David A Knowles

List of Publications by Year
in descending order

27 papers	4,862 citations	361413 20 h-index	526287 27 g-index
42 all docs	42 docs citations	42 times ranked	12091 citing authors

#	Article	IF	Citations
1	Mapping cis- and trans-regulatory effects across multiple tissues in twins. Nature Genetics, 2012, 44, 1084-1089.	21.4	701
2	Opportunities and challenges for transcriptome-wide association studies. Nature Genetics, 2019, 51, 592-599.	21.4	592
3	RNA splicing is a primary link between genetic variation and disease. Science, 2016, 352, 600-604.	12.6	574
4	Annotation-free quantification of RNA splicing using LeafCutter. Nature Genetics, 2018, 50, 151-158.	21.4	520
5	Therapeutic reduction of ataxin-2 extends lifespan and reduces pathology in TDP-43 mice. Nature, 2017, 544, 367-371.	27.8	422
6	Batch effects and the effective design of single-cell gene expression studies. Scientific Reports, 2017, 7, 39921.	3.3	275
7	Molecular Choreography of Acute Exercise. Cell, 2020, 181, 1112-1130.e16.	28.9	261
8	Distinct Epigenomic Features in End-Stage Failing Human Hearts. Circulation, 2011, 124, 2411-2422.	1.6	245
9	Landscape of stimulation-responsive chromatin across diverse human immune cells. Nature Genetics, 2019, 51, 1494-1505.	21.4	196
10	Distinct Classes of Complex Structural Variation Uncovered across Thousands of Cancer Genome Graphs. Cell, 2020, 183, 197-210.e32.	28.9	141
11	Allele-specific expression reveals interactions between genetic variation and environment. Nature Methods, 2017, 14, 699-702.	19.0	135
12	Inferring Relevant Cell Types for Complex Traits by Using Single-Cell Gene Expression. American Journal of Human Genetics, 2017, 101, 686-699.	6.2	102
13	Determining the genetic basis of anthracycline-cardiotoxicity by molecular response QTL mapping in induced cardiomyocytes. ELife, 2018, 7, .	6.0	94
14	An Efficient Multiple-Testing Adjustment for eQTL Studies that Accounts for Linkage Disequilibrium between Variants. American Journal of Human Genetics, 2016, 98, 216-224.	6.2	91
15	Impact of the X Chromosome and sex on regulatory variation. Genome Research, 2016, 26, 768-777.	5.5	88
16	Fixed-Form Variational Posterior Approximation through Stochastic Linear Regression. Bayesian Analysis, 2013, 8, .	3.0	65
17	Transcriptome Sequencing of a Large Human Family Identifies the Impact of Rare Noncoding Variants. American Journal of Human Genetics, 2014, 95, 245-256.	6.2	63
18	Allelic Expression of Deleterious Protein-Coding Variants across Human Tissues. PLoS Genetics, 2014, 10, e1004304.	3.5	60

#	Article	IF	Citations
19	Genetic regulation of gene expression and splicing during a 10-year period of human aging. Genome Biology, 2019, 20, 230.	8.8	57
20	A human lung tumor microenvironment interactome identifies clinically relevant cell-type cross-talk. Genome Biology, 2020, 21, 107.	8.8	33
21	Interactions between genetic variation and cellular environment in skeletal muscle gene expression. PLoS ONE, 2018, 13, e0195788.	2.5	18
22	Small RNA Sequencing in Cells and Exosomes Identifies eQTLs and 14q32 as a Region of Active Export. G3: Genes, Genomes, Genetics, 2017, 7, 31-39.	1.8	16
23	Pitman Yor Diffusion Trees for Bayesian Hierarchical Clustering. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2015, 37, 271-289.	13.9	11
24	An integrated approach to identify environmental modulators of genetic risk factors for complex traits. American Journal of Human Genetics, 2021, 108, 1866-1879.	6.2	9
25	Relational Learning and Network Modelling Using Infinite Latent Attribute Models. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2015, 37, 462-474.	13.9	8
26	Welch-weighted Egger regression reduces false positives due to correlated pleiotropy in Mendelian randomization. American Journal of Human Genetics, 2021, 108, 2319-2335.	6.2	8
27	Sparse discriminative latent characteristics for predicting cancer drug sensitivity from genomic features. PLoS Computational Biology, 2019, 15, e1006743.	3.2	4