Claudia Bank

List of Publications by Year in descending order

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361296 434063 2,491 31 20 31 citations h-index g-index papers 52 52 52 3393 all docs docs citations times ranked citing authors

#	Article	IF	CITATIONS
1	Genomics and the origin of species. Nature Reviews Genetics, 2014, 15, 176-192.	7.7	850
2	The Limits to Parapatric Speciation: Dobzhansky–Muller Incompatibilities in a Continent–Island Model. Genetics, 2012, 191, 845-863.	1.2	147
3	Influenza Virus Drug Resistance: A Time-Sampled Population Genetics Perspective. PLoS Genetics, 2014, 10, e1004185.	1.5	126
4	Evolution in the light of fitness landscape theory. Trends in Ecology and Evolution, 2019, 34, 69-82.	4.2	124
5	Thinking too positive? Revisiting current methods of population genetic selection inference. Trends in Genetics, 2014, 30, 540-546.	2.9	121
6	A Systematic Survey of an Intragenic Epistatic Landscape. Molecular Biology and Evolution, 2015, 32, 229-238.	3.5	118
7	SHIFTING FITNESS LANDSCAPES IN RESPONSE TO ALTERED ENVIRONMENTS. Evolution; International Journal of Organic Evolution, 2013, 67, 3512-3522.	1.1	114
8	On the (un)predictability of a large intragenic fitness landscape. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14085-14090.	3.3	104
9	A Bayesian MCMC Approach to Assess the Complete Distribution of Fitness Effects of New Mutations: Uncovering the Potential for Adaptive Walks in Challenging Environments. Genetics, 2014, 196, 841-852.	1.2	100
10	Deleterious mutation accumulation and the long-term fate of chromosomal inversions. PLoS Genetics, 2021, 17, e1009411.	1.5	71
11	Low mutational load and high mutation rate variation in gut commensal bacteria. PLoS Biology, 2020, 18, e3000617.	2.6	59
12	Renal control of disease tolerance to malaria. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 5681-5686.	3.3	58
13	Comprehensive fitness maps of Hsp90 show widespread environmental dependence. ELife, 2020, 9, .	2.8	49
14	On the importance of skewed offspring distributions and background selection in virus population genetics. Heredity, 2016, 117, 393-399.	1.2	48
15	A Statistical Guide to the Design of Deep Mutational Scanning Experiments. Genetics, 2016, 204, 77-87.	1.2	45
16	CAN REINFORCEMENT COMPLETE SPECIATION?. Evolution; International Journal of Organic Evolution, 2012, 66, 229-239.	1.1	44
17	An experimental evaluation of drugâ€induced mutational meltdown as an antiviral treatment strategy. Evolution; International Journal of Organic Evolution, 2016, 70, 2470-2484.	1.1	36
18	A Balance between Inhibitor Binding and Substrate Processing Confers Influenza Drug Resistance. Journal of Molecular Biology, 2016, 428, 538-553.	2.0	36

#	Article	IF	CITATIONS
19	In search of the Goldilocks zone for hybrid speciation. PLoS Genetics, 2018, 14, e1007613.	1.5	31
20	The Combined Effect of Oseltamivir and Favipiravir on Influenza A Virus Evolution. Genome Biology and Evolution, 2017, 9, 1913-1924.	1.1	28
21	Environment changes epistasis to alter tradeâ€offs along alternative evolutionary paths. Evolution; International Journal of Organic Evolution, 2019, 73, 2094-2105.	1.1	28
22	The fitness landscape of the codon space across environments. Heredity, 2018, 121, 422-437.	1.2	21
23	Two sides of the same coin: A population genetics perspective on lethal mutagenesis and mutational meltdown. Virus Evolution, 2017, 3, vex004.	2.2	19
24	The limits to parapatric speciation 3: evolution of strong reproductive isolation in presence of gene flow despite limited ecological differentiation. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190532.	1.8	14
25	Homage to Felsenstein 1981, or why are there so few/many species?. Evolution; International Journal of Organic Evolution, 2021, 75, 978-988.	1.1	13
26	Understanding Admixture: Haplodiploidy to the Rescue. Trends in Ecology and Evolution, 2020, 35, 34-42.	4.2	12
27	The Adaptive Potential of the Middle Domain of Yeast Hsp90. Molecular Biology and Evolution, 2021, 38, 368-379.	3.5	10
28	Conflict between heterozygote advantage and hybrid incompatibility in haplodiploids (and sex) Tj ETQq0 0 0 rgBT	/Overlock	10 Tf 50 38
29	Patterns of selection against centrosome amplification in human cell lines. PLoS Computational Biology, 2021, 17, e1008765.	1.5	8
30	The extinction time under mutational meltdown driven by high mutation rates. Ecology and Evolution, 2022, 12, .	0.8	4
31	Imbalanced segregation of recombinant haplotypes in hybrid populations reveals inter- and intrachromosomal Dobzhansky-Muller incompatibilities. PLoS Genetics, 2022, 18, e1010120.	1.5	2