# David A Knowles

List of Publications by Year
in descending order



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|---|---|---|---|
| 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 | 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 |
| 2 | 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 |
| 3 | Distinct Classes of Complex Structural Variation Uncovered across Thousands of Cancer Genome Graphs. Cell, 2020, 183, 197-210.e32. | 28.9 | 141 |
| 4 | A human lung tumor microenvironment interactome identifies clinically relevant cell-type cross-talk. Genome Biology, 2020, 21, 107. | 8.8 | 33 |
| 5 | Molecular Choreography of Acute Exercise. Cell, 2020, 181, 1112-1130.e16. | 28.9 | 261 |
| 6 | Genetic regulation of gene expression and splicing during a 10-year period of human aging. Genome Biology, 2019, 20, 230. | 8.8 | 57 |
| 7 | Sparse discriminative latent characteristics for predicting cancer drug sensitivity from genomic features. PLoS Computational Biology, 2019, 15, e1006743. | 3.2 | 4 |
| 8 | Opportunities and challenges for transcriptome-wide association studies. Nature Genetics, 2019, 51, 592-599. | 21.4 | 592 |
| 9 | Landscape of stimulation-responsive chromatin across diverse human immune cells. Nature Genetics, 2019, 51, 1494-1505. | 21.4 | 196 |
| 10 | Annotation-free quantification of RNA splicing using LeafCutter. Nature Genetics, 2018, 50, 151-158. | 21.4 | 520 |
| 11 | Interactions between genetic variation and cellular environment in skeletal muscle gene expression. PLoS ONE, 2018, 13, e0195788. | 2.5 | 18 |
| 12 | Determining the genetic basis of anthracycline-cardiotoxicity by molecular response QTL mapping in induced cardiomyocytes. ELife, 2018, 7, . | 6.0 | 94 |
| 13 | Therapeutic reduction of ataxin-2 extends lifespan and reduces pathology in TDP-43 mice. Nature, 2017, 544, 367-371. | 27.8 | 422 |
| 14 | Allele-specific expression reveals interactions between genetic variation and environment. Nature Methods, 2017, 14, 699-702. | 19.0 | 135 |
| 15 | Batch effects and the effective design of single-cell gene expression studies. Scientific Reports, 2017, 7, 39921. | 3.3 | 275 |
| 16 | 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 |
| 17 | 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 |
| 18 | Impact of the X Chromosome and sex on regulatory variation. Genome Research, 2016, 26, 768-777. | 5.5 | 88 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | RNA splicing is a primary link between genetic variation and disease. Science, 2016, 352, 600-604. | 12.6 | 574 |
| 20 | 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 |
| 21 | 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 |
| 22 | Pitman Yor Diffusion Trees for Bayesian Hierarchical Clustering. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2015, 37, 271-289. | 13.9 | 11 |
| 23 | Allelic Expression of Deleterious Protein-Coding Variants across Human Tissues. PLoS Genetics, 2014, 10, e1004304. | 3.5 | 60 |
| 24 | 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 |
| 25 | Fixed-Form Variational Posterior Approximation through Stochastic Linear Regression. Bayesian Analysis, 2013, 8, . | 3.0 | 65 |
| 26 | Mapping cis- and trans-regulatory effects across multiple tissues in twins. Nature Genetics, 2012, 44, 1084-1089. | 21.4 | 701 |
| 27 | Distinct Epigenomic Features in End-Stage Failing Human Hearts. Circulation, 2011, 124, 2411-2422. | 1.6 | 245 |