

Jochen B W Wolf

List of Publications by Year in descending order

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Version: 2024-02-01

91
papers

9,190
citations

87401

40
h-index

54771

88
g-index

112
all docs

112
docs citations

112
times ranked

12939
citing authors

#	ARTICLE	IF	CITATIONS
1	Accumulation and ineffective silencing of transposable elements on an avian W Chromosome. <i>Genome Research</i> , 2022, 32, 671-681.	2.4	13
2	The genomic architecture of the passerine MHC region: High repeat content and contrasting evolutionary histories of single copy and tandemly duplicated MHC genes. <i>Molecular Ecology Resources</i> , 2022, 22, 2379-2395.	2.2	14
3	Reactivation of transposable elements following hybridization in fission yeast. <i>Genome Research</i> , 2022, 32, 324-336.	2.4	13
4	A genome-wide investigation of adaptive signatures in protein-coding genes related to tool behaviour in New Caledonian and Hawaiian crows. <i>Molecular Ecology</i> , 2021, 30, 973-986.	2.0	2
5	Experimental evolution of adaptive divergence under varying degrees of gene flow. <i>Nature Ecology and Evolution</i> , 2021, 5, 338-349.	3.4	15
6	Hi-C scaffolded short- and long-read genome assemblies of the California sea lion are broadly consistent for syntenic inference across 45 million years of evolution. <i>Molecular Ecology Resources</i> , 2021, 21, 2455-2470.	2.2	7
7	A sex chromosome inversion is associated with copy number variation of mitochondrial DNA in zebra finch sperm. <i>Royal Society Open Science</i> , 2021, 8, 211025.	1.1	3
8	Runs of homozygosity in killer whale genomes provide a global record of demographic histories. <i>Molecular Ecology</i> , 2021, 30, 6162-6177.	2.0	39
9	Phylogenomic Discordance in the Eared Seals is best explained by Incomplete Lineage Sorting following Explosive Radiation in the Southern Hemisphere. <i>Systematic Biology</i> , 2021, 70, 786-802.	2.7	25
10	Assortative mating and epistatic mating-trait architecture induce complex movement of the crow hybrid zone. <i>Evolution; International Journal of Organic Evolution</i> , 2021, 75, 3154-3174.	1.1	10
11	Community genomics: a community-wide perspective on within-species genetic diversity. <i>American Journal of Botany</i> , 2021, 108, 2108-2111.	0.8	5
12	Polymorphism Data Assist Estimation of the Nonsynonymous over Synonymous Fixation Rate Ratio $\tilde{\omega}$ for Closely Related Species. <i>Molecular Biology and Evolution</i> , 2020, 37, 260-279.	3.5	27
13	Purifying Selection in Corvids Is Less Efficient on Islands. <i>Molecular Biology and Evolution</i> , 2020, 37, 469-474.	3.5	24
14	A test for meiotic drive in hybrids between Australian and Timor zebra finches. <i>Ecology and Evolution</i> , 2020, 10, 13464-13475.	0.8	3
15	From molecules to populations: appreciating and estimating recombination rate variation. <i>Nature Reviews Genetics</i> , 2020, 21, 476-492.	7.7	81
16	Determinants of genetic variation across eco-evolutionary scales in pinnipeds. <i>Nature Ecology and Evolution</i> , 2020, 4, 1095-1104.	3.4	47
17	Discovery and population genomics of structural variation in a songbird genus. <i>Nature Communications</i> , 2020, 11, 3403.	5.8	83
18	Near-chromosome level genome assembly of the fruit pest <i>Drosophila suzukii</i> using long-read sequencing. <i>Scientific Reports</i> , 2020, 10, 11227.	1.6	42

