

Konrad Lohse

List of Publications by Year in descending order

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Version: 2024-02-01

51
papers

1,511
citations

430874

18
h-index

395702

33
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66
all docs

66
docs citations

66
times ranked

2004
citing authors

#	ARTICLE	IF	CITATIONS
1	The genome sequence of the lesser marbled fritillary, <i>Brenthis ino</i> , and evidence for a segregating neo-Z chromosome. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	8
2	Efficient ancestry and mutation simulation with msprime 1.0. <i>Genetics</i> , 2022, 220, .	2.9	133
3	The Pleistocene species pump past its prime: Evidence from European butterfly sister species. <i>Molecular Ecology</i> , 2021, 30, 3575-3589.	3.9	35
4	Sweeps in time: leveraging the joint distribution of branch lengths. <i>Genetics</i> , 2021, 219, .	2.9	14
5	Discordant Pleistocene population size histories in a guild of hymenopteran parasitoids. <i>Molecular Ecology</i> , 2021, 30, 4538-4550.	3.9	5
6	The genome sequence of the large tortoiseshell, <i>Nymphalis polychloros</i> (Linnaeus, 1758). <i>Wellcome Open Research</i> , 2021, 6, 238.	1.8	3
7	The genome sequence of the heath fritillary, <i>Melitaea athalia</i> (Rottemburg, 1775). <i>Wellcome Open Research</i> , 2021, 6, 304.	1.8	1
8	The impact of global selection on local adaptation and reproductive isolation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190531.	4.0	11
9	Low-coverage genomic data resolve the population divergence and gene flow history of an Australian rain forest fig wasp. <i>Molecular Ecology</i> , 2020, 29, 3649-3666.	3.9	4
10	Coalescent Simulation with msprime. <i>Methods in Molecular Biology</i> , 2020, 2090, 191-230.	0.9	23
11	The determinants of genetic diversity in butterflies. <i>Nature Communications</i> , 2019, 10, 3466.	12.8	80
12	Maintaining their genetic distance: Little evidence for introgression between widely hybridizing species of <i>Geum</i> with contrasting mating systems. <i>Molecular Ecology</i> , 2018, 27, 1214-1228.	3.9	19
13	Divergent evolution in the genomes of closely-related lacertids, <i>Lacerta viridis</i> and <i>L. bilineata</i> and implications for speciation. <i>GigaScience</i> , 2018, 8, .	6.4	10
14	ABLE: blockwise site frequency spectra for inferring complex population histories and recombination. <i>Genome Biology</i> , 2018, 19, 145.	8.8	16
15	Whole-genome data reveal the complex history of a diverse ecological community. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E6507-E6515.	7.1	45
16	Come on feel the noise – from metaphors to null models. <i>Journal of Evolutionary Biology</i> , 2017, 30, 1506-1508.	1.7	17
17	Para-allopatry in hybridizing fire-bellied toads (<i>Bombina bombina</i> and <i>B. variegata</i>): Inference from transcriptome-wide coalescence analyses. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 1803-1818.	2.3	25
18	Efficient Strategies for Calculating Blockwise Likelihoods Under the Coalescent. <i>Genetics</i> , 2016, 202, 775-786.	2.9	62

