

Marcus R Kronforst

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

3,892
citations

201658

27
h-index

144002

57
g-index

64
all docs

64
docs citations

64
times ranked

3785
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>optix</i> Drives the Repeated Convergent Evolution of Butterfly Wing Pattern Mimicry. <i>Science</i> , 2011, 333, 1137-1141.	12.6	431
2	Genomic architecture and introgression shape a butterfly radiation. <i>Science</i> , 2019, 366, 594-599.	12.6	365
3	Linkage of butterfly mate preference and wing color preference cue at the genomic location of <i>wingless</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 6575-6580.	7.1	312
4	The genetics of monarch butterfly migration and warning colouration. <i>Nature</i> , 2014, 514, 317-321.	27.8	264
5	Diversification of complex butterfly wing patterns by repeated regulatory evolution of a <i>Wnt</i> ligand. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 12632-12637.	7.1	244
6	Outbred genome sequencing and CRISPR/Cas9 gene editing in butterflies. <i>Nature Communications</i> , 2015, 6, 8212.	12.8	146
7	Macroevolutionary shifts of <i>WntA</i> function potentiate butterfly wing-pattern diversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 10701-10706.	7.1	137
8	Polymorphic Butterfly Reveals the Missing Link in Ecological Speciation. <i>Science</i> , 2009, 326, 847-850.	12.6	135
9	Hybridization Reveals the Evolving Genomic Architecture of Speciation. <i>Cell Reports</i> , 2013, 5, 666-677.	6.4	118
10	Genome-wide introgression among distantly related <i>Heliconius</i> butterfly species. <i>Genome Biology</i> , 2016, 17, 25.	8.8	115
11	The Functional Basis of Wing Patterning in <i>Heliconius</i> Butterflies: The Molecules Behind Mimicry. <i>Genetics</i> , 2015, 200, 1-19.	2.9	106
12	Wing patterning gene redefines the mimetic history of <i>Heliconius</i> butterflies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 19666-19671.	7.1	104
13	Genomic Hotspots for Adaptation: The Population Genetics of MÅ¼llerian Mimicry in the <i>Heliconius melpomene</i> Clade. <i>PLoS Genetics</i> , 2010, 6, e1000794.	3.5	97
14	Sex Chromosome Mosaicism and Hybrid Speciation among Tiger Swallowtail Butterflies. <i>PLoS Genetics</i> , 2011, 7, e1002274.	3.5	88
15	Ancient homology underlies adaptive mimetic diversity across butterflies. <i>Nature Communications</i> , 2014, 5, 4817.	12.8	87
16	<i>Aristaless</i> Controls Butterfly Wing Color Variation Used in Mimicry and Mate Choice. <i>Current Biology</i> , 2018, 28, 3469-3474.e4.	3.9	79
17	Do <i>Heliconius</i> butterfly species exchange mimicry alleles?. <i>Biology Letters</i> , 2013, 9, 20130503.	2.3	76
18	Serial founder effects and genetic differentiation during worldwide range expansion of monarch butterflies. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20142230.	2.6	73

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19	DNA methylation is widespread across social Hymenoptera. <i>Current Biology</i> , 2008, 18, R287-R288.	3.9	72
20	The molecular genetic basis of herbivory between butterflies and their host plants. <i>Nature Ecology and Evolution</i> , 2018, 2, 1418-1427.	7.8	56
21	A shared genetic basis of mimicry across swallowtail butterflies points to ancestral co-option of doublesex. <i>Nature Communications</i> , 2020, 11, 6.	12.8	55
22	Parallel Genetic Architecture of Parallel Adaptive Radiations in Mimetic <i>Heliconius</i> Butterflies. <i>Genetics</i> , 2006, 174, 535-539.	2.9	49
23	Dissecting comimetic radiations in <i>Heliconius</i> reveals divergent histories of convergent butterflies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 7365-7370.	7.1	47
24	Genomic takeover by transposable elements in the Strawberry poison frog. <i>Molecular Biology and Evolution</i> , 2014, 35, 2913-2927.	8.9	45
25	Contemporary loss of migration in monarch butterflies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 14671-14676.	7.1	41
26	Monarch butterflies use an environmentally sensitive, internal timer to control overwintering dynamics. <i>Molecular Ecology</i> , 2019, 28, 3642-3655.	3.9	37
27	Tracing the origin and evolution of supergene mimicry in butterflies. <i>Nature Communications</i> , 2017, 8, 1269.	12.8	36
28	Genomic evidence for gene flow between monarchs with divergent migratory phenotypes and flight performance. <i>Molecular Ecology</i> , 2020, 29, 2567-2582.	3.9	35
29	Frequency dependence shapes the adaptive landscape of imperfect Batesian mimicry. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20172786.	2.6	30
30	Butterfly Mimicry Polymorphisms Highlight Phylogenetic Limits of Gene Reuse in the Evolution of Diverse Adaptations. <i>Molecular Biology and Evolution</i> , 2019, 36, 2842-2853.	8.9	30
31	Genome-Wide Characterization of Adaptation and Speciation in Tiger Swallowtail Butterflies Using De Novo Transcriptome Assemblies. <i>Genome Biology and Evolution</i> , 2013, 5, 1233-1245.	2.5	29
32	Transitions from Single- to Multi-Locus Processes during Speciation with Gene Flow. <i>Genes</i> , 2018, 9, 274.	2.4	25
33	Lack of genetic differentiation among widely spaced subpopulations of a butterfly with home range behaviour. <i>Heredity</i> , 2001, 86, 243-250.	2.6	22
34	The population genetics of mimetic diversity in <i>Heliconius</i> butterflies. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2008, 275, 493-500.	2.6	22
35	Phylogeography of <i>Heliconius cydno</i> and its closest relatives: disentangling their origin and diversification. <i>Molecular Ecology</i> , 2014, 23, 4137-4152.	3.9	21
36	No genomic mosaicism in a putative hybrid butterfly species. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2007, 274, 1255-1264.	2.6	17