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19	Extra-pair paternity as a strategy to reduce the costs of heterospecific reproduction? Insights from the crow hybrid zone. <i>Journal of Evolutionary Biology</i> , 2020, 33, 727-733.	0.8	4
20	Dominance relationships and coalitionary aggression against conspecifics in female carrion crows. <i>Scientific Reports</i> , 2019, 9, 15922.	1.6	11
21	Intraspecific Diversity of Fission Yeast Mitochondrial Genomes. <i>Genome Biology and Evolution</i> , 2019, 11, 2312-2329.	1.1	24
22	Killer whale genomes reveal a complex history of recurrent admixture and vicariance. <i>Molecular Ecology</i> , 2019, 28, 3427-3444.	2.0	46
23	Ancestral Admixture Is the Main Determinant of Global Biodiversity in Fission Yeast. <i>Molecular Biology and Evolution</i> , 2019, 36, 1975-1989.	3.5	50
24	Epistatic mutations under divergent selection govern phenotypic variation in the crow hybrid zone. <i>Nature Ecology and Evolution</i> , 2019, 3, 570-576.	3.4	65
25	Fur seal microbiota are shaped by the social and physical environment, show mother-offspring similarities and are associated with host genetic quality. <i>Molecular Ecology</i> , 2019, 28, 2406-2422.	2.0	27
26	<i>In situ</i> quantification of individual mRNA transcripts in melanocytes discloses gene regulation of relevance to speciation. <i>Journal of Experimental Biology</i> , 2019, 222, .	0.8	7
27	Host-derived population genomics data provides insights into bacterial and diatom composition of the killer whale skin. <i>Molecular Ecology</i> , 2019, 28, 484-502.	2.0	42
28	Repeated evolution of self-compatibility for reproductive assurance. <i>Nature Communications</i> , 2018, 9, 1639.	5.8	19
29	Demographic histories and genetic diversity across pinnipeds are shaped by human exploitation, ecology and life-history. <i>Nature Communications</i> , 2018, 9, 4836.	5.8	49
30	RAD Sequencing and a Hybrid Antarctic Fur Seal Genome Assembly Reveal Rapidly Decaying Linkage Disequilibrium, Global Population Structure and Evidence for Inbreeding. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2709-2722.	0.8	30
31	Colonisation of subterranean ecosystems leads to larger genome in waterlouse (Aselloidea). <i>Peer Community in Evolutionary Biology</i> , 2018, , 100029.	0.0	0
32	Covariation in levels of nucleotide diversity in homologous regions of the avian genome long after completion of lineage sorting. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20162756.	1.2	50
33	Genomewide patterns of variation in genetic diversity are shared among populations, species and higher-order taxa. <i>Molecular Ecology</i> , 2017, 26, 4284-4295.	2.0	75
34	Combination of short-read, long-read, and optical mapping assemblies reveals large-scale tandem repeat arrays with population genetic implications. <i>Genome Research</i> , 2017, 27, 697-708.	2.4	94
35	Parallelism in genomic landscapes of differentiation, conserved genomic features and the role of linked selection. <i>Journal of Evolutionary Biology</i> , 2017, 30, 1516-1518.	0.8	25
36	Bioinformatic processing of RAD-seq data dramatically impacts downstream population genetic inference. <i>Methods in Ecology and Evolution</i> , 2017, 8, 907-917.	2.2	253

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37	Making sense of genomic islands of differentiation in light of speciation. <i>Nature Reviews Genetics</i> , 2017, 18, 87-100.	7.7	389
38	On the Challenge of Interpreting Census Data: Insights from a Study of an Endangered Pinniped. <i>PLoS ONE</i> , 2016, 11, e0154588.	1.1	21
39	A draft fur seal genome provides insights into factors affecting SNP validation and how to mitigate them. <i>Molecular Ecology Resources</i> , 2016, 16, 909-921.	2.2	29
40	Disruptive selection without genome-wide evolution across a migratory divide. <i>Molecular Ecology</i> , 2016, 25, 2529-2541.	2.0	32
41	Genome-culture coevolution promotes rapid divergence of killer whale ecotypes. <i>Nature Communications</i> , 2016, 7, 11693.	5.8	222
42	Evolution of heterogeneous genome differentiation across multiple contact zones in a crow species complex. <i>Nature Communications</i> , 2016, 7, 13195.	5.8	156
43	Reply to Garner et al.. <i>Trends in Ecology and Evolution</i> , 2016, 31, 83-84.	4.2	24
44	Forecasting Ecological Genomics: High-Tech Animal Instrumentation Meets High-Throughput Sequencing. <i>PLoS Biology</i> , 2016, 14, e1002350.	2.6	22
45	Transcriptomics of colour patterning and coloration shifts in crows. <i>Molecular Ecology</i> , 2015, 24, 4617-4628.	2.0	71
46	Differences in foraging ecology align with genetically divergent ecotypes of a highly mobile marine top predator. <i>Oecologia</i> , 2015, 179, 1041-1052.	0.9	24
47	Convergent evolution of the genomes of marine mammals. <i>Nature Genetics</i> , 2015, 47, 272-275.	9.4	392
48	Low-budget ready-to-fly unmanned aerial vehicles: an effective tool for evaluating the nesting status of canopy-breeding bird species. <i>Journal of Avian Biology</i> , 2015, 46, 425-430.	0.6	77
49	Fine-scale matrilineal population structure in the Galapagos fur seal and its implications for conservation management. <i>Conservation Genetics</i> , 2015, 16, 1099-1113.	0.8	25
50	Transcontinental migratory connectivity predicts parasite prevalence in breeding populations of the European barn swallow. <i>Journal of Evolutionary Biology</i> , 2015, 28, 535-546.	0.8	30
51	Single Nucleotides in the mtDNA Sequence Modify Mitochondrial Molecular Function and Are Associated with Sex-Specific Effects on Fertility and Aging. <i>Current Biology</i> , 2015, 25, 2717-2722.	1.8	93
52	Genomics and the challenging translation into conservation practice. <i>Trends in Ecology and Evolution</i> , 2015, 30, 78-87.	4.2	469
53	Demographic inferences using short-read genomic data in an approximate Bayesian computation framework: in silico evaluation of power, biases and proof of concept in Atlantic walrus. <i>Molecular Ecology</i> , 2015, 24, 328-345.	2.0	54
54	Why Time Matters: Codon Evolution and the Temporal Dynamics of dN/dS. <i>Molecular Biology and Evolution</i> , 2014, 31, 212-231.	3.5	110

