, 5, 4. | 4.6 | 154 |
| 79 | The ITS2 Database III—sequences and structures for phylogeny. <i>Nucleic Acids Research</i> , 2010, 38, D275-D279. | 14.5 | 223 |
| 80 | 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 |
| 81 | ITS2 secondary structure improves phylogeny estimation in a radiation of blue butterflies of the subgenus <i>Agrodiaetus</i> (Lepidoptera: Lycaenidae: Polyommatus). <i>BMC Evolutionary Biology</i> , 2009, 9, 300. | 3.2 | 69 |
| 82 | 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 |
| 83 | 5.8S-28S rRNA interaction and HMM-based ITS2 annotation. <i>Gene</i> , 2009, 430, 50-57. | 2.2 | 394 |
| 84 | ITS2 data corroborate a monophyletic chlorophycean DO-group (Sphaeropleales). <i>BMC Evolutionary Biology</i> , 2008, 8, 218. | 3.2 | 56 |