Farhad Hormozdiari

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/5085128/publications.pdf

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36 papers	4,867 citations	279798 23 h-index	377865 34 g-index

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

#	Article	IF	Citations
1	Colocalization of GWAS and eQTL Signals Detects Target Genes. American Journal of Human Genetics, 2016, 99, 1245-1260.	6.2	569
2	Chromosome conformation elucidates regulatory relationships in developing human brain. Nature, 2016, 538, 523-527.	27.8	507
3	Genome Sequencing Highlights the Dynamic Early History of Dogs. PLoS Genetics, 2014, 10, e1004016.	3.5	481
4	Integrating Functional Data to Prioritize Causal Variants in Statistical Fine-Mapping Studies. PLoS Genetics, 2014, 10, e1004722.	3.5	475
5	Identifying Causal Variants at Loci with Multiple Signals of Association. Genetics, 2014, 198, 497-508.	2.9	400
6	Using an atlas of gene regulation across 44 human tissues to inform complex disease- and trait-associated variation. Nature Genetics, 2018, 50, 956-967.	21.4	389
7	Loci associated with skin pigmentation identified in African populations. Science, 2017, 358, .	12.6	260
8	Functionally informed fine-mapping and polygenic localization of complex trait heritability. Nature Genetics, 2020, 52, 1355-1363.	21.4	185
9	Extreme Polygenicity of Complex Traits Is Explained by Negative Selection. American Journal of Human Genetics, 2019, 105, 456-476.	6.2	175
10	Leveraging molecular quantitative trait loci to understand the genetic architecture of diseases and complex traits. Nature Genetics, 2018, 50, 1041-1047.	21.4	154
11	Exploiting the GTEx resources to decipher the mechanisms at GWAS loci. Genome Biology, 2021, 22, 49.	8.8	150
12	Selection in Europeans on Fatty Acid Desaturases Associated with Dietary Changes. Molecular Biology and Evolution, 2017, 34, 1307-1318.	8.9	90
13	Demographically-Based Evaluation of Genomic Regions under Selection in Domestic Dogs. PLoS Genetics, 2016, 12, e1005851.	3.5	77
14	Widespread Allelic Heterogeneity in Complex Traits. American Journal of Human Genetics, 2017, 100, 789-802.	6.2	74
15	Identification of causal genes for complex traits. Bioinformatics, 2015, 31, i206-i213.	4.1	72
16	Multiple testing correction in linear mixed models. Genome Biology, 2016, 17, 62.	8.8	72
17	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.	6.2	68
18	Combining SNP-to-gene linking strategies to identify disease genes and assess disease omnigenicity. Nature Genetics, 2022, 54, 827-836.	21.4	61

#	Article	IF	Citations
19	Detecting genome-wide directional effects of transcription factor binding on polygenic disease risk. Nature Genetics, 2018, 50, 1483-1493.	21.4	55
20	mrsFAST-Ultra: a compact, SNP-aware mapper for high performance sequencing applications. Nucleic Acids Research, 2014, 42, W494-W500.	14.5	54
21	Genes with High Network Connectivity Are Enriched for Disease Heritability. American Journal of Human Genetics, 2019, 104, 896-913.	6.2	46
22	Imputing Phenotypes for Genome-wide Association Studies. American Journal of Human Genetics, 2016, 99, 89-103.	6.2	40
23	Large-scale machine-learning-based phenotyping significantly improves genomic discovery for optic nerve head morphology. American Journal of Human Genetics, 2021, 108, 1217-1230.	6.2	35
24	Hypothalamic transcriptomes of 99 mouse strains reveal trans eQTL hotspots, splicing QTLs and novel non-coding genes. ELife, 2016, 5, .	6.0	35
25	Identifying causal variants by fine mapping across multiple studies. PLoS Genetics, 2021, 17, e1009733.	3.5	34
26	Efficient and Accurate Multiple-Phenotype Regression Method for High Dimensional Data Considering Population Structure. Genetics, 2016, 204, 1379-1390.	2.9	26
27	Evaluating the informativeness of deep learning annotations for human complex diseases. Nature Communications, 2020, 11, 4703.	12.8	21
28	DeepNull models non-linear covariate effects to improve phenotypic prediction and association power. Nature Communications, 2022, 13, 241.	12.8	17
29	Annotations capturing cell type-specific TF binding explain a large fraction of disease heritability. Human Molecular Genetics, 2020, 29, 1057-1067.	2.9	16
30	Using genomic annotations increases statistical power to detect eGenes. Bioinformatics, 2016, 32, i156-i163.	4.1	14
31	Functional disease architectures reveal unique biological role of transposable elements. Nature Communications, 2019, 10, 4054.	12.8	14
32	Privacy preserving protocol for detecting genetic relatives using rare variants. Bioinformatics, 2014, 30, i204-i211.	4.1	10
33	Fast and accurate mapping of Complete Genomics reads. Methods, 2015, 79-80, 3-10.	3.8	5
34	MARS: leveraging allelic heterogeneity to increase power of association testing. Genome Biology, 2021, 22, 128.	8.8	2
35	Memory efficient assembly of human genome. Journal of Bioinformatics and Computational Biology, 2015, 13, 1550008.	0.8	0
36	Improving Imputation Accuracy by Inferring Causal Variants in Genetic Studies. Journal of Computational Biology, 2019, 26, 1203-1213.	1.6	0