Farhad Hormozdiari

List of Publications by Year
in descending order

36	4,867	23	34
papers	citations	h-index	g-index
		279487	377514

45	45	45	11115
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	DeepNull models non-linear covariate effects to improve phenotypic prediction and association power. Nature Communications, 2022, 13, 241.	5.8	17
2	Combining SNP-to-gene linking strategies to identify disease genes and assess disease omnigenicity. Nature Genetics, 2022, 54, 827-836.	9.4	61
3	Exploiting the GTEx resources to decipher the mechanisms at GWAS loci. Genome Biology, 2021, 22, 49.	3.8	150
4	MARS: leveraging allelic heterogeneity to increase power of association testing. Genome Biology, 2021, 22, 128.	3.8	2
5	Large-scale machine-learning-based phenotyping significantly improves genomic discovery for optic nerve head morphology. American Journal of Human Genetics, 2021, 108, 1217-1230.	2.6	35
6	Identifying causal variants by fine mapping across multiple studies. PLoS Genetics, 2021, 17, e1009733.	1.5	34
7	Annotations capturing cell type-specific TF binding explain a large fraction of disease heritability. Human Molecular Genetics, 2020, 29, 1057-1067.	1.4	16
8	Functionally informed fine-mapping and polygenic localization of complex trait heritability. Nature Genetics, 2020, 52, 1355-1363.	9.4	185
9	Evaluating the informativeness of deep learning annotations for human complex diseases. Nature Communications, 2020, 11, 4703.	5.8	21
10	Extreme Polygenicity of Complex Traits Is Explained by Negative Selection. American Journal of Human Genetics, 2019, 105, 456-476.	2.6	175
11	Functional disease architectures reveal unique biological role of transposable elements. Nature Communications, 2019, 10, 4054.	5.8	14
12	Genes with High Network Connectivity Are Enriched for Disease Heritability. American Journal of Human Genetics, 2019, 104, 896-913.	2.6	46
13	Disease Heritability Enrichment of Regulatory Elements Is Concentrated in Elements with Ancient Sequence Age and Conserved Function across Species. American Journal of Human Genetics, 2019, 104, 611-624.	2.6	68
14	Improving Imputation Accuracy by Inferring Causal Variants in Genetic Studies. Journal of Computational Biology, 2019, 26, 1203-1213.	0.8	0
15	Detecting genome-wide directional effects of transcription factor binding on polygenic disease risk. Nature Genetics, 2018, 50, 1483-1493.	9.4	55
16	Using an atlas of gene regulation across 44 human tissues to inform complex disease- and trait-associated variation. Nature Genetics, 2018, 50, 956-967.	9.4	389
17	Leveraging molecular quantitative trait loci to understand the genetic architecture of diseases and complex traits. Nature Genetics, 2018, 50, 1041-1047.	9.4	154
18	Selection in Europeans on Fatty Acid Desaturases Associated with Dietary Changes. Molecular Biology and Evolution, 2017, 34, 1307-1318.	3.5	90

#	Article	IF	Citations
19	Widespread Allelic Heterogeneity in Complex Traits. American Journal of Human Genetics, 2017, 100, 789-802.	2.6	74
20	Loci associated with skin pigmentation identified in African populations. Science, 2017, 358, .	6.0	260
21	Efficient and Accurate Multiple-Phenotype Regression Method for High Dimensional Data Considering Population Structure. Genetics, 2016, 204, 1379-1390.	1.2	26
22	Using genomic annotations increases statistical power to detect eGenes. Bioinformatics, 2016, 32, i156-i163.	1.8	14
23	Colocalization of GWAS and eQTL Signals Detects Target Genes. American Journal of Human Genetics, 2016, 99, 1245-1260.	2.6	569
24	Chromosome conformation elucidates regulatory relationships in developing human brain. Nature, 2016, 538, 523-527.	13.7	507
25	Multiple testing correction in linear mixed models. Genome Biology, 2016, 17, 62.	3.8	72
26	Imputing Phenotypes for Genome-wide Association Studies. American Journal of Human Genetics, 2016, 99, 89-103.	2.6	40
27	Demographically-Based Evaluation of Genomic Regions under Selection in Domestic Dogs. PLoS Genetics, 2016, 12, e1005851.	1.5	77
28	Hypothalamic transcriptomes of 99 mouse strains reveal trans eQTL hotspots, splicing QTLs and novel non-coding genes. ELife, 2016, 5, .	2.8	35
29	Identification of causal genes for complex traits. Bioinformatics, 2015, 31, i206-i213.	1.8	72
30	Memory efficient assembly of human genome. Journal of Bioinformatics and Computational Biology, 2015, 13, 1550008.	0.3	0
31	Fast and accurate mapping of Complete Genomics reads. Methods, 2015, 79-80, 3-10.	1.9	5
32	Privacy preserving protocol for detecting genetic relatives using rare variants. Bioinformatics, 2014, 30, i204-i211.	1.8	10
33	mrsFAST-Ultra: a compact, SNP-aware mapper for high performance sequencing applications. Nucleic Acids Research, 2014, 42, W494-W500.	6.5	54
34	Integrating Functional Data to Prioritize Causal Variants in Statistical Fine-Mapping Studies. PLoS Genetics, 2014, 10, e1004722.	1.5	475
35	Genome Sequencing Highlights the Dynamic Early History of Dogs. PLoS Genetics, 2014, 10, e1004016.	1.5	481
36	Identifying Causal Variants at Loci with Multiple Signals of Association. Genetics, 2014, 198, 497-508.	1.2	400