

Naoki Nariai

List of Publications by Year in descending order

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

Version: 2024-02-01

19
papers

1,343
citations

686830

13
h-index

794141

19
g-index

22
all docs

22
docs citations

22
times ranked

2793
citing authors

#	ARTICLE	IF	CITATIONS
1	Systematic analysis of binding of transcription factors to noncoding variants. <i>Nature</i> , 2021, 591, 147-151.	13.7	89
2	Pancreatic islet chromatin accessibility and conformation reveals distal enhancer networks of type 2 diabetes risk. <i>Nature Communications</i> , 2019, 10, 2078.	5.8	82
3	Construction of full-length Japanese reference panel of class I HLA genes with single-molecule, real-time sequencing. <i>Pharmacogenomics Journal</i> , 2019, 19, 136-146.	0.9	12
4	Systematic genetic analysis of the MHC region reveals mechanistic underpinnings of HLA type associations with disease. <i>ELife</i> , 2019, 8, .	2.8	34
5	Large-Scale Profiling Reveals the Influence of Genetic Variation on Gene Expression in Human Induced Pluripotent Stem Cells. <i>Cell Stem Cell</i> , 2017, 20, 533-546.e7.	5.2	157
6	iPSCORE: A Resource of 222 iPSC Lines Enabling Functional Characterization of Genetic Variation across a Variety of Cell Types. <i>Stem Cell Reports</i> , 2017, 8, 1086-1100.	2.3	147
7	Efficient Prioritization of Multiple Causal eQTL Variants via Sparse Polygenic Modeling. <i>Genetics</i> , 2017, 207, 1301-1312.	1.2	10
8	Pgltools: a genomic arithmetic tool suite for manipulation of Hi-C peak and other chromatin interaction data. <i>BMC Bioinformatics</i> , 2017, 18, 207.	1.2	35
9	Monitoring of minimal residual disease in early Tâ€cell precursor acute lymphoblastic leukaemia by nextâ€generation sequencing. <i>British Journal of Haematology</i> , 2017, 176, 318-321.	1.2	7
10	Short tandem repeat number estimation from paired-end reads for multiple individuals by considering coalescent tree. <i>BMC Genomics</i> , 2016, 17, 494.	1.2	4
11	A Bayesian approach for estimating allele-specific expression from RNA-Seq data with diploid genomes. <i>BMC Genomics</i> , 2016, 17, 2.	1.2	22
12	ijGVD: an integrative Japanese genome variation database based on whole-genome sequencing. <i>Human Genome Variation</i> , 2015, 2, 15050.	0.4	100
13	Japonica array: improved genotype imputation by designing a population-specific SNP array with 1070 Japanese individuals. <i>Journal of Human Genetics</i> , 2015, 60, 581-587.	1.1	120
14	Rare variant discovery by deep whole-genome sequencing of 1,070 Japanese individuals. <i>Nature Communications</i> , 2015, 6, 8018.	5.8	352
15	SUGAR: graphical user interface-based data refiner for high-throughput DNA sequencing. <i>BMC Genomics</i> , 2014, 15, 664.	1.2	12
16	HapMonster: A Statistically Unified Approach for Variant Calling and Haplotyping Based on Phase-Informative Reads. <i>Lecture Notes in Computer Science</i> , 2014, , 107-118.	1.0	6
17	TIGAR: transcript isoform abundance estimation method with gapped alignment of RNA-Seq data by variational Bayesian inference. <i>Bioinformatics</i> , 2013, 29, 2292-2299.	1.8	36
18	Integration of relational and hierarchical network information for protein function prediction. <i>BMC Bioinformatics</i> , 2008, 9, 350.	1.2	33

#	ARTICLE	IF	CITATIONS
19	Probabilistic Protein Function Prediction from Heterogeneous Genome-Wide Data. PLoS ONE, 2007, 2, e337.	1.1	84