Omer Weissbrod

List of Publications by Year
in descending order

29	4,938	394421 19	477307 29
papers	citations	h-index	g-index

41	41	41	8536
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Environment dominates over host genetics in shaping human gut microbiota. Nature, 2018, 555, 210-215.	27.8	1,958
2	Large-scale association analyses identify host factors influencing human gut microbiome composition. Nature Genetics, 2021, 53, 156-165.	21.4	676
3	Prediction of acute myeloid leukaemia risk in healthy individuals. Nature, 2018, 559, 400-404.	27.8	617
4	Bread Affects Clinical Parameters and Induces Gut Microbiome-Associated Personal Glycemic Responses. Cell Metabolism, 2017, 25, 1243-1253.e5.	16.2	233
5	A reference map of potential determinants for the human serum metabolome. Nature, 2020, 588, 135-140.	27.8	230
6	Functionally informed fine-mapping and polygenic localization of complex trait heritability. Nature Genetics, 2020, 52, 1355-1363.	21.4	185
7	Quantitative analysis of population-scale family trees with millions of relatives. Science, 2018, 360, 171-175.	12.6	157
8	Leveraging fine-mapping and multipopulation training data to improve cross-population polygenic risk scores. Nature Genetics, 2022, 54, 450-458.	21.4	109
9	Estimating SNP-Based Heritability and Genetic Correlation in Case-Control Studies Directly and with Summary Statistics. American Journal of Human Genetics, 2018, 103, 89-99.	6.2	102
10	Titin Mutation in Familial Restrictive Cardiomyopathy. International Journal of Cardiology, 2014, 171, 24-30.	1.7	84
11	Further Improvements to Linear Mixed Models for Genome-Wide Association Studies. Scientific Reports, 2014, 4, 6874.	3.3	61
12	Combining SNP-to-gene linking strategies to identify disease genes and assess disease omnigenicity. Nature Genetics, 2022, 54, 827-836.	21.4	61
13	Multikernel linear mixed models for complex phenotype prediction. Genome Research, 2016, 26, 969-979.	5.5	57
14	Loss of CD55 in Eculizumab-Responsive Protein-Losing Enteropathy. New England Journal of Medicine, 2017, 377, 87-89.	27.0	41
15	Paradoxical Hypersusceptibility of Drug-resistant M ycobacterium tuberculosis to Î²-lactam Antibiotics. EBioMedicine, 2016, 9, 170-179.	6.1	39
16	Accurate liability estimation improves power in ascertained case-control studies. Nature Methods, 2015, 12, 332-334.	19.0	36
17	Utility of polygenic embryo screening for disease depends on the selection strategy. ELife, 2021, 10, .	6.0	34
18	Host genetics and microbiome associations through the lens of genome wide association studies. Current Opinion in Microbiology, 2018, 44, 9-19.	5.1	33

#	Article	IF	Citations
19	Open problems in human trait genetics. Genome Biology, 2022, 23, .	8.8	33
20	RL-SKAT: An Exact and Efficient Score Test for Heritability and Set Tests. Genetics, 2017, 207, 1275-1283.	2.9	19
21	Fatal thoracic aortic aneurysm and dissection in a large family with a novel MYLK gene mutation: delineation of the clinical phenotype. Orphanet Journal of Rare Diseases, 2018, 13, 41.	2.7	16
22	Whole-genome sequencing reveals that variants in the Interleukin 18 Receptor Accessory Protein 3â€²UTR protect against ALS. Nature Neuroscience, 2022, 25, 433-445.	14.8	16
23	An atlas of robust microbiome associations with phenotypic traits based on large-scale cohorts from two continents. PLoS ONE, 2022, 17, e0265756.	2.5	15
24	Functional disease architectures reveal unique biological role of transposable elements. Nature Communications, 2019, 10, 4054.	12.8	14
25	Estimating variance components in population scale family trees. PLoS Genetics, 2019, 15, e1008124.	3.5	11
26	Association testing of bisulfite-sequencing methylation data via a Laplace approximation. Bioinformatics, 2017, 33, i325-i332.	4.1	9
27	Fast and Efficient Feature Engineering for Multi-Cohort Analysis of EHR Data. Studies in Health Technology and Informatics, 2017, 235, 181-185.	0.3	9
28	Improving the informativeness of Mendelian disease-derived pathogenicity scores for common disease. Nature Communications, 2020, 11, 6258.	12.8	8
29	Detecting heritable phenotypes without a model using fast permutation testing for heritability and set-tests. Nature Communications, 2018, 9, 4919.	12.8	6