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37	Divergence and gene flow among Darwin's finches: A genome-wide view of adaptive radiation driven by interspecies allele sharing. <i>BioEssays</i> , 2015, 37, 968-974.	2.5	16
38	Genetic differentiation between body size biotypes of the parasitoid fly <i>Pseudacteon obtusus</i> (Diptera: Tj ETQq0 0,0,rgBT /Oyerlock 10	2.7	15
39	Museum genomics reveals the Xerces blue butterfly (<i>Glaucopsyche xerces</i>) was a distinct species driven to extinction. <i>Biology Letters</i> , 2021, 17, 20210123.	2.3	15
40	Divergence, gene flow, and the origin of leapfrog geographic distributions: The history of colour pattern variation in <i>Phyllobates</i> poison dart frogs. <i>Molecular Ecology</i> , 2020, 29, 3702-3719.	3.9	14
41	The roles of hybridization and habitat fragmentation in the evolution of Brazil's enigmatic longwing butterflies, <i>Heliconius nattereri</i> and <i>H. hermathena</i> . <i>BMC Biology</i> , 2020, 18, 84.	3.8	14
42	Primers for the amplification of nuclear introns in <i>Heliconius</i> butterflies. <i>Molecular Ecology Notes</i> , 2005, 5, 158-162.	1.7	13
43	Genetic diversity in the social amoeba <i>Dictyostelium discoideum</i> : Population differentiation and cryptic species. <i>Molecular Phylogenetics and Evolution</i> , 2011, 60, 455-462.	2.7	13
44	Diversification of the silverspot butterflies (Nymphalidae) in the Neotropics inferred from multi-locus DNA sequences. <i>Molecular Phylogenetics and Evolution</i> , 2015, 82, 156-165.	2.7	13
45	Migration behaviour of commercial monarchs reared outdoors and wild-derived monarchs reared indoors. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20201326.	2.6	13
46	Are eastern and western monarch butterflies distinct populations? A review of evidence for ecological, phenotypic, and genetic differentiation and implications for conservation. <i>Conservation Science and Practice</i> , 2021, 3, e432.	2.0	13
47	Species boundaries in <i>Philaethria</i> butterflies: an integrative taxonomic analysis based on genitalia ultrastructure, wing geometric morphometrics, DNA sequences, and amplified fragment length polymorphisms. <i>Zoological Journal of the Linnean Society</i> , 2014, 170, 690-709.	2.3	11
48	Subtle variation in size and shape of the whole forewing and the red band among co-mimics revealed by geometric morphometric analysis in <i>Heliconius</i> butterflies. <i>Ecology and Evolution</i> , 2018, 8, 3280-3295.	1.9	11
49	Female mate choice is a reproductive isolating barrier in <i>Heliconius</i> butterflies. <i>Ethology</i> , 2018, 124, 862-869.	1.1	11
50	Effectiveness of DNA Barcoding in <i>Speyeria</i> Butterflies at Small Geographic Scales. <i>Diversity</i> , 2018, 10, 130.	1.7	10
51	A neutral view of the evolving genomic architecture of speciation. <i>Ecology and Evolution</i> , 2017, 7, 6358-6366.	1.9	8
52	Experimental field tests of Batesian mimicry in the swallowtail butterfly <i>Papilio polytes</i> . <i>Ecology and Evolution</i> , 2018, 8, 7657-7666.	1.9	8
53	Behaviour before beauty: Signal weighting during mate selection in the butterfly <i>Papilio polytes</i> . <i>Ethology</i> , 2019, 125, 565-574.	1.1	8
54	Comparative Transcriptomics Provides Insights into Reticulate and Adaptive Evolution of a Butterfly Radiation. <i>Genome Biology and Evolution</i> , 2019, 11, 2963-2975.	2.5	7

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55	The evolution and genetics of sexually dimorphic "dual" mimicry in the butterfly <i>Elymnias hypermnestra</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20202192.	2.6	6
56	Disentangling Population History and Character Evolution among Hybridizing Lineages. <i>Molecular Biology and Evolution</i> , 2020, 37, 1295-1305.	8.9	5
57	Mimetic Butterflies Introgress to Impress. <i>PLoS Genetics</i> , 2012, 8, e1002802.	3.5	3
58	Exploring the molecular basis of monarch butterfly color pattern variation. <i>Pigment Cell and Melanoma Research</i> , 2015, 28, 127-130.	3.3	3
59	Development of a microsatellite library for the passion flower butterfly <i>Dione moneta</i> (Lepidoptera: Nymphalidae: Heliconiinae). <i>Conservation Genetics Resources</i> , 2012, 4, 719-724.	0.8	2
60	Species boundaries in <i>Philaethria</i> butterflies: an integrative taxonomic analysis based on genitalia ultrastructure, wing geometric morphometrics, DNA sequences, and amplified fragment length polymorphisms. <i>Zoological Journal of the Linnean Society</i> , 2014, , .	2.3	0