

# Robin D Dowell

## List of Publications by Year in descending order

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Version: 2024-02-01

69  
papers

3,753  
citations

218592

26  
h-index

149623

56  
g-index

82  
all docs

82  
docs citations

82  
times ranked

6816  
citing authors

#	ARTICLE	IF	CITATIONS
1	Protocol variations in run-on transcription dataset preparation produce detectable signatures in sequencing libraries. <i>BMC Genomics</i> , 2022, 23, 187.	1.2	5
2	Suppression of p53 response by targeting p53-Mediator binding with a stapled peptide. <i>Cell Reports</i> , 2022, 39, 110630.	2.9	5
3	Metabolic and Transcriptomic Effects of Mediator Kinase Inhibition on the Interferon Response in Down Syndrome. <i>FASEB Journal</i> , 2022, 36, .	0.2	0
4	Competition between PRC2.1 and 2.2 subcomplexes regulates PRC2 chromatin occupancy in human stem cells. <i>Molecular Cell</i> , 2021, 81, 488-501.e9.	4.5	38
5	The MUC5B-associated variant rs35705950 resides within an enhancer subject to lineage- and disease-dependent epigenetic remodeling. <i>JCI Insight</i> , 2021, 6, .	2.3	21
6	Application of a bioinformatic pipeline to RNA-seq data identifies novel virus-like sequence in human blood. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	4
7	Nuclear mechanosensing drives chromatin remodelling in persistently activated fibroblasts. <i>Nature Biomedical Engineering</i> , 2021, 5, 1485-1499.	11.6	71
8	Transcription factor enrichment analysis (TFEA) quantifies the activity of multiple transcription factors from a single experiment. <i>Communications Biology</i> , 2021, 4, 661.	2.0	21
9	The $\hat{\tau}$ 40p53 isoform inhibits p53-dependent eRNA transcription and enables regulation by signal-specific transcription factors during p53 activation. <i>PLoS Biology</i> , 2021, 19, e3001364.	2.6	14
10	Characterization of Global Gene Expression, Regulation of Metal Ions, and Infection Outcomes in Immune-Competent 129S6 Mouse Macrophages. <i>Infection and Immunity</i> , 2021, 89, e0027321.	1.0	2
11	Chromatin remodeling due to degradation of citrate carrier impairs osteogenesis of aged mesenchymal stem cells. <i>Nature Aging</i> , 2021, 1, 810-825.	5.3	37
12	Deconvolution of multiplexed transcriptional responses to wood smoke particles defines rapid aryl hydrocarbon receptor signaling dynamics. <i>Journal of Biological Chemistry</i> , 2021, 297, 101147.	1.6	9
13	Escape of hair follicle stem cells causes stem cell exhaustion during aging. <i>Nature Aging</i> , 2021, 1, 889-903.	5.3	31
14	Lessons from eRNAs: understanding transcriptional regulation through the lens of nascent RNAs. <i>Transcription</i> , 2020, 11, 3-18.	1.7	13
15	Selective inhibition of CDK7 reveals high-confidence targets and new models for TFIIF function in transcription. <i>Genes and Development</i> , 2020, 34, 1452-1473.	2.7	47
16	Remodeling of Zn <sup>2+</sup> homeostasis upon differentiation of mammary epithelial cells. <i>Metallomics</i> , 2020, 12, 346-362.	1.0	7
17	Combining signal and sequence to detect RNA polymerase initiation in ATAC-seq data. <i>PLoS ONE</i> , 2020, 15, e0232332.	1.1	1
18	TFIID Enables RNA Polymerase II Promoter-Proximal Pausing. <i>Molecular Cell</i> , 2020, 78, 785-793.e8.	4.5	55

