

Gregory I Lang

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

1,755
citations

623188

14
h-index

752256

20
g-index

31
all docs

31
docs citations

31
times ranked

2283
citing authors

#	ARTICLE	IF	CITATIONS
1	Pervasive genetic hitchhiking and clonal interference in forty evolving yeast populations. <i>Nature</i> , 2013, 500, 571-574.	13.7	523
2	Estimating the Per-Base-Pair Mutation Rate in the Yeast <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2008, 178, 67-82.	1.2	306
3	Genetic Variation and the Fate of Beneficial Mutations in Asexual Populations. <i>Genetics</i> , 2011, 188, 647-661.	1.2	183
4	The cost of gene expression underlies a fitness trade-off in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 5755-5760.	3.3	142
5	Mutation Rates across Budding Yeast Chromosome VI Are Correlated with Replication Timing. <i>Genome Biology and Evolution</i> , 2011, 3, 799-811.	1.1	137
6	The spectrum of adaptive mutations in experimental evolution. <i>Genomics</i> , 2014, 104, 412-416.	1.3	71
7	Adaptive genome duplication affects patterns of molecular evolution in <i>Saccharomyces cerevisiae</i> . <i>PLoS Genetics</i> , 2018, 14, e1007396.	1.5	69
8	Hitchhiking and epistasis give rise to cohort dynamics in adapting populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 8330-8335.	3.3	61
9	Crowded growth leads to the spontaneous evolution of semistable coexistence in laboratory yeast populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 11306-11311.	3.3	47
10	Altered access to beneficial mutations slows adaptation and biases fixed mutations in diploids. <i>Nature Ecology and Evolution</i> , 2018, 2, 882-889.	3.4	46
11	A Test of the Coordinated Expression Hypothesis for the Origin and Maintenance of the GAL Cluster in Yeast. <i>PLoS ONE</i> , 2011, 6, e25290.	1.1	31
12	Experimental evolution in fungi: An untapped resource. <i>Fungal Genetics and Biology</i> , 2016, 94, 88-94.	0.9	29
13	Measuring Mutation Rates Using the Luria-Delbrück Fluctuation Assay. <i>Methods in Molecular Biology</i> , 2018, 1672, 21-31.	0.4	26
14	Adaptive evolution of nontransitive fitness in yeast. <i>ELife</i> , 2020, 9, .	2.8	23
15	Detecting genetic interactions using parallel evolution in experimental populations. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180237.	1.8	21
16	Overdominant and partially dominant mutations drive clonal adaptation in diploid <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2022, 221, .	1.2	9
17	Exploring a Local Genetic Interaction Network Using Evolutionary Replay Experiments. <i>Molecular Biology and Evolution</i> , 2021, 38, 3144-3152.	3.5	7
18	Overdominant Mutations Restrict Adaptive Loss of Heterozygosity at Linked Loci. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	6

#	ARTICLE	IF	CITATIONS
19	Integrative Meta-Assembly Pipeline (IMAP): Chromosome-level genome assembler combining multiple de novo assemblies. PLoS ONE, 2019, 14, e0221858.	1.1	3
20	Evolution of Epistasis: Small Populations Go Their Separate Ways. Journal of Molecular Evolution, 2020, 88, 418-420.	0.8	1