

# Ayal B Gussow

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2462746/publications.pdf>

Version: 2024-02-01

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