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19	Applying knowledge-driven mechanistic inference to toxicogenomics. <i>Toxicology in Vitro</i> , 2020, 66, 104877.	1.1	11
20	Systems genetics analysis of the LXS recombinant inbred mouse strains: Genetic and molecular insights into acute ethanol tolerance. <i>PLoS ONE</i> , 2020, 15, e0240253.	1.1	1
21	Title is missing!. , 2020, 15, e0240253.		0
22	Title is missing!. , 2020, 15, e0240253.		0
23	Title is missing!. , 2020, 15, e0240253.		0
24	Title is missing!. , 2020, 15, e0240253.		0
25	Transcriptional Responses to IFN- $\beta$ Require Mediator Kinase-Dependent Pause Release and Mechanistically Distinct CDK8 and CDK19 Functions. <i>Molecular Cell</i> , 2019, 76, 485-499.e8.	4.5	52
26	Nascent transcript analysis of glucocorticoid crosstalk with TNF defines primary and cooperative inflammatory repression. <i>Genome Research</i> , 2019, 29, 1753-1765.	2.4	36
27	Identification and characterization of a novel anti-inflammatory lipid isolated from <i>Mycobacterium vaccae</i> , a soil-derived bacterium with immunoregulatory and stress resilience properties. <i>Psychopharmacology</i> , 2019, 236, 1653-1670.	1.5	28
28	Heat shock in <i>C. elegans</i> induces downstream of gene transcription and accumulation of double-stranded RNA. <i>PLoS ONE</i> , 2019, 14, e0206715.	1.1	14
29	Two-stage ML Classifier for Identifying Host Protein Targets of the Dengue Protease. , 2019, , .		2
30	Enhancer RNA profiling predicts transcription factor activity. <i>Genome Research</i> , 2018, 28, 334-344.	2.4	88
31	Genome-wide dose-dependent inhibition of histone deacetylases studies reveal their roles in enhancer remodeling and suppression of oncogenic super-enhancers. <i>Nucleic Acids Research</i> , 2018, 46, 1756-1776.	6.5	58
32	PI(3,5)P <sub>2</sub> controls vacuole potassium transport to support cellular osmoregulation. <i>Molecular Biology of the Cell</i> , 2018, 29, 1718-1731.	0.9	19
33	miR-MaGiC improves quantification accuracy for small RNA-seq. <i>BMC Research Notes</i> , 2018, 11, 296.	0.6	9
34	Detecting Differential Transcription Factor Activity from ATAC-Seq Data. <i>Molecules</i> , 2018, 23, 1136.	1.7	33
35	Control of inducible gene expression links cohesin to hematopoietic progenitor self-renewal and differentiation. <i>Nature Immunology</i> , 2018, 19, 932-941.	7.0	175
36	An Annotation Agnostic Algorithm for Detecting Nascent RNA Transcripts in GRO-Seq. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 1070-1081.	1.9	19