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19	What haplodiploids can teach us about hybridization and speciation. <i>Molecular Ecology</i> , 2015, 24, 5075-5077.	3.9	20
20	Genome-wide tests for introgression between cactophilic <i>Drosophila</i> implicate a role of inversions during speciation. <i>Evolution; International Journal of Organic Evolution</i> , 2015, 69, 1178-1190.	2.3	70
21	Inferring Bottlenecks from Genome-Wide Samples of Short Sequence Blocks. <i>Genetics</i> , 2015, 201, 1157-1169.	2.9	40
22	Likelihood-based inference of population history from low-coverage <i>de novo</i> genome assemblies. <i>Molecular Ecology</i> , 2014, 23, 198-211.	3.9	28
23	Testing models of speciation from genome sequences: divergence and asymmetric admixture in <i>S. olearia</i> and <i>S. aegyptia</i> species during the Pliocene climatic fluctuations. <i>Molecular Ecology</i> , 2014, 23, 5566-5574.	3.9	32
24	RECOMMENDATIONS FOR USING MSBAYES TO INCORPORATE UNCERTAINTY IN SELECTING AN ABC MODEL PRIOR: A RESPONSE TO OAKS ET AL.. <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 284-294.	2.3	29
25	Neandertal Admixture in Eurasia Confirmed by Maximum-Likelihood Analysis of Three Genomes. <i>Genetics</i> , 2014, 196, 1241-1251.	2.9	78
26	A new genus of oak gallwasp, <i>Cyclocynips melika</i> , Tang & Sinclair (Hymenoptera: Cynipidae: Cynipini), with descriptions of two new species from Taiwan. <i>Zootaxa</i> , 2013, 3630, 534-548.	0.5	13
27	A likelihood-based comparison of population histories in a parasitoid guild. <i>Molecular Ecology</i> , 2012, 21, 4605-4617.	3.9	19
28	Reconstructing Community Assembly in Time and Space Reveals Enemy Escape in a Western Palearctic Insect Community. <i>Current Biology</i> , 2012, 22, 532-537.	3.9	95
29	Model-based comparisons of phylogeographic scenarios resolve the intraspecific divergence of cactophilic <i>Drosophila mojavensis</i> . <i>Molecular Ecology</i> , 2012, 21, 3293-3307.	3.9	36
30	Developing EPIC markers for chalcidoid Hymenoptera from EST and genomic data. <i>Molecular Ecology Resources</i> , 2011, 11, 521-529.	4.8	17
31	Inferring the colonization of a mountain range-refugia vs. nunatak survival in high alpine ground beetles. <i>Molecular Ecology</i> , 2011, 20, 394-408.	3.9	44
32	A General Method for Calculating Likelihoods Under the Coalescent Process. <i>Genetics</i> , 2011, 189, 977-987.	2.9	108
33	QUANTIFYING THE PLEISTOCENE HISTORY OF THE OAK GALL PARASITOID <i>CECIDOSTIBA FUNGOSA</i> USING TWENTY INTRON LOCI. <i>Evolution; International Journal of Organic Evolution</i> , 2010, 64, 2664-2681.	2.3	26
34	Revealing secret liaisons: DNA barcoding changes our understanding of food webs. <i>Ecological Entomology</i> , 2010, 35, 623-638.	2.2	118
35	Can mtDNA Barcodes Be Used to Delimit Species? A Response to Pons et al. (2006). <i>Systematic Biology</i> , 2009, 58, 439-442.	5.6	161
36	Measuring the degree of starshape in genealogies – summary statistics and demographic inference. <i>Genetical Research</i> , 2009, 91, 281-292.	0.9	6

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37	EXPERIMENTAL EVOLUTION OF RESISTANCE IN PARAMECIUM CAUDATUM AGAINST THE BACTERIAL PARASITE HOLOSPORA UNDULATA. <i>Evolution; International Journal of Organic Evolution</i> , 2006, 60, 1177.	2.3	4
38	The genome sequence of the small tortoiseshell butterfly, <i>Aglaia urticae</i> (Linnaeus, 1758). <i>Wellcome Open Research</i> , 0, 6, 233.	1.8	4
39	The genome sequence of the Glanville fritillary, <i>Melitaea cinxia</i> (Linnaeus, 1758). <i>Wellcome Open Research</i> , 0, 6, 266.	1.8	1
40	The genome sequence of the small white, <i>Pieris rapae</i> (Linnaeus, 1758). <i>Wellcome Open Research</i> , 0, 6, 273.	1.8	2
41	The genome sequence of the speckled wood butterfly, <i>Pararge aegeria</i> (Linnaeus, 1758). <i>Wellcome Open Research</i> , 0, 6, 287.	1.8	3
42	The genome sequence of the European peacock butterfly, <i>Aglaia io</i> (Linnaeus, 1758). <i>Wellcome Open Research</i> , 0, 6, 258.	1.8	4
43	The genome sequence of the large white, <i>Pieris brassicae</i> (Linnaeus, 1758). <i>Wellcome Open Research</i> , 0, 6, 262.	1.8	2
44	The genome sequence of the small copper, <i>Lycaena phlaeas</i> (Linnaeus, 1760). <i>Wellcome Open Research</i> , 0, 6, 294.	1.8	1
45	The genome sequence of the meadow brown, <i>Maniola jurtina</i> (Linnaeus, 1758). <i>Wellcome Open Research</i> , 0, 6, 296.	1.8	1
46	The genome sequence of the painted lady, <i>Vanessa cardui</i> Linnaeus 1758. <i>Wellcome Open Research</i> , 0, 6, 324.	1.8	11
47	The genome sequence of the grizzled skipper, <i>Pyrgus malvae</i> (Linnaeus, 1758). <i>Wellcome Open Research</i> , 0, 7, 114.	1.8	0
48	The genome sequence of the small pearl-bordered fritillary butterfly, <i>Boloria selene</i> (Schifferrmüller.) <i>Tj ETQqO O O rgBT /Overlock 10 Tf 5</i>	1.8	2
49	The genome sequence of the black-veined white butterfly, <i>Aporia crataegi</i> (Linnaeus, 1758). <i>Wellcome Open Research</i> , 0, 7, 81.	1.8	1
50	The genome sequence of the marbled white butterfly, <i>Melanargia galathea</i> (Linnaeus, 1758). <i>Wellcome Open Research</i> , 0, 7, 123.	1.8	1
51	The genome sequence of the red admiral, <i>Vanessa atalanta</i> (Linnaeus, 1758). <i>Wellcome Open Research</i> , 0, 6, 356.	1.8	2