

# Julien F Ayroles

## List of Publications by Year in descending order

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Version: 2024-02-01

35  
papers

5,652  
citations

279798

23  
h-index

361022

35  
g-index

49  
all docs

49  
docs citations

49  
times ranked

7324  
citing authors

#	ARTICLE	IF	CITATIONS
1	The <i>Drosophila melanogaster</i> Genetic Reference Panel. <i>Nature</i> , 2012, 482, 173-178.	27.8	1,756
2	The genetics of quantitative traits: challenges and prospects. <i>Nature Reviews Genetics</i> , 2009, 10, 565-577.	16.3	1,061
3	Systems genetics of complex traits in <i>Drosophila melanogaster</i> . <i>Nature Genetics</i> , 2009, 41, 299-307.	21.4	490
4	Epistasis dominates the genetic architecture of <i>Drosophila</i> quantitative traits. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 15553-15559.	7.1	348
5	Genetic incompatibilities are widespread within species. <i>Nature</i> , 2013, 504, 135-137.	27.8	200
6	Using Whole-Genome Sequence Data to Predict Quantitative Trait Phenotypes in <i>Drosophila melanogaster</i> . <i>PLoS Genetics</i> , 2012, 8, e1002685.	3.5	191
7	Behavioral idiosyncrasy reveals genetic control of phenotypic variability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6706-6711.	7.1	159
8	The microbiome extends host evolutionary potential. <i>Nature Communications</i> , 2021, 12, 5141.	12.8	138
9	Museum genomics: low-cost and high-accuracy genetic data from historical specimens. <i>Molecular Ecology Resources</i> , 2011, 11, 1082-1092.	4.8	122
10	Modulated Modularity Clustering as an Exploratory Tool for Functional Genomic Inference. <i>PLoS Genetics</i> , 2009, 5, e1000479.	3.5	118
11	Genomic Variation and Its Impact on Gene Expression in <i>Drosophila melanogaster</i> . <i>PLoS Genetics</i> , 2012, 8, e1003055.	3.5	102
12	Supervised machine learning reveals introgressed loci in the genomes of <i>Drosophila simulans</i> and <i>D. sechellia</i> . <i>PLoS Genetics</i> , 2018, 14, e1007341.	3.5	97
13	Co-regulated transcriptional networks contribute to natural genetic variation in <i>Drosophila</i> sleep. <i>Nature Genetics</i> , 2009, 41, 371-375.	21.4	91
14	Systems genetics analysis of body weight and energy metabolism traits in <i>Drosophila melanogaster</i> . <i>BMC Genomics</i> , 2010, 11, 297.	2.8	84
15	Segregating Variation in the Transcriptome: Cis Regulation and Additivity of Effects. <i>Genetics</i> , 2006, 173, 1347-1355.	2.9	63
16	A Genomewide Assessment of Inbreeding Depression: Gene Number, Function, and Mode of Action. <i>Conservation Biology</i> , 2009, 23, 920-930.	4.7	61
17	Individual Variation in Pheromone Response Correlates with Reproductive Traits and Brain Gene Expression in Worker Honey Bees. <i>PLoS ONE</i> , 2010, 5, e9116.	2.5	54
18	A transcriptional network associated with natural variation in <i>Drosophila</i> aggressive behavior. <i>Genome Biology</i> , 2009, 10, R76.	9.6	53

#	ARTICLE	IF	CITATIONS
19	Alcohol Sensitivity in <i>Drosophila</i> : Translational Potential of Systems Genetics. <i>Genetics</i> , 2009, 183, 733-745.	2.9	45
20	Overexpression of Myocilin in the <i>Drosophila</i> Eye Activates the Unfolded Protein Response: Implications for Glaucoma. <i>PLoS ONE</i> , 2009, 4, e4216.	2.5	41
21	The Evolution of Variance Control. <i>Trends in Ecology and Evolution</i> , 2020, 35, 22-33.	8.7	40
22	Genetic and environmental perturbations lead to regulatory decoherence. <i>ELife</i> , 2019, 8, .	6.0	34
23	TM3 <sup>seq</sup> : A Tagmentation-Mediated 3 <sup>seq</sup> Sequencing Approach for Improving Scalability of RNAseq Experiments. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 143-150.	1.8	32
24	Natural selection for imprecise vertical transmission in host-microbiota systems. <i>Nature Ecology and Evolution</i> , 2022, 6, 77-87.	7.8	31
25	The structure of behavioral variation within a genotype. <i>ELife</i> , 2021, 10, .	6.0	30
26	[11] Analysis of Variance of Microarray Data. <i>Methods in Enzymology</i> , 2006, 411, 214-233.	1.0	29
27	Functional genome annotation of <i>Drosophila</i> seminal fluid proteins using transcriptional genetic networks. <i>Genetical Research</i> , 2011, 93, 387-395.	0.9	29
28	Statistical tests for detecting variance effects in quantitative trait studies. <i>Bioinformatics</i> , 2019, 35, 200-210.	4.1	28
29	Urbanization and market integration have strong, nonlinear effects on cardiometabolic health in the Turkana. <i>Science Advances</i> , 2020, 6, .	10.3	23
30	Ancestral polymorphisms shape the adaptive radiation of <i>Metrosideros</i> across the Hawaiian Islands. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	19
31	Meta-analysis suggests the microbiome responds to Evolve and Resequencing experiments in <i>Drosophila melanogaster</i> . <i>BMC Microbiology</i> , 2021, 21, 108.	3.3	10
32	Modeling epistasis in mice and yeast using the proportion of two or more distinct genetic backgrounds: Evidence for polygenic epistasis. <i>PLoS Genetics</i> , 2020, 16, e1009165.	3.5	7
33	Socioeconomic status effects on health vary between rural and urban Turkana. <i>Evolution, Medicine and Public Health</i> , 2021, 9, 406-419.	2.5	7
34	Precise Quantification of Behavioral Individuality From 80 Million Decisions Across 183,000 Flies. <i>Frontiers in Behavioral Neuroscience</i> , 0, 16, .	2.0	7
35	Genetic basis of offspring number-body weight tradeoff in <i>Drosophila melanogaster</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	5