Naoki Nariai

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/11980218/publications.pdf

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19	1,343	687363 13	794594 19
papers	citations	h-index	g-index

22	22	22	2793
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Rare variant discovery by deep whole-genome sequencing of 1,070 Japanese individuals. Nature Communications, 2015, 6, 8018.	12.8	352
2	Large-Scale Profiling Reveals the Influence of Genetic Variation on Gene Expression in Human Induced Pluripotent Stem Cells. Cell Stem Cell, 2017, 20, 533-546.e7.	11.1	157
3	iPSCORE: A Resource of 222 iPSC Lines Enabling Functional Characterization of Genetic Variation across a Variety of Cell Types. Stem Cell Reports, 2017, 8, 1086-1100.	4.8	147
4	Japonica array: improved genotype imputation by designing a population-specific SNP array with 1070 Japanese individuals. Journal of Human Genetics, 2015, 60, 581-587.	2.3	120
5	iJGVD: an integrative Japanese genome variation database based on whole-genome sequencing. Human Genome Variation, 2015, 2, 15050.	0.7	100
6	Systematic analysis of binding of transcription factors to noncoding variants. Nature, 2021, 591, 147-151.	27.8	89
7	Probabilistic Protein Function Prediction from Heterogeneous Genome-Wide Data. PLoS ONE, 2007, 2, e337.	2.5	84
8	Pancreatic islet chromatin accessibility and conformation reveals distal enhancer networks of type 2 diabetes risk. Nature Communications, 2019, 10, 2078.	12.8	82
9	TIGAR: transcript isoform abundance estimation method with gapped alignment of RNA-Seq data by variational Bayesian inference. Bioinformatics, 2013, 29, 2292-2299.	4.1	36
10	Pgltools: a genomic arithmetic tool suite for manipulation of Hi-C peak and other chromatin interaction data. BMC Bioinformatics, 2017, 18, 207.	2.6	35
11	Systematic genetic analysis of the MHC region reveals mechanistic underpinnings of HLA type associations with disease. ELife, 2019, 8, .	6.0	34
12	Integration of relational and hierarchical network information for protein function prediction. BMC Bioinformatics, 2008, 9, 350.	2.6	33
13	A Bayesian approach for estimating allele-specific expression from RNA-Seq data with diploid genomes. BMC Genomics, 2016, 17, 2.	2.8	22
14	SUGAR: graphical user interface-based data refiner for high-throughput DNA sequencing. BMC Genomics, 2014, 15, 664.	2.8	12
15	Construction of full-length Japanese reference panel of class I HLA genes with single-molecule, real-time sequencing. Pharmacogenomics Journal, 2019, 19, 136-146.	2.0	12
16	Efficient Prioritization of Multiple Causal eQTL Variants via Sparse Polygenic Modeling. Genetics, 2017, 207, 1301-1312.	2.9	10
17	Monitoring of minimal residual disease in early Tâ€cell precursor acute lymphoblastic leukaemia by nextâ€generation sequencing. British Journal of Haematology, 2017, 176, 318-321.	2.5	7
18	HapMonster: A Statistically Unified Approach for Variant Calling and Haplotyping Based on Phase-Informative Reads. Lecture Notes in Computer Science, 2014, , 107-118.	1.3	6

#	Article	IF	Citations
19	Short tandem repeat number estimation from paired-end reads for multiple individuals by considering coalescent tree. BMC Genomics, 2016, 17, 494.	2.8	4