

# Lawrence H Uricchio

## List of Publications by Year in descending order

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Version: 2024-02-01

19  
papers

935  
citations

687363

13  
h-index

794594

19  
g-index

26  
all docs

26  
docs citations

26  
times ranked

1897  
citing authors

#	ARTICLE	IF	CITATIONS
1	Revisiting the malaria hypothesis: accounting for polygenicity and pleiotropy. <i>Trends in Parasitology</i> , 2022, 38, 290-301.	3.3	5
2	Understanding the emergence of contingent and deterministic exclusion in multispecies communities. <i>Ecology Letters</i> , 2021, 24, 2155-2168.	6.4	8
3	How will mosquitoes adapt to climate warming?. <i>ELife</i> , 2021, 10, .	6.0	46
4	Evolutionary perspectives on polygenic selection, missing heritability, and GWAS. <i>Human Genetics</i> , 2020, 139, 5-21.	3.8	37
5	Priority Effects and Nonhierarchical Competition Shape Species Composition in a Complex Grassland Community. <i>American Naturalist</i> , 2019, 193, 213-226.	2.1	31
6	Ultrarare variants drive substantial cis heritability of human gene expression. <i>Nature Genetics</i> , 2019, 51, 1349-1355.	21.4	98
7	An evolutionary compass for detecting signals of polygenic selection and mutational bias. <i>Evolution Letters</i> , 2019, 3, 69-79.	3.3	29
8	Exploiting selection at linked sites to infer the rate and strength of adaptation. <i>Nature Ecology and Evolution</i> , 2019, 3, 977-984.	7.8	43
9	An admixture mapping meta-analysis implicates genetic variation at 18q21 with asthma susceptibility in Latinos. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 143, 957-969.	2.9	33
10	Singleton Variants Dominate the Genetic Architecture of Human Gene Expression. <i>SSRN Electronic Journal</i> , 2018, , .	0.4	4
11	Selection and explosive growth alter genetic architecture and hamper the detection of causal rare variants. <i>Genome Research</i> , 2016, 26, 863-873.	5.5	63
12	An analytical upper bound on the number of loci required for all splits of a species tree to appear in a set of gene trees. <i>BMC Bioinformatics</i> , 2016, 17, 417.	2.6	1
13	Population Genetic Simulations of Complex Phenotypes with Implications for Rare Variant Association Tests. <i>Genetic Epidemiology</i> , 2015, 39, 35-44.	1.3	16
14	Robust Forward Simulations of Recurrent Hitchhiking. <i>Genetics</i> , 2014, 197, 221-236.	2.9	24
15	Population Genetics of Rare Variants and Complex Diseases. <i>Human Heredity</i> , 2012, 74, 118-128.	0.8	53
16	Accurate Imputation of Rare and Common Variants in a Founder Population From a Small Number of Sequenced Individuals. <i>Genetic Epidemiology</i> , 2012, 36, 312-319.	1.3	19
17	Exome sequencing reveals a novel mutation for autosomal recessive non-syndromic mental retardation in the <i>TECR</i> gene on chromosome 19p13. <i>Human Molecular Genetics</i> , 2011, 20, 1285-1289.	2.9	94
18	Inflammasome-Mediated Production of IL-1 $\beta$ Is Required for Neutrophil Recruitment against <i>Staphylococcus aureus</i> In Vivo. <i>Journal of Immunology</i> , 2007, 179, 6933-6942.	0.8	294

#	ARTICLE	IF	CITATIONS
19	Coarse-grained entropy decrease and phase-space focusing in Hamiltonian dynamics. Physical Review A, 2005, 72, .	2.5	2