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55	DISENTANGLING THE CONTRIBUTION OF SEXUAL SELECTION AND ECOLOGY TO THE EVOLUTION OF SIZE DIMORPHISM IN PINNIPEDS. <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 1485-1496.	1.1	45
56	A field guide to whole-genome sequencing, assembly and annotation. <i>Evolutionary Applications</i> , 2014, 7, 1026-1042.	1.5	296
57	The genomic landscape underlying phenotypic integrity in the face of gene flow in crows. <i>Science</i> , 2014, 344, 1410-1414.	6.0	490
58	An extensive candidate gene approach to speciation: diversity, divergence and linkage disequilibrium in candidate pigmentation genes across the European crow hybrid zone. <i>Heredity</i> , 2013, 111, 467-473.	1.2	30
59	Divergent allele advantage at MHC-DRB through direct and maternal genotypic effects and its consequences for allele pool composition and mating. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2013, 280, 20130714.	1.2	54
60	Hybridization and speciation. <i>Journal of Evolutionary Biology</i> , 2013, 26, 229-246.	0.8	1,735
61	Challenges and strategies in transcriptome assembly and differential gene expression quantification. A comprehensive <i>in silico</i> assessment of RNA-seq experiments. <i>Molecular Ecology</i> , 2013, 22, 620-634.	2.0	210
62	Widespread evidence for incipient ecological speciation: a meta-analysis of isolation-by-environment. <i>Ecology Letters</i> , 2013, 16, 940-950.	3.0	262
63	Principles of transcriptome analysis and gene expression quantification: an RNA-seq tutorial. <i>Molecular Ecology Resources</i> , 2013, 13, 559-572.	2.2	167
64	High Levels of Gene Expression Explain the Strong Evolutionary Constraint of Mitochondrial Protein-Coding Genes. <i>Molecular Biology and Evolution</i> , 2013, 30, 272-284.	3.5	67
65	The genomic landscape of species divergence in <i>Ficedula</i> flycatchers. <i>Nature</i> , 2012, 491, 756-760.	13.7	589
66	Exploring the Link between Genetic Relatedness and Social Contact Structure in Animal Social Networks. <i>American Naturalist</i> , 2011, 177, 135-142.	1.0	10
67	Growth under uncertainty: The influence of marine variability on early development of Galapagos sea lions. <i>Marine Mammal Science</i> , 2011, 27, 350-365.	0.9	34
68	General lack of global dosage compensation in ZZ/ZW systems? Broadening the perspective with RNA-seq. <i>BMC Genomics</i> , 2011, 12, 91.	1.2	86
69	Conservation of Neutral Substitution Rate and Substitutional Asymmetries in Mammalian Genes. <i>Genome Biology and Evolution</i> , 2010, 2, 19-28.	1.1	12
70	A TEST OF THE NEUTRAL MODEL OF EXPRESSION CHANGE IN NATURAL POPULATIONS OF HOUSE MOUSE SUBSPECIES. <i>Evolution; International Journal of Organic Evolution</i> , 2010, 64, 549-560.	1.1	17
71	Nucleotide divergence vs. gene expression differentiation: comparative transcriptome sequencing in natural isolates from the carrion crow and its hybrid zone with the hooded crow. <i>Molecular Ecology</i> , 2010, 19, 162-175.	2.0	125
72	Comparative genomics based on massive parallel transcriptome sequencing reveals patterns of substitution and selection across 10 bird species. <i>Molecular Ecology</i> , 2010, 19, 266-276.	2.0	105

