

Robin D Dowell

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1276486/publications.pdf>

Version: 2024-02-01

69
papers

3,753
citations

218662

26
h-index

149686

56
g-index

82
all docs

82
docs citations

82
times ranked

6816
citing authors

#	ARTICLE	IF	CITATIONS
1	Tissue-specific transcriptional regulation has diverged significantly between human and mouse. <i>Nature Genetics</i> , 2007, 39, 730-732.	21.4	491
2	Polyploidy can drive rapid adaptation in yeast. <i>Nature</i> , 2015, 519, 349-352.	27.8	376
3	Genotype to Phenotype: A Complex Problem. <i>Science</i> , 2010, 328, 469-469.	12.6	358
4	HIF1A Employs CDK8-Mediator to Stimulate RNAPII Elongation in Response to Hypoxia. <i>Cell</i> , 2013, 153, 1327-1339.	28.9	300
5	Global analysis of p53-regulated transcription identifies its direct targets and unexpected regulatory mechanisms. <i>ELife</i> , 2014, 3, e02200.	6.0	205
6	Control of inducible gene expression links cohesin to hematopoietic progenitor self-renewal and differentiation. <i>Nature Immunology</i> , 2018, 19, 932-941.	14.5	175
7	Toggle involving <i>cis</i> -interfering noncoding RNAs controls variegated gene expression in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 18321-18326.	7.1	174
8	Human TFIID Kinase CDK7 Regulates Transcription-Associated Chromatin Modifications. <i>Cell Reports</i> , 2017, 20, 1173-1186.	6.4	123
9	Identification of Mediator Kinase Substrates in Human Cells using Cortistatin A and Quantitative Phosphoproteomics. <i>Cell Reports</i> , 2016, 15, 436-450.	6.4	117
10	Foxc1 reinforces quiescence in self-renewing hair follicle stem cells. <i>Science</i> , 2016, 351, 613-617.	12.6	109
11	Prolonged Cre expression driven by the β -myosin heavy chain promoter can be cardiotoxic. <i>Journal of Molecular and Cellular Cardiology</i> , 2015, 86, 54-61.	1.9	90
12	Enhancer RNA profiling predicts transcription factor activity. <i>Genome Research</i> , 2018, 28, 334-344.	5.5	88
13	High-resolution computational models of genome binding events. <i>Nature Biotechnology</i> , 2006, 24, 963-970.	17.5	82
14	Nuclear mechanosensing drives chromatin remodelling in persistently activated fibroblasts. <i>Nature Biomedical Engineering</i> , 2021, 5, 1485-1499.	22.5	71
15	Transcription factor binding variation in the evolution of gene regulation. <i>Trends in Genetics</i> , 2010, 26, 468-475.	6.7	60
16	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.	14.5	58
17	A Kinase-Independent Role for Cyclin-Dependent Kinase 19 in p53 Response. <i>Molecular and Cellular Biology</i> , 2017, 37, .	2.3	57
18	TFIID Enables RNA Polymerase II Promoter-Proximal Pausing. <i>Molecular Cell</i> , 2020, 78, 785-793.e8.	9.7	55

#	ARTICLE	IF	CITATIONS
19	Transcriptional Responses to IFN- β Require Mediator Kinase-Dependent Pause Release and Mechanistically Distinct CDK8 and CDK19 Functions. <i>Molecular Cell</i> , 2019, 76, 485-499.e8.	9.7	52
20	Selective inhibition of CDK7 reveals high-confidence targets and new models for TFIID function in transcription. <i>Genes and Development</i> , 2020, 34, 1452-1473.	5.9	47
21	A generative model for the behavior of RNA polymerase. <i>Bioinformatics</i> , 2017, 33, 227-234.	4.1	46
22	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.	9.7	38
23	Chromatin remodeling due to degradation of citrate carrier impairs osteogenesis of aged mesenchymal stem cells. <i>Nature Aging</i> , 2021, 1, 810-825.	11.6	37
24	Nascent transcript analysis of glucocorticoid crosstalk with TNF defines primary and cooperative inflammatory repression. <i>Genome Research</i> , 2019, 29, 1753-1765.	5.5	36
25	Detecting Differential Transcription Factor Activity from ATAC-Seq Data. <i>Molecules</i> , 2018, 23, 1136.	3.8	33
26	Feed-Forward Regulation of a Cell Fate Determinant by an RNA-Binding Protein Generates Asymmetry in Yeast. <i>Genetics</i> , 2010, 185, 513-522.	2.9	32
27	Transcriptome and Functional Profile of Cardiac Myocytes Is Influenced by Biological Sex. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	31
28	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.	8.9	31
29	Escape of hair follicle stem cells causes stem cell exhaustion during aging. <i>Nature Aging</i> , 2021, 1, 889-903.	11.6	31
30	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.	3.1	28
31	The similarity of gene expression between human and mouse tissues. <i>Genome Biology</i> , 2011, 12, 101.	9.6	25
32	The MUC5B-associated variant rs35705950 resides within an enhancer subject to lineage- and disease-dependent epigenetic remodeling. <i>JCI Insight</i> , 2021, 6, .	5.0	21
33	Transcription factor enrichment analysis (TFEA) quantifies the activity of multiple transcription factors from a single experiment. <i>Communications Biology</i> , 2021, 4, 661.	4.4	21
34	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.	3.0	19
35	PI(3,5)P ₂ controls vacuole potassium transport to support cellular osmoregulation. <i>Molecular Biology of the Cell</i> , 2018, 29, 1718-1731.	2.1	19
36	Discriminating between HuR and TTP binding sites using the k-spectrum kernel method. <i>PLoS ONE</i> , 2017, 12, e0174052.	2.5	15

