Ayal B Gussow

List of Publications by Year
in descending order

14 papers	1,184 citations	687363 13 h-index	1058476 14 g-index
17 all docs	17 docs citations	17 times ranked	2681 citing authors

#	Article	IF	Citations
1	Discovery of an expansive bacteriophage family that includes the most abundant viruses from the human gut. Nature Microbiology, 2018, 3, 38-46.	13.3	245
2	Genomic determinants of pathogenicity in SARS-CoV-2 and other human coronaviruses. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 15193-15199.	7.1	196
3	The Intolerance of Regulatory Sequence to Genetic Variation Predicts Gene Dosage Sensitivity. PLoS Genetics, 2015, 11, e1005492.	3.5	123
4	The intolerance to functional genetic variation of protein domains predicts the localization of pathogenic mutations within genes. Genome Biology, 2016, 17, 9.	8.8	118
5	Thousands of previously unknown phages discovered in whole-community human gut metagenomes. Microbiome, 2021, 9, 78.	11.1	101
6	Seeker: alignment-free identification of bacteriophage genomes by deep learning. Nucleic Acids Research, 2020, 48, e121-e121.	14.5	78
7	Evolutionary and functional classification of the CARF domain superfamily, key sensors in prokaryotic antivirus defense. Nucleic Acids Research, 2020, 48, 8828-8847.	14.5	66
8	Machine-learning approach expands the repertoire of anti-CRISPR protein families. Nature Communications, 2020, 11, 3784.	12.8	64
9	Incorporating Machine Learning into Established Bioinformatics Frameworks. International Journal of Molecular Sciences, 2021, 22, 2903.	4.1	48
10	Prioritizing non-coding regions based on human genomic constraint and sequence context with deep learning. Nature Communications, 2021, 12, 1504.	12.8	40
11	Inhibition of microRNA 128 promotes excitability of cultured cortical neuronal networks. Genome Research, 2016, 26, 1411-1416.	5.5	34
12	Orion: Detecting regions of the human non-coding genome that are intolerant to variation using population genetics. PLoS ONE, 2017, 12, e0181604.	2.5	31
13	Prediction of the incubation period for COVID-19 and future virus disease outbreaks. BMC Biology, 2020, 18, 186.	3.8	16
14	Identification of combinations of somatic mutations that predict cancer survival and immunotherapy benefit. NAR Cancer, 2021, 3, zcab017.	3.1	2