

David R Kelley

List of Publications by Citations

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Version: 2024-04-28

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

49
papers

11,864
citations

23
h-index

57
g-index

57
ext. papers

15,471
ext. citations

17
avg, IF

6.34
L-index

#	Paper	IF	Citations
49	Differential gene and transcript expression analysis of RNA-seq experiments with TopHat and Cufflinks. <i>Nature Protocols</i> , 2012 , 7, 562-78	18.8	8342
48	Basset: learning the regulatory code of the accessible genome with deep convolutional neural networks. <i>Genome Research</i> , 2016 , 26, 990-9	9.7	500
47	Topological organization of multichromosomal regions by the long intergenic noncoding RNA Firre. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 198-206	17.6	455
46	Quake: quality-aware detection and correction of sequencing errors. <i>Genome Biology</i> , 2010 , 11, R116	18.3	404
45	Transposable elements reveal a stem cell-specific class of long noncoding RNAs. <i>Genome Biology</i> , 2012 , 13, R107	18.3	361
44	Transcriptional and epigenetic dynamics during specification of human embryonic stem cells. <i>Cell</i> , 2013 , 153, 1149-63	56.2	332
43	Long noncoding RNAs regulate adipogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 3387-92	11.5	315
42	Widespread RNA binding by chromatin-associated proteins. <i>Genome Biology</i> , 2016 , 17, 28	18.3	143
41	Sequential regulatory activity prediction across chromosomes with convolutional neural networks. <i>Genome Research</i> , 2018 , 28, 739-750	9.7	134
40	Gene prediction with Glimmer for metagenomic sequences augmented by classification and clustering. <i>Nucleic Acids Research</i> , 2012 , 40, e9	20.1	120
39	Genetic determinants and epigenetic effects of pioneer-factor occupancy. <i>Nature Genetics</i> , 2018 , 50, 250-258	36.3	85
38	Clustering metagenomic sequences with interpolated Markov models. <i>BMC Bioinformatics</i> , 2010 , 11, 544	3.6	75
37	Detection and correction of false segmental duplications caused by genome mis-assembly. <i>Genome Biology</i> , 2010 , 11, R28	18.3	65
36	Transposable elements modulate human RNA abundance and splicing via specific RNA-protein interactions. <i>Genome Biology</i> , 2014 , 15, 537	18.3	64
35	Murine single-cell RNA-seq reveals cell-identity- and tissue-specific trajectories of aging. <i>Genome Research</i> , 2019 , 29, 2088-2103	9.7	55
34	Recurrent noncoding regulatory mutations in pancreatic ductal adenocarcinoma. <i>Nature Genetics</i> , 2017 , 49, 825-833	36.3	41
33	Predicting 3D genome folding from DNA sequence with Akita. <i>Nature Methods</i> , 2020 , 17, 1111-1117	21.6	39

32	Detecting genome-wide directional effects of transcription factor binding on polygenic disease risk. <i>Nature Genetics</i> , 2018 , 50, 1483-1493	36.3	34
31	Solo: Doublet Identification in Single-Cell RNA-Seq via Semi-Supervised Deep Learning. <i>Cell Systems</i> , 2020 , 11, 95-101.e5	10.6	31
30	lncRNA requirements for mouse acute myeloid leukemia and normal differentiation. <i>ELife</i> , 2017 , 6,	8.9	31
29	Cross-species regulatory sequence activity prediction. <i>PLoS Computational Biology</i> , 2020 , 16, e1008050	5	25
28	Effective gene expression prediction from sequence by integrating long-range interactions. <i>Nature Methods</i> , 2021 , 18, 1196-1203	21.6	24
27	Basset: Learning the regulatory code of the accessible genome with deep convolutional neural networks		19
26	Semisupervised adversarial neural networks for single-cell classification. <i>Genome Research</i> , 2021 , 31, 1781-1793	9.7	14
25	Leveraging supervised learning for functionally-informed fine-mapping of cis-eQTLs identifies an additional 20,913 putative causal eQTLs. <i>Nature Communications</i> , 2021 , 12, 3394	17.4	9
24	Effective gene expression prediction from sequence by integrating long-range interactions		8
23	Sequential regulatory activity prediction across chromosomes with convolutional neural networks		7
22	Evaluating the informativeness of deep learning annotations for human complex diseases. <i>Nature Communications</i> , 2020 , 11, 4703	17.4	7
21	Detecting genome-wide directional effects of transcription factor binding on polygenic disease risk		6
20	Cross-species regulatory sequence activity prediction		6
19	A murine aging cell atlas reveals cell identity and tissue-specific trajectories of aging		5
18	scNym: Semi-supervised adversarial neural networks for single cell classification		4
17	Predicting 3D genome folding from DNA sequence		4
16	Differentiation reveals latent features of aging and an energy barrier in murine myogenesis. <i>Cell Reports</i> , 2021 , 35, 109046	10.6	4
15	The landscape of alternative polyadenylation in single cells of the developing mouse embryo. <i>Nature Communications</i> , 2021 , 12, 5101	17.4	4

14	Extracting between-pathway models from E-MAP interactions using expected graph compression. <i>Journal of Computational Biology</i> , 2011 , 18, 379-90	1.7	3
13	Evaluating the informativeness of deep learning annotations for human complex diseases		3
12	Differentiation reveals the plasticity of age-related change in murine muscle progenitors		2
11	Leveraging supervised learning for functionally-informed fine-mapping of cis-eQTLs identifies an additional 20,913 putative causal eQTLs		2
10	Solo: doublet identification via semi-supervised deep learning		1
9	The landscape of alternative polyadenylation in single cells of the developing mouse embryo		1
8	Cross-species regulatory sequence activity prediction 2020 , 16, e1008050		
7	Cross-species regulatory sequence activity prediction 2020 , 16, e1008050		
6	Cross-species regulatory sequence activity prediction 2020 , 16, e1008050		
5	Cross-species regulatory sequence activity prediction 2020 , 16, e1008050		
4	Cross-species regulatory sequence activity prediction 2020 , 16, e1008050		
3	Cross-species regulatory sequence activity prediction 2020 , 16, e1008050		
2	Cross-species regulatory sequence activity prediction 2020 , 16, e1008050		
1	Cross-species regulatory sequence activity prediction 2020 , 16, e1008050		