

# Riccardo Papa

## List of Publications by Year in descending order

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Version: 2024-02-01

30  
papers

2,563  
citations

394421

19  
h-index

454955

30  
g-index

36  
all docs

36  
docs citations

36  
times ranked

2614  
citing authors

#	ARTICLE	IF	CITATIONS
1	Origin of the green iguana ( <i>Iguana iguana</i> ) invasion in the greater Caribbean Region and Fiji. <i>Biological Invasions</i> , 2021, 23, 2591.	2.4	6
2	Selection and isolation define a heterogeneous divergence landscape between hybridizing <i>Heliconius</i> butterflies. <i>Evolution; International Journal of Organic Evolution</i> , 2021, 75, 2251-2268.	2.3	18
3	Cortex cis-regulatory switches establish scale colour identity and pattern diversity in <i>Heliconius</i> . <i>ELife</i> , 2021, 10, .	6.0	40
4	Novel <i>Doublesex</i> Duplication Associated with Sexually Dimorphic Development of Dogface Butterfly Wings. <i>Molecular Biology and Evolution</i> , 2021, 38, 5021-5033.	8.9	19
5	<i>Heliconius</i> butterflies: a window into the evolution and development of diversity. <i>Current Opinion in Genetics and Development</i> , 2021, 69, 72-81.	3.3	8
6	Balanced polymorphisms and their divergence in a <i>Heliconius</i> butterfly. <i>Ecology and Evolution</i> , 2021, 11, 18319-18330.	1.9	1
7	Many functionally connected loci foster adaptive diversification along a neotropical hybrid zone. <i>Science Advances</i> , 2020, 6, .	10.3	18
8	Perfect mimicry between <i>Heliconius</i> butterflies is constrained by genetics and development. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20201267.	2.6	20
9	Visual mate preference evolution during butterfly speciation is linked to neural processing genes. <i>Nature Communications</i> , 2020, 11, 4763.	12.8	24
10	Divergence of chemosensing during the early stages of speciation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 16438-16447.	7.1	25
11	Multiple Loci Control Eyespot Number Variation on the Hindwings of <i>Bicyclus anynana</i> Butterflies. <i>Genetics</i> , 2020, 214, 1059-1078.	2.9	4
12	Genomic architecture and introgression shape a butterfly radiation. <i>Science</i> , 2019, 366, 594-599.	12.6	365
13	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
14	Parallel evolution of ancient, pleiotropic enhancers underlies butterfly wing pattern mimicry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24174-24183.	7.1	102
15	Interplay between Developmental Flexibility and Determinism in the Evolution of Mimetic <i>Heliconius</i> Wing Patterns. <i>Current Biology</i> , 2019, 29, 3996-4009.e4.	3.9	55
16	Patterns of Z chromosome divergence among <i>Heliconius</i> species highlight the importance of historical demography. <i>Molecular Ecology</i> , 2018, 27, 3852-3872.	3.9	69
17	patternize: An R package for quantifying colour pattern variation. <i>Methods in Ecology and Evolution</i> , 2018, 9, 390-398.	5.2	96
18	Conserved microbiota among young <i>Heliconius</i> butterfly species. <i>PeerJ</i> , 2018, 6, e5502.	2.0	25

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19	Complex modular architecture around a simple toolkit of wing pattern genes. <i>Nature Ecology and Evolution</i> , 2017, 1, 52.	7.8	179
20	Genome-wide analysis of ionotropic receptors provides insight into their evolution in <i>Heliconius</i> butterflies. <i>BMC Genomics</i> , 2016, 17, 254.	2.8	38
21	Divergence with gene flow across a speciation continuum of <i>Heliconius</i> butterflies. <i>BMC Evolutionary Biology</i> , 2015, 15, 204.	3.2	38
22	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
23	Population genomics of parallel hybrid zones in the mimetic butterflies, <i>H. melpomene</i> and <i>H. erato</i> . <i>Genome Research</i> , 2014, 24, 1316-1333.	5.5	114
24	Multi-Allelic Major Effect Genes Interact with Minor Effect QTLs to Control Adaptive Color Pattern Variation in <i>Heliconius erato</i> . <i>PLoS ONE</i> , 2013, 8, e57033.	2.5	38
25	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
26	Transcriptome analysis reveals novel patterning and pigmentation genes underlying <i>Heliconius</i> butterfly wing pattern variation. <i>BMC Genomics</i> , 2012, 13, 288.	2.8	56
27	<i>optix</i> Drives the Repeated Convergent Evolution of Butterfly Wing Pattern Mimicry. <i>Science</i> , 2011, 333, 1137-1141.	12.6	431
28	Genomic Hotspots for Adaptation: The Population Genetics of Allergic Mimicry in <i>Heliconius erato</i> . <i>PLoS Genetics</i> , 2010, 6, e1000796.	3.5	99
29	Highly conserved gene order and numerous novel repetitive elements in genomic regions linked to wing pattern variation in <i>Heliconius</i> butterflies. <i>BMC Genomics</i> , 2008, 9, 345.	2.8	51
30	A Conserved Supergene Locus Controls Colour Pattern Diversity in <i>Heliconius</i> Butterflies. <i>PLoS Biology</i> , 2006, 4, e303.	5.6	242