Omer Weissbrod

List of Publications by Year
in descending order

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

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

#	Article	IF	Citations
1	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
2	Whole-genome sequencing reveals that variants in the Interleukin 18 Receptor Accessory Protein 3′UTR protect against ALS. Nature Neuroscience, 2022, 25, 433-445.	14.8	16
3	Leveraging fine-mapping and multipopulation training data to improve cross-population polygenic risk scores. Nature Genetics, 2022, 54, 450-458.	21.4	109
4	Combining SNP-to-gene linking strategies to identify disease genes and assess disease omnigenicity. Nature Genetics, 2022, 54, 827-836.	21.4	61
5	Open problems in human trait genetics. Genome Biology, 2022, 23, .	8.8	33
6	Large-scale association analyses identify host factors influencing human gut microbiome composition. Nature Genetics, 2021, 53, 156-165.	21.4	676
7	Utility of polygenic embryo screening for disease depends on the selection strategy. ELife, 2021, 10, .	6.0	34
8	Functionally informed fine-mapping and polygenic localization of complex trait heritability. Nature Genetics, 2020, 52, 1355-1363.	21.4	185
9	A reference map of potential determinants for the human serum metabolome. Nature, 2020, 588, 135-140.	27.8	230
10	Improving the informativeness of Mendelian disease-derived pathogenicity scores for common disease. Nature Communications, 2020, 11, 6258.	12.8	8
11	Estimating variance components in population scale family trees. PLoS Genetics, 2019, 15, e1008124.	3.5	11
12	Functional disease architectures reveal unique biological role of transposable elements. Nature Communications, 2019, 10, 4054.	12.8	14
13	Environment dominates over host genetics in shaping human gut microbiota. Nature, 2018, 555, 210-215.	27.8	1,958
14	Quantitative analysis of population-scale family trees with millions of relatives. Science, 2018, 360, 171-175.	12.6	157
15	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
16	Detecting heritable phenotypes without a model using fast permutation testing for heritability and set-tests. Nature Communications, 2018, 9, 4919.	12.8	6
17	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
18	Prediction of acute myeloid leukaemia risk in healthy individuals. Nature, 2018, 559, 400-404.	27.8	617

#	Article	IF	Citations
19	Host genetics and microbiome associations through the lens of genome wide association studies. Current Opinion in Microbiology, 2018, 44, 9-19.	5.1	33
20	Bread Affects Clinical Parameters and Induces Gut Microbiome-Associated Personal Glycemic Responses. Cell Metabolism, 2017, 25, 1243-1253.e5.	16.2	233
21	RL-SKAT: An Exact and Efficient Score Test for Heritability and Set Tests. Genetics, 2017, 207, 1275-1283.	2.9	19
22	Loss of CD55 in Eculizumab-Responsive Protein-Losing Enteropathy. New England Journal of Medicine, 2017, 377, 87-89.	27.0	41
23	Association testing of bisulfite-sequencing methylation data via a Laplace approximation. Bioinformatics, 2017, 33, i325-i332.	4.1	9
24	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
25	Paradoxical Hypersusceptibility of Drug-resistant M ycobacterium tuberculosis to Î²-lactam Antibiotics. EBioMedicine, 2016, 9, 170-179.	6.1	39
26	Multikernel linear mixed models for complex phenotype prediction. Genome Research, 2016, 26, 969-979.	5.5	57
27	Accurate liability estimation improves power in ascertained case-control studies. Nature Methods, 2015, 12, 332-334.	19.0	36
28	Titin Mutation in Familial Restrictive Cardiomyopathy. International Journal of Cardiology, 2014, 171, 24-30.	1.7	84
29	Further Improvements to Linear Mixed Models for Genome-Wide Association Studies. Scientific Reports, 2014, 4, 6874.	3.3	61