David R Kelley

List of Publications by Year
in descending order

37 papers	**17,015** citations	293460 **24** h-index	511568 **30** g-index
57 all docs	**57** docs citations	**57** times ranked	**38949** citing authors

#	Article	IF	Citations
1	Novel insights from a multiomics dissection of the Hayflick limit. ELife, 2022, 11, .	2.8	38
2	Semisupervised adversarial neural networks for single-cell classification. Genome Research, 2021, 31, 1781-1793.	2.4	60
3	Differentiation reveals latent features of aging and an energy barrier in murine myogenesis. Cell Reports, 2021, 35, 109046.	2.9	23
4	Leveraging supervised learning for functionallyÂinformed fine-mapping of cis-eQTLs identifies an additional 20,913 putative causal eQTLs. Nature Communications, 2021, 12, 3394.	5.8	44
5	The landscape of alternative polyadenylation in single cells of the developing mouse embryo. Nature Communications, 2021, 12, 5101.	5.8	33
6	Effective gene expression prediction from sequence by integrating long-range interactions. Nature Methods, 2021, 18, 1196-1203.	9.0	385
7	Predicting 3D genome folding from DNA sequence with Akita. Nature Methods, 2020, 17, 1111-1117.	9.0	149
8	Cross-species regulatory sequence activity prediction. PLoS Computational Biology, 2020, 16, e1008050.	1.5	116
9	Evaluating the informativeness of deep learning annotations for human complex diseases. Nature Communications, 2020, 11, 4703.	5.8	21
10	Solo: Doublet Identification in Single-Cell RNA-Seq via Semi-Supervised Deep Learning. Cell Systems, 2020, 11, 95-101.e5.	2.9	104
11	Cross-species regulatory sequence activity prediction. , 2020, 16, e1008050.		0
12	Cross-species regulatory sequence activity prediction. , 2020, 16, e1008050.		0
13	Cross-species regulatory sequence activity prediction. , 2020, 16, e1008050.		0
14	Cross-species regulatory sequence activity prediction. , 2020, 16, e1008050.		0
15	Cross-species regulatory sequence activity prediction. , 2020, 16, e1008050.		0
16	Cross-species regulatory sequence activity prediction. , 2020, 16, e1008050.		0
17	Cross-species regulatory sequence activity prediction. , 2020, 16, e1008050.		0
18	Cross-species regulatory sequence activity prediction. , 2020, 16, e1008050.		0

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19	Murine single-cell RNA-seq reveals cell-identity- and tissue-specific trajectories of aging. Genome Research, 2019, 29, 2088-2103.	2.4	132
20	Genetic determinants and epigenetic effects of pioneer-factor occupancy. Nature Genetics, 2018, 50, 250-258.	9.4	139
21	Sequential regulatory activity prediction across chromosomes with convolutional neural networks. Genome Research, 2018, 28, 739-750.	2.4	324
22	Detecting genome-wide directional effects of transcription factor binding on polygenic disease risk. Nature Genetics, 2018, 50, 1483-1493.	9.4	55
23	Recurrent noncoding regulatory mutations in pancreatic ductal adenocarcinoma. Nature Genetics, 2017, 49, 825-833.	9.4	55
24	lncRNA requirements for mouse acute myeloid leukemia and normal differentiation. ELife, 2017, 6, .	2.8	54
25	Widespread RNA binding by chromatin-associated proteins. Genome Biology, 2016, 17, 28.	3.8	197
26	Basset: learning the regulatory code of the accessible genome with deep convolutional neural networks. Genome Research, 2016, 26, 990-999.	2.4	790
27	Transposable elements modulate human RNA abundance and splicing via specific RNA-protein interactions. Genome Biology, 2014, 15, 537.	3.8	88
28	Topological organization of multichromosomal regions by the long intergenic noncoding RNA Firre. Nature Structural and Molecular Biology, 2014, 21, 198-206.	3.6	565
29	Long noncoding RNAs regulate adipogenesis. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 3387-3392.	3.3	371
30	Transcriptional and Epigenetic Dynamics during Specification of Human Embryonic Stem Cells. Cell, 2013, 153, 1149-1163.	13.5	419
31	Gene prediction with Glimmer for metagenomic sequences augmented by classification and clustering. Nucleic Acids Research, 2012, 40, e9-e9.	6.5	150
32	Transposable elements reveal a stem cell-specific class of long noncoding RNAs. Genome Biology, 2012, 13, R107.	13.9	462
33	Differential gene and transcript expression analysis of RNA-seq experiments with TopHat and Cufflinks. Nature Protocols, 2012, 7, 562-578.	5.5	11,433
34	Extracting Between-Pathway Models from E-MAP Interactions Using Expected Graph Compression. Journal of Computational Biology, 2011, 18, 379-390.	0.8	4
35	Clustering metagenomic sequences with interpolated Markov models. BMC Bioinformatics, 2010, 11, 544.	1.2	90
36	Quake: quality-aware detection and correction of sequencing errors. Genome Biology, 2010, 11, R116.	13.9	470

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37	Detection and correction of false segmental duplications caused by genome mis-assembly. Genome Biology, 2010, 11, R28.	13.9	96