#	ARTICLE	IF	CITATIONS
37	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.	2.5	14
38	The $\hat{\gamma}$ 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.	5.6	14
39	Survey of cryptic unstable transcripts in yeast. <i>BMC Genomics</i> , 2016, 17, 305.	2.8	13
40	Lessons from eRNAs: understanding transcriptional regulation through the lens of nascent RNAs. <i>Transcription</i> , 2020, 11, 3-18.	3.1	13
41	Model based heritability scores for high-throughput sequencing data. <i>BMC Bioinformatics</i> , 2017, 18, 143.	2.6	11
42	Applying knowledge-driven mechanistic inference to toxicogenomics. <i>Toxicology in Vitro</i> , 2020, 66, 104877.	2.4	11
43	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.	3.5	11
44	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.	2.4	9
45	RNA Pol II transcription model and interpretation of GRO-seq data. <i>Journal of Mathematical Biology</i> , 2017, 74, 77-97.	1.9	9
46	miR-MaGiC improves quantification accuracy for small RNA-seq. <i>BMC Research Notes</i> , 2018, 11, 296.	1.4	9
47	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.	3.4	9
48	FStitch. , 2014, , .		8
49	Remodeling of Zn ²⁺ homeostasis upon differentiation of mammary epithelial cells. <i>Metallomics</i> , 2020, 12, 346-362.	2.4	7
50	Genome characterization of the selected long- and short-sleep mouse lines. <i>Mammalian Genome</i> , 2016, 27, 574-586.	2.2	6
51	Protocol variations in run-on transcription dataset preparation produce detectable signatures in sequencing libraries. <i>BMC Genomics</i> , 2022, 23, 187.	2.8	5
52	Suppression of p53 response by targeting p53-Mediator binding with a stapled peptide. <i>Cell Reports</i> , 2022, 39, 110630.	6.4	5
53	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, .	1.8	4
54	CodaChrome: a tool for the visualization of proteome conservation across all fully sequenced bacterial genomes. <i>BMC Genomics</i> , 2014, 15, 65.	2.8	3

#	ARTICLE	IF	CITATIONS
55	Two-stage ML Classifier for Identifying Host Protein Targets of the Dengue Protease. , 2019, , .		2
56	Characterization of Global Gene Expression, Regulation of Metal Ions, and Infection Outcomes in Immune-Competent 129S6 Mouse Macrophages. Infection and Immunity, 2021, 89, e0027321.	2.2	2
57	Discovering Regulatory Overlapping RNA Transcripts. Journal of Computational Biology, 2011, 18, 295-303.	1.6	1
58	Combining signal and sequence to detect RNA polymerase initiation in ATAC-seq data. PLoS ONE, 2020, 15, e0232332.	2.5	1
59	The Naturally Occurring α^{40p53} Isoform Inhibits eRNA Transcription and Enables Context-Specific Regulation During p53 Activation. SSRN Electronic Journal, 0, , .	0.4	1
60	Discovering Regulatory Overlapping RNA Transcripts. Lecture Notes in Computer Science, 2010, , 110-122.	1.3	1
61	Systems genetics analysis of the LXS recombinant inbred mouse strains:Genetic and molecular insights into acute ethanol tolerance. PLoS ONE, 2020, 15, e0240253.	2.5	1
62	Inferring ancestry in mouse genomes using a hidden Markov model. , 2014, , .		0
63	A Modeling Framework for Generation of Positional and Temporal Simulations of Transcriptional Regulation. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 459-471.	3.0	0
64	Automated discovery of functional generality of human gene expression programs. PLoS Computational Biology, 2005, preprint, e148.	3.2	0
65	Title is missing!. , 2020, 15, e0240253.		0
66	Title is missing!. , 2020, 15, e0240253.		0
67	Title is missing!. , 2020, 15, e0240253.		0
68	Title is missing!. , 2020, 15, e0240253.		0
69	Metabolic and Transcriptomic Effects of Mediator Kinase Inhibition on the Interferon Response in Down Syndrome. FASEB Journal, 2022, 36, .	0.5	0