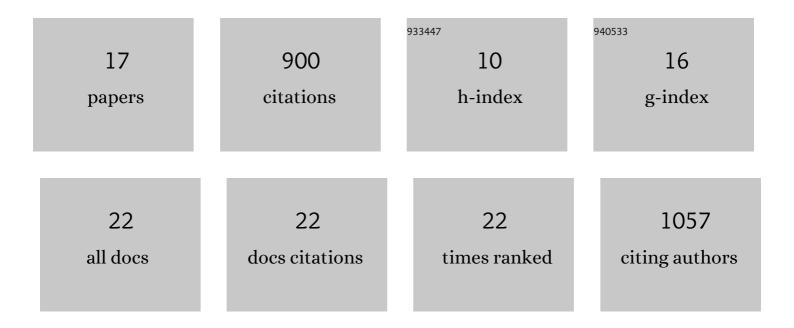
## Laurence Loewe

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5388784/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Clonal polymorphism and high heterozygosity in the celibate genome of the Amazon molly. Nature Ecology and Evolution, 2018, 2, 669-679.	7.8	117
2	Stochasticity, Selection, and the Evolution of Cooperation in a Two-Level Moran Model of the Snowdrift Game. Complexity, 2018, 2018, 1-14.	1.6	10
3	Evolvix BEST Names for semantic reproducibility across code2brain interfaces. Annals of the New York Academy of Sciences, 2017, 1387, 124-144.	3.8	1
4	Lazy Updating of hubs can enable more realistic models by speeding up stochastic simulations. Journal of Chemical Physics, 2014, 141, 204109.	3.0	5
5	How Evolutionary Systems Biology Will Help Understand Adaptive Landscapes and Distributions of Mutational Effects. Advances in Experimental Medicine and Biology, 2012, 751, 399-410.	1.6	5
6	The population genetics of mutations: good, bad and indifferent. Philosophical Transactions of the Royal Society B: Biological Sciences, 2010, 365, 1153-1167.	4.0	163
7	A framework for evolutionary systems biology. BMC Systems Biology, 2009, 3, 27.	3.0	65
8	On the potential for extinction by Muller's Ratchet in Caenorhabditis elegans. BMC Evolutionary Biology, 2008, 8, 125.	3.2	38
9	Quantifying the threat of extinction from Muller's ratchet in the diploid Amazon molly (Poecilia) Tj ETQq1 1 0.78	4314 rgBT	- /Qyerlock 1
10	Background Selection in Single Genes May Explain Patterns of Codon Bias. Genetics, 2007, 175, 1381-1393.	2.9	60
11	Evolution@home: observations on participant choice, work unit variation and low-effort global computing. Software - Practice and Experience, 2007, 37, 1289-1318.	3.6	8
12	Inferring the distribution of mutational effects on fitness in Drosophila. Biology Letters, 2006, 2, 426-430.	2.3	81
13	Quantifying the genomic decay paradox due to Muller's ratchet in human mitochondrial DNA. Genetical Research, 2006, 87, 133-159.	0.9	78
14	Estimating Selection on Nonsynonymous Mutations. Genetics, 2006, 172, 1079-1092.	2.9	111
15	High Deleterious Genomic Mutation Rate in Stationary Phase of Escherichia coli. Science, 2003, 302, 1558-1560.	12.6	80
16	Global computing for bioinformatics. Briefings in Bioinformatics, 2002, 3, 377-388.	6.5	10
17	Quantifying the implicit process flow abstraction in SBGN-PD diagrams with Bio-PEPA. Electronic Proceedings in Theoretical Computer Science, EPTCS, 0, 6, 93-107.	0.8	1