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37	RNA Pol II transcription model and interpretation of GRO-seq data. <i>Journal of Mathematical Biology</i> , 2017, 74, 77-97.	0.8	9
38	Model based heritability scores for high-throughput sequencing data. <i>BMC Bioinformatics</i> , 2017, 18, 143.	1.2	11
39	A Kinase-Independent Role for Cyclin-Dependent Kinase 19 in p53 Response. <i>Molecular and Cellular Biology</i> , 2017, 37, .	1.1	57
40	Transcriptome and Functional Profile of Cardiac Myocytes Is Influenced by Biological Sex. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	31
41	Human TFIIH Kinase CDK7 Regulates Transcription-Associated Chromatin Modifications. <i>Cell Reports</i> , 2017, 20, 1173-1186.	2.9	123
42	A generative model for the behavior of RNA polymerase. <i>Bioinformatics</i> , 2017, 33, 227-234.	1.8	46
43	The Influence of Polyploidy on the Evolution of Yeast Grown in a Sub-Optimal Carbon Source. <i>Molecular Biology and Evolution</i> , 2017, 34, 2690-2703.	3.5	31
44	Discriminating between HuR and TTP binding sites using the k-spectrum kernel method. <i>PLoS ONE</i> , 2017, 12, e0174052.	1.1	15
45	Identification of Mediator Kinase Substrates in Human Cells using Cortistatin A and Quantitative Phosphoproteomics. <i>Cell Reports</i> , 2016, 15, 436-450.	2.9	117
46	Genome characterization of the selected long- and short-sleep mouse lines. <i>Mammalian Genome</i> , 2016, 27, 574-586.	1.0	6
47	Survey of cryptic unstable transcripts in yeast. <i>BMC Genomics</i> , 2016, 17, 305.	1.2	13
48	A Modeling Framework for Generation of Positional and Temporal Simulations of Transcriptional Regulation. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2016, 13, 459-471.	1.9	0
49	Foxc1 reinforces quiescence in self-renewing hair follicle stem cells. <i>Science</i> , 2016, 351, 613-617.	6.0	109
50	A trans-acting Variant within the Transcription Factor RIM101 Interacts with Genetic Background to Determine its Regulatory Capacity. <i>PLoS Genetics</i> , 2016, 12, e1005746.	1.5	11
51	Quantitative Trait Locus Mapping of Acute Functional Tolerance in the LXS Recombinant Inbred Strains. <i>Alcoholism: Clinical and Experimental Research</i> , 2015, 39, 611-620.	1.4	9
52	Prolonged Cre expression driven by the $\beta$ -myosin heavy chain promoter can be cardiotoxic. <i>Journal of Molecular and Cellular Cardiology</i> , 2015, 86, 54-61.	0.9	90
53	Polyploidy can drive rapid adaptation in yeast. <i>Nature</i> , 2015, 519, 349-352.	13.7	376
54	Inferring ancestry in mouse genomes using a hidden Markov model. , 2014, , .		0

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55	FStitch. , 2014, , .		8
56	CodaChrome: a tool for the visualization of proteome conservation across all fully sequenced bacterial genomes. BMC Genomics, 2014, 15, 65.	1.2	3
57	Global analysis of p53-regulated transcription identifies its direct targets and unexpected regulatory mechanisms. ELife, 2014, 3, e02200.	2.8	205
58	HIF1A Employs CDK8-Mediator to Stimulate RNAPII Elongation in Response to Hypoxia. Cell, 2013, 153, 1327-1339.	13.5	300
59	The similarity of gene expression between human and mouse tissues. Genome Biology, 2011, 12, 101.	13.9	25
60	Discovering Regulatory Overlapping RNA Transcripts. Journal of Computational Biology, 2011, 18, 295-303.	0.8	1
61	Transcription factor binding variation in the evolution of gene regulation. Trends in Genetics, 2010, 26, 468-475.	2.9	60
62	Feed-Forward Regulation of a Cell Fate Determinant by an RNA-Binding Protein Generates Asymmetry in Yeast. Genetics, 2010, 185, 513-522.	1.2	32
63	Genotype to Phenotype: A Complex Problem. Science, 2010, 328, 469-469.	6.0	358
64	Discovering Regulatory Overlapping RNA Transcripts. Lecture Notes in Computer Science, 2010, , 110-122.	1.0	1
65	Toggle involving <i>cis</i> -interfering noncoding RNAs controls variegated gene expression in yeast. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 18321-18326.	3.3	174
66	Tissue-specific transcriptional regulation has diverged significantly between human and mouse. Nature Genetics, 2007, 39, 730-732.	9.4	491
67	High-resolution computational models of genome binding events. Nature Biotechnology, 2006, 24, 963-970.	9.4	82
68	Automated discovery of functional generality of human gene expression programs. PLoS Computational Biology, 2005, preprint, e148.	1.5	0
69	The Naturally Occurring $\beta$ 40p53 Isoform Inhibits eRNA Transcription and Enables Context-Specific Regulation During p53 Activation. SSRN Electronic Journal, 0, , .	0.4	1