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	Prediction of Neurodevelopmental Disorders Based on De Novo Coding Variation. Journal of Autism and Developmental Disorders, 2023, 53, 963-976.	2.7	2
2	MAGI-MS: multiple seed-centric module discovery. Bioinformatics Advances, 2022, 2, .	2.4	0
3	Nebula: ultra-efficient mapping-free structural variant genotyper. Nucleic Acids Research, 2021, 49, e47-e47.	14.5	14
4	Comparative genome analysis using sample-specific string detection in accurate long reads. Bioinformatics Advances, 2021, 1, .	2.4	5
5	Meltos: multi-sample tumor phylogeny reconstruction for structural variants. Bioinformatics, 2020, 36, 1082-1090.	4.1	9
6	Kevlar: A Mapping-Free Framework for Accurate Discovery of De Novo Variants. IScience, 2019, 18, 28-36.	4.1	20
7	Dissecting the genetic basis of comorbid epilepsy phenotypes in neurodevelopmental disorders. Genome Medicine, 2019, 11, 65.	8.2	35
8	Functional disease architectures reveal unique biological role of transposable elements. Nature Communications, 2019, 10, 4054.	12.8	14
9	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	12.8	636
10	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
11	TAD fusion score: discovery and ranking the contribution of deletions to genome structure. Genome Biology, 2019, 20, 60.	8.8	32
12	Discovery of tandem and interspersed segmental duplications using high-throughput sequencing. Bioinformatics, 2019, 35, 3923-3930.	4.1	29
13	Neurodevelopmental disease genes implicated by de novo mutation and copy number variation morbidity. Nature Genetics, 2019, 51, 106-116.	21.4	231
14	Combinatorial Approach for Complex Disorder Prediction: Case Study of Neurodevelopmental Disorders. Genetics, 2018, 210, 1483-1495.	2.9	1
15	Genetic variation associated with increased insecticide resistance in the malaria mosquito, Anopheles coluzzii. Parasites and Vectors, 2018, 11, 225.	2.5	25
16	High-resolution comparative analysis of great ape genomes. Science, 2018, 360, .	12.6	304
17	Targeted sequencing identifies 91 neurodevelopmental-disorder risk genes with autism and developmental-disability biases. Nature Genetics, 2017, 49, 515-526.	21.4	443
18	Toolkit for automated and rapid discovery of structural variants. Methods, 2017, 129, 3-7.	3.8	28

#	Article	IF	Citations
19	Genomic Patterns of De Novo Mutation in Simplex Autism. Cell, 2017, 171, 710-722.e12.	28.9	308
20	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
21	Global diversity, population stratification, and selection of human copy-number variation. Science, 2015, 349, aab3761.	12.6	293
22	Characteristics of de novo structural changes in the human genome. Genome Research, 2015, 25, 792-801.	5.5	115
23	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	27.8	1,994
24	The discovery of integrated gene networks for autism and related disorders. Genome Research, 2015, 25, 142-154.	5.5	259
25	Resolving the complexity of the human genome using single-molecule sequencing. Nature, 2015, 517, 608-611.	27.8	714
26	Whole-Genome Sequencing of Individuals from a Founder Population Identifies Candidate Genes for Asthma. PLoS ONE, 2014, 9, e104396.	2.5	42
27	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
28	Great ape genetic diversity and population history. Nature, 2013, 499, 471-475.	27.8	768
29	Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65.	27.8	991
30	Alu repeat discovery and characterization within human genomes. Genome Research, 2011, 21, 840-849.	5.5	94
31	deFuse: An Algorithm for Gene Fusion Discovery in Tumor RNA-Seq Data. PLoS Computational Biology, 2011, 7, e1001138.	3.2	477
32	Simultaneous structural variation discovery among multiple paired-end sequenced genomes. Genome Research, 2011, 21, 2203-2212.	5.5	60
33	Gorilla genome structural variation reveals evolutionary parallelisms with chimpanzee. Genome Research, 2011, 21, 1640-1649.	5.5	65
34	mrsFAST: a cache-oblivious algorithm for short-read mapping. Nature Methods, 2010, 7, 576-577.	19.0	248
35	Detection and characterization of novel sequence insertions using paired-end next-generation sequencing. Bioinformatics, 2010, 26, 1277-1283.	4.1	98
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	Protein-Protein Interaction Network Evaluation for Identifying Potential Drug Targets. Journal of Computational Biology, 2010, 17, 669-684.	1.6	30
38	Next-generation VariationHunter: combinatorial algorithms for transposon insertion discovery. Bioinformatics, 2010, 26, i350-i357.	4.1	190
39	Personalized copy number and segmental duplication maps using next-generation sequencing. Nature Genetics, 2009, 41, 1061-1067.	21.4	656
40	MoDIL: detecting small indels from clone-end sequencing with mixtures of distributions. Nature Methods, 2009, 6, 473-474.	19.0	115
41	Combinatorial algorithms for structural variation detection in high-throughput sequenced genomes. Genome Research, 2009, 19, 1270-1278.	5.5	266
42	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
43	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