Fereydoun Hormozdiari

List of Publications by Year
in descending order

43	10,109	201674	265206
papers	citations	27 h-index	42 g-index

50	50	50	17648
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	27.8	1,994
2	Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65.	27.8	991
3	Great ape genetic diversity and population history. Nature, 2013, 499, 471-475.	27.8	768
4	Resolving the complexity of the human genome using single-molecule sequencing. Nature, 2015, 517, 608-611.	27.8	714
5	Personalized copy number and segmental duplication maps using next-generation sequencing. Nature Genetics, 2009, 41, 1061-1067.	21.4	656
6	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	12.8	636
7	deFuse: An Algorithm for Gene Fusion Discovery in Tumor RNA-Seq Data. PLoS Computational Biology, 2011, 7, e1001138.	3.2	477
8	Targeted sequencing identifies 91 neurodevelopmental-disorder risk genes with autism and developmental-disability biases. Nature Genetics, 2017, 49, 515-526.	21.4	443
9	Genomic Patterns of De Novo Mutation in Simplex Autism. Cell, 2017, 171, 710-722.e12.	28.9	308
10	High-resolution comparative analysis of great ape genomes. Science, 2018, 360, .	12.6	304
11	Global diversity, population stratification, and selection of human copy-number variation. Science, 2015, 349, aab3761.	12.6	293
12	Combinatorial algorithms for structural variation detection in high-throughput sequenced genomes. Genome Research, 2009, 19, 1270-1278.	5.5	266
13	The discovery of integrated gene networks for autism and related disorders. Genome Research, 2015, 25, 142-154.	5.5	259
14	mrsFAST: a cache-oblivious algorithm for short-read mapping. Nature Methods, 2010, 7, 576-577.	19.0	248
15	Genome Sequencing of Autism-Affected Families Reveals Disruption of Putative Noncoding Regulatory DNA. American Journal of Human Genetics, 2016, 98, 58-74.	6.2	248
16	Neurodevelopmental disease genes implicated by de novo mutation and copy number variation morbidity. Nature Genetics, 2019, 51, 106-116.	21.4	231
17	Next-generation VariationHunter: combinatorial algorithms for transposon insertion discovery. Bioinformatics, 2010, 26, i350-i357.	4.1	190
18	MoDIL: detecting small indels from clone-end sequencing with mixtures of distributions. Nature Methods, 2009, 6, 473-474.	19.0	115

#	Article	IF	Citations
19	Characteristics of de novo structural changes in the human genome. Genome Research, 2015, 25, 792-801.	5.5	115
20	Detection and characterization of novel sequence insertions using paired-end next-generation sequencing. Bioinformatics, 2010, 26, 1277-1283.	4.1	98
21	Alu repeat discovery and characterization within human genomes. Genome Research, 2011, 21, 840-849.	5.5	94
22	Not All Scale-Free Networks Are Born Equal: The Role of the Seed Graph in PPI Network Evolution. PLoS Computational Biology, 2007, 3, e118.	3.2	77
23	Gorilla genome structural variation reveals evolutionary parallelisms with chimpanzee. Genome Research, 2011, 21, 1640-1649.	5.5	65
24	Simultaneous structural variation discovery among multiple paired-end sequenced genomes. Genome Research, 2011, 21, 2203-2212.	5.5	60
25	Rates and patterns of great ape retrotransposition. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 13457-13462.	7.1	57
26	Whole-Genome Sequencing of Individuals from a Founder Population Identifies Candidate Genes for Asthma. PLoS ONE, 2014, 9, e104396.	2.5	42
27	Dissecting the genetic basis of comorbid epilepsy phenotypes in neurodevelopmental disorders. Genome Medicine, 2019, 11, 65.	8.2	35
28	TAD fusion score: discovery and ranking the contribution of deletions to genome structure. Genome Biology, 2019, 20, 60.	8.8	32
29	Protein-Protein Interaction Network Evaluation for Identifying Potential Drug Targets. Journal of Computational Biology, 2010, 17, 669-684.	1.6	30
30	Discovery of tandem and interspersed segmental duplications using high-throughput sequencing. Bioinformatics, 2019, 35, 3923-3930.	4.1	29
31	Toolkit for automated and rapid discovery of structural variants. Methods, 2017, 129, 3-7.	3.8	28
32	The Effect of Insertions and Deletions on Wirings in Protein-Protein Interaction Networks: A Large-Scale Study. Journal of Computational Biology, 2009, 16, 159-167.	1.6	25
33	Genetic variation associated with increased insecticide resistance in the malaria mosquito, Anopheles coluzzii. Parasites and Vectors, 2018, 11, 225.	2.5	25
34	How bioinformatics and open data can boost basic science in countries and universities with limited resources. Nature Biotechnology, 2019, 37, 324-326.	17.5	25
35	Kevlar: A Mapping-Free Framework for Accurate Discovery of De Novo Variants. IScience, 2019, 18, 28-36.	4.1	20
36	Towards Improved Assessment of Functional Similarity in Large-Scale Screens: A Study on Indel Length. Journal of Computational Biology, 2010, 17, 1-20.	1.6	15

#	Article	IF	Citations
37	Functional disease architectures reveal unique biological role of transposable elements. Nature Communications, 2019, 10, 4054.	12.8	14
38	Nebula: ultra-efficient mapping-free structural variant genotyper. Nucleic Acids Research, 2021, 49, e47-e47.	14.5	14
39	Meltos: multi-sample tumor phylogeny reconstruction for structural variants. Bioinformatics, 2020, 36, 1082-1090.	4.1	9
40	Comparative genome analysis using sample-specific string detection in accurate long reads. Bioinformatics Advances, 2021, 1, .	2.4	5
41	Prediction of Neurodevelopmental Disorders Based on De Novo Coding Variation. Journal of Autism and Developmental Disorders, 2023, 53, 963-976.	2.7	2
42	Combinatorial Approach for Complex Disorder Prediction: Case Study of Neurodevelopmental Disorders. Genetics, 2018, 210, 1483-1495.	2.9	1
43	MAGI-MS: multiple seed-centric module discovery. Bioinformatics Advances, 2022, 2, .	2.4	0