Dongwon Lee

List of Publications by Year
in descending order

18 papers	**3,731** citations	686830 **13** h-index	839053 **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. Genome Research, 2021, 31, 1638-1645.	2.4	3
2	Analysis of putative cis-regulatory elements regulating blood pressure variation. Human Molecular Genetics, 2020, 29, 1922-1932.	1.4	7
3	Multiple SCN5A variant enhancers modulate its cardiac gene expression and the QT interval. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 10636-10645.	3.3	22
4	Cardiomyocytes have mosaic patterns of protein expression. Cardiovascular Pathology, 2018, 34, 50-57.	0.7	18
5	Human cardiac *cis*-regulatory elements, their cognate transcription factors, and regulatory DNA sequence variants. Genome Research, 2018, 28, 1577-1588.	2.4	25
6	Design of a synthetic yeast genome. Science, 2017, 355, 1040-1044.	6.0	464
7	Testing the Ret and Sema3d genetic interaction in mouse enteric nervous system development. Human Molecular Genetics, 2017, 26, 1811-1820.	1.4	8
8	gkmSVM: an R package for gapped-kmer SVM. Bioinformatics, 2016, 32, 2205-2207.	1.8	155
9	Enhancer Variants Synergistically Drive Dysfunction of a Gene Regulatory Network In Hirschsprung Disease. Cell, 2016, 167, 355-368.e10.	13.5	112
10	Rare coding TTN variants are associated with electrocardiographic QT interval in the general population. Scientific Reports, 2016, 6, 28356.	1.6	6
11	LS-GKM: a new gkm-SVM for large-scale datasets. Bioinformatics, 2016, 32, 2196-2198.	1.8	126
12	A method to predict the impact of regulatory variants from DNA sequence. Nature Genetics, 2015, 47, 955-961.	9.4	416
13	Enhanced Regulatory Sequence Prediction Using Gapped k-mer Features. PLoS Computational Biology, 2014, 10, e1003711.	1.5	426
14	Divergent functions of hematopoietic transcription factors in lineage priming and differentiation during erythro-megakaryopoiesis. Genome Research, 2014, 24, 1932-1944.	2.4	88
15	A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364.	13.7	1,444
16	kmer-SVM: a web server for identifying predictive regulatory sequence features in genomic data sets. Nucleic Acids Research, 2013, 41, W544-W556.	6.5	118
17	Integration of ChIP-seq and machine learning reveals enhancers and a predictive regulatory sequence vocabulary in melanocytes. Genome Research, 2012, 22, 2290-2301.	2.4	64
18	Discriminative prediction of mammalian enhancers from DNA sequence. Genome Research, 2011, 21, 2167-2180.	2.4	222