

# Sasha F Levy

## List of Publications by Year in descending order

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Version: 2024-02-01

26  
papers

2,362  
citations

331670

21  
h-index

526287

27  
g-index

35  
all docs

35  
docs citations

35  
times ranked

3062  
citing authors

#	ARTICLE	IF	CITATIONS
1	The interplay of additivity, dominance, and epistasis on fitness in a diploid yeast cross. <i>Nature Communications</i> , 2022, 13, 1463.	12.8	19
2	Overdominant and partially dominant mutations drive clonal adaptation in diploid <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2022, 221, .	2.9	9
3	The genotype-phenotype landscape of an allosteric protein. <i>Molecular Systems Biology</i> , 2021, 17, e10179.	7.2	40
4	A large accessory protein interactome is rewired across environments. <i>ELife</i> , 2020, 9, .	6.0	24
5	High-resolution lineage tracking reveals travelling wave of adaptation in laboratory yeast. <i>Nature</i> , 2019, 575, 494-499.	27.8	119
6	iSeq 2.0: A Modular and Interchangeable Toolkit for Interaction Screening in Yeast. <i>Cell Systems</i> , 2019, 8, 338-344.e8.	6.2	20
7	Improved discovery of genetic interactions using CRISPRiSeq across multiple environments. <i>Genome Research</i> , 2019, 29, 668-681.	5.5	34
8	The dynamics of adaptive genetic diversity during the early stages of clonal evolution. <i>Nature Ecology and Evolution</i> , 2019, 3, 293-301.	7.8	45
9	Bartender: a fast and accurate clustering algorithm to count barcode reads. <i>Bioinformatics</i> , 2018, 34, 739-747.	4.1	71
10	Unbiased Fitness Estimation of Pooled Barcode or Amplicon Sequencing Studies. <i>Cell Systems</i> , 2018, 7, 521-525.e4.	6.2	27
11	Single-cell copy number variant detection reveals the dynamics and diversity of adaptation. <i>PLoS Biology</i> , 2018, 16, e3000069.	5.6	106
12	iSeq: A New Double-Barcode Method for Detecting Dynamic Genetic Interactions in Yeast. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 143-153.	1.8	32
13	A scalable double-barcode sequencing platform for characterization of dynamic protein-protein interactions. <i>Nature Communications</i> , 2017, 8, 15586.	12.8	35
14	A method for high-throughput production of sequence-verified <i>scp</i> -DNA libraries and strain collections. <i>Molecular Systems Biology</i> , 2017, 13, 913.	7.2	41
15	Gene Architectures that Minimize Cost of Gene Expression. <i>Molecular Cell</i> , 2017, 65, 142-153.	9.7	77
16	Cellular Heterogeneity: Benefits Besides Bet-Hedging. <i>Current Biology</i> , 2016, 26, R355-R357.	3.9	31
17	Development of a Comprehensive Genotype-to-Fitness Map of Adaptation-Driving Mutations in Yeast. <i>Cell</i> , 2016, 166, 1585-1596.e22.	28.9	205
18	Quantitative evolutionary dynamics using high-resolution lineage tracking. <i>Nature</i> , 2015, 519, 181-186.	27.8	372

#	ARTICLE	IF	CITATIONS
19	Beyond genome sequencing: Lineage tracking with barcodes to study the dynamics of evolution, infection, and cancer. <i>Genomics</i> , 2014, 104, 417-430.	2.9	81
20	Histone Variant HTZ1 Shows Extensive Epistasis with, but Does Not Increase Robustness to, New Mutations. <i>PLoS Genetics</i> , 2013, 9, e1003733.	3.5	42
21	Bet Hedging in Yeast by Heterogeneous, Age-Related Expression of a Stress Protectant. <i>PLoS Biology</i> , 2012, 10, e1001325.	5.6	324
22	The Robustness Continuum. <i>Advances in Experimental Medicine and Biology</i> , 2012, 751, 431-452.	1.6	27
23	FTDP-17 Mutations in Tau Alter the Regulation of Microtubule Dynamics. <i>Journal of Biological Chemistry</i> , 2008, 283, 36406-36415.	3.4	37
24	Network Hubs Buffer Environmental Variation in <i>Saccharomyces cerevisiae</i> . <i>PLoS Biology</i> , 2008, 6, e264.	5.6	270
25	Somatodendritic microRNAs identified by laser capture and multiplex RT-PCR. <i>Rna</i> , 2007, 13, 1224-1234.	3.5	166
26	Three- and Four-repeat Tau Regulate the Dynamic Instability of Two Distinct Microtubule Subpopulations in Qualitatively Different Manners. <i>Journal of Biological Chemistry</i> , 2005, 280, 13520-13528.	3.4	81