

Dongwon Lee

List of Publications by Year in descending order

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Version: 2024-02-01

18
papers

3,731
citations

687363

13
h-index

839539

18
g-index

23
all docs

23
docs citations

23
times ranked

7809
citing authors

#	ARTICLE	IF	CITATIONS
1	Sequence-based correction of barcode bias in massively parallel reporter assays. <i>Genome Research</i> , 2021, 31, 1638-1645.	5.5	3
2	Analysis of putative cis-regulatory elements regulating blood pressure variation. <i>Human Molecular Genetics</i> , 2020, 29, 1922-1932.	2.9	7
3	Multiple SCN5A variant enhancers modulate its cardiac gene expression and the QT interval. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 10636-10645.	7.1	22
4	Cardiomyocytes have mosaic patterns of protein expression. <i>Cardiovascular Pathology</i> , 2018, 34, 50-57.	1.6	18
5	Human cardiac cis-regulatory elements, their cognate transcription factors, and regulatory DNA sequence variants. <i>Genome Research</i> , 2018, 28, 1577-1588.	5.5	25
6	Design of a synthetic yeast genome. <i>Science</i> , 2017, 355, 1040-1044.	12.6	464
7	Testing the Ret and Sema3d genetic interaction in mouse enteric nervous system development. <i>Human Molecular Genetics</i> , 2017, 26, 1811-1820.	2.9	8
8	gkmSVM: an R package for gapped-kmer SVM. <i>Bioinformatics</i> , 2016, 32, 2205-2207.	4.1	155
9	Enhancer Variants Synergistically Drive Dysfunction of a Gene Regulatory Network In Hirschsprung Disease. <i>Cell</i> , 2016, 167, 355-368.e10.	28.9	112
10	Rare coding TTN variants are associated with electrocardiographic QT interval in the general population. <i>Scientific Reports</i> , 2016, 6, 28356.	3.3	6
11	LS-GKM: a new gkm-SVM for large-scale datasets. <i>Bioinformatics</i> , 2016, 32, 2196-2198.	4.1	126
12	A method to predict the impact of regulatory variants from DNA sequence. <i>Nature Genetics</i> , 2015, 47, 955-961.	21.4	416
13	Enhanced Regulatory Sequence Prediction Using Gapped k-mer Features. <i>PLoS Computational Biology</i> , 2014, 10, e1003711.	3.2	426
14	Divergent functions of hematopoietic transcription factors in lineage priming and differentiation during erythro-megakaryopoiesis. <i>Genome Research</i> , 2014, 24, 1932-1944.	5.5	88
15	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364.	27.8	1,444
16	kmer-SVM: a web server for identifying predictive regulatory sequence features in genomic data sets. <i>Nucleic Acids Research</i> , 2013, 41, W544-W556.	14.5	118
17	Integration of ChIP-seq and machine learning reveals enhancers and a predictive regulatory sequence vocabulary in melanocytes. <i>Genome Research</i> , 2012, 22, 2290-2301.	5.5	64
18	Discriminative prediction of mammalian enhancers from DNA sequence. <i>Genome Research</i> , 2011, 21, 2167-2180.	5.5	222