

# Robert Kofler

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2375731/publications.pdf>

Version: 2024-02-01

33  
papers

4,173  
citations

331670

21  
h-index

395702

33  
g-index

41  
all docs

41  
docs citations

41  
times ranked

4438  
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolutionary dynamics of piRNA clusters in <i>Drosophila</i> . <i>Molecular Ecology</i> , 2023, 32, 1306-1322.	3.9	20
2	Novel quality metrics allow identifying and generating high-quality assemblies of piRNA clusters. <i>Molecular Ecology Resources</i> , 2022, 22, 102-121.	4.8	13
3	The Transposition Rate Has Little Influence on the Plateauing Level of the P-element. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	11
4	Tirant Stealthily Invaded Natural <i>Drosophila melanogaster</i> Populations during the Last Century. <i>Molecular Biology and Evolution</i> , 2021, 38, 1482-1497.	8.9	10
5	Reconstructing the Invasion Route of the P-Element in <i>Drosophila melanogaster</i> Using Extant Population Samples. <i>Genome Biology and Evolution</i> , 2020, 12, 2139-2152.	2.5	2
6	piRNA Clusters Need a Minimum Size to Control Transposable Element Invasions. <i>Genome Biology and Evolution</i> , 2020, 12, 736-749.	2.5	20
7	Evolutionary genomics can improve prediction of species' responses to climate change. <i>Evolution Letters</i> , 2020, 4, 4-18.	3.3	190
8	Rapid sex-specific adaptation to high temperature in <i>Drosophila</i> . <i>ELife</i> , 2020, 9, .	6.0	25
9	Benchmarking software tools for detecting and quantifying selection in evolve and resequencing studies. <i>Genome Biology</i> , 2019, 20, 169.	8.8	33
10	Optimizing the Power to Identify the Genetic Basis of Complex Traits with Evolve and Resequence Studies. <i>Molecular Biology and Evolution</i> , 2019, 36, 2890-2905.	8.9	14
11	DeviaTE: Assembly-free analysis and visualization of mobile genetic element composition. <i>Molecular Ecology Resources</i> , 2019, 19, 1346-1354.	4.8	28
12	Dynamics of Transposable Element Invasions with piRNA Clusters. <i>Molecular Biology and Evolution</i> , 2019, 36, 1457-1472.	8.9	54
13	Genetic redundancy fuels polygenic adaptation in <i>Drosophila</i> . <i>PLoS Biology</i> , 2019, 17, e3000128.	5.6	212
14	Molecular dissection of a natural transposable element invasion. <i>Genome Research</i> , 2018, 28, 824-835.	5.5	64
15	SimulaTE: simulating complex landscapes of transposable elements of populations. <i>Bioinformatics</i> , 2018, 34, 1419-1420.	4.1	3
16	MimicEE2: Genome-wide forward simulations of Evolve and Resequencing studies. <i>PLoS Computational Biology</i> , 2018, 14, e1006413.	3.2	43
17	Regulation of transposable elements: Interplay between TE-encoded regulatory sequences and host-specific trans-acting factors in <i>Drosophila melanogaster</i> . <i>Molecular Ecology</i> , 2017, 26, 5149-5159.	3.9	12
18	Suitability of Different Mapping Algorithms for Genome-Wide Polymorphism Scans with Pool-Seq Data. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3507-3515.	1.8	38

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19	The impact of library preparation protocols on the consistency of allele frequency estimates in Pool-Seq data. <i>Molecular Ecology Resources</i> , 2016, 16, 118-122.	4.8	22
20	PoPoolationTE2: Comparative Population Genomics of Transposable Elements Using Pool-Seq. <i>Molecular Biology and Evolution</i> , 2016, 33, 2759-2764.	8.9	86
21	Tempo and Mode of Transposable Element Activity in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2015, 11, e1005406.	3.5	97
22	The recent invasion of natural <i>Drosophila simulans</i> populations by the P-element. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6659-6663.	7.1	101
23	Gaussian process test for high-throughput sequencing time series: application to experimental evolution. <i>Bioinformatics</i> , 2015, 31, 1762-1770.	4.1	41
24	Massive Habitat-Specific Genomic Response in <i>D. melanogaster</i> Populations during Experimental Evolution in Hot and Cold Environments. <i>Molecular Biology and Evolution</i> , 2014, 31, 364-375.	8.9	138
25	Sequencing pools of individuals " mining genome-wide polymorphism data without big funding. <i>Nature Reviews Genetics</i> , 2014, 15, 749-763.	16.3	654
26	A Guide for the Design of Evolve and Resequencing Studies. <i>Molecular Biology and Evolution</i> , 2014, 31, 474-483.	8.9	138
27	Genome-wide patterns of natural variation reveal strong selective sweeps and ongoing genomic conflict in <i>Drosophila mauritiana</i> . <i>Genome Research</i> , 2013, 23, 99-110.	5.5	73
28	PoolChmm: a Python program for estimating the allele frequency spectrum and detecting selective sweeps from next generation sequencing of pooled samples. <i>Molecular Ecology Resources</i> , 2013, 13, 337-340.	4.8	55
29	Sequencing of Pooled DNA Samples (Pool-Seq) Uncovers Complex Dynamics of Transposable Element Insertions in <i>Drosophila melanogaster</i> . <i>PLoS Genetics</i> , 2012, 8, e1002487.	3.5	223
30	Genome-wide patterns of latitudinal differentiation among populations of <i>Drosophila melanogaster</i> from North America. <i>Molecular Ecology</i> , 2012, 21, 4748-4769.	3.9	256
31	Adaptation of <i>Drosophila</i> to a novel laboratory environment reveals temporally heterogeneous trajectories of selected alleles. <i>Molecular Ecology</i> , 2012, 21, 4931-4941.	3.9	194
32	PoPoolation: A Toolbox for Population Genetic Analysis of Next Generation Sequencing Data from Pooled Individuals. <i>PLoS ONE</i> , 2011, 6, e15925.	2.5	556
33	PoPoolation2: identifying differentiation between populations using sequencing of pooled DNA samples (Pool-Seq). <i>Bioinformatics</i> , 2011, 27, 3435-3436.	4.1	729