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73	Male reproductive success and its behavioural correlates in a polygynous mammal, the Galápagos sea lion (<i>Zalophus wollebaeki</i>). <i>Molecular Ecology</i> , 2010, 19, no-no.	2.0	53
74	Speciation genetics: current status and evolving approaches. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2010, 365, 1717-1733.	1.8	174
75	Molecular evolution of genes in avian genomes. <i>Genome Biology</i> , 2010, 11, R68.	13.9	125
76	Nonlinear Dynamics of Nonsynonymous (dN) and Synonymous (dS) Substitution Rates Affects Inference of Selection. <i>Genome Biology and Evolution</i> , 2009, 1, 308-319.	1.1	95
77	Effects of brood size on multiple-paternity rates: a case for "paternity share"™ as an offspring-based estimate. <i>Animal Behaviour</i> , 2009, 78, 563-571.	0.8	14
78	Parent-offspring and sibling conflict in Galápagos fur seals and sea lions. <i>Behavioral Ecology and Sociobiology</i> , 2008, 62, 363-375.	0.6	99
79	Age-related changes in hematocrit in the Galápagos sea lion (<i>Zalophus wollebaeki</i>) and the Weddell seal (<i>Leptonychotes weddellii</i>). <i>Marine Mammal Science</i> , 2008, 24, 303-314.	0.9	20
80	Seasonal Changes of Vocal Rates and Their Relation to Territorial Status in Male Galápagos Sea Lions (<i>Zalophus wollebaeki</i>). <i>Ethology</i> , 2008, 114, 381-388.	0.5	26
81	Tracing early stages of species differentiation: Ecological, morphological and genetic divergence of Galápagos sea lion populations. <i>BMC Evolutionary Biology</i> , 2008, 8, 150.	3.2	73
82	Kin in space: social viscosity in a spatially and genetically substructured network. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2008, 275, 2063-2069.	1.2	65
83	Genetic dissimilarity predicts paternity in the smooth newt (<i>Lissotriton vulgaris</i>). <i>Biology Letters</i> , 2007, 3, 526-528.	1.0	27
84	Galápagos and Californian sea lions are separate species: Genetic analysis of the genus <i>Zalophus</i> and its implications for conservation management. <i>Frontiers in Zoology</i> , 2007, 4, 20.	0.9	53
85	Social structure in a colonial mammal: unravelling hidden structural layers and their foundations by network analysis. <i>Animal Behaviour</i> , 2007, 74, 1293-1302.	0.8	150
86	Beyond habitat requirements: individual fine-scale site fidelity in a colony of the Galapagos sea lion (<i>Zalophus wollebaeki</i>) creates conditions for social structuring. <i>Oecologia</i> , 2007, 152, 553-567.	0.9	89
87	Ten novel dinucleotide microsatellite loci cloned from the Galápagos sea lion (<i>Zalophus</i>) Tj ETQq1 1 0.784314 rgBT/Overlock 10 Tf 50 7, 103-105.	1.7	32
88	Development of new microsatellite loci and evaluation of loci from other pinniped species for the Galápagos sea lion (<i>Zalophus californianus wollebaeki</i>). <i>Conservation Genetics</i> , 2006, 7, 461-465.	0.8	21
89	Males in the shade: habitat use and sexual segregation in the Galápagos sea lion (<i>Zalophus</i>) Tj ETQq1 1 0.784314 rgBT/Overlock 10 Tf 50	0.6	90
90	Activation-tagged tobacco mutants that are tolerant to antimicrotubular herbicides are cross-resistant to chilling stress. <i>Transgenic Research</i> , 2003, 12, 615-629.	1.3	31

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91	Biotic interactions, community assembly, and eco-evolutionary dynamics as drivers of long-term biodiversityâ€“ecosystem functioning relationships. Research Ideas and Outcomes, 0, 5, .	1.0	23