

Christoph Dieterich

List of Publications by Year in descending order

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Version: 2024-02-01

115
papers

8,849
citations

53751

45
h-index

49868

87
g-index

135
all docs

135
docs citations

135
times ranked

14923
citing authors

#	ARTICLE	IF	CITATIONS
1	The mRNA-Bound Proteome and Its Global Occupancy Profile on Protein-Coding Transcripts. <i>Molecular Cell</i> , 2012, 46, 674-690.	4.5	1,077
2	Analysis of Intron Sequences Reveals Hallmarks of Circular RNA Biogenesis in Animals. <i>Cell Reports</i> , 2015, 10, 170-177.	2.9	918
3	FLEXBAR—Flexible Barcode and Adapter Processing for Next-Generation Sequencing Platforms. <i>Biology</i> , 2012, 1, 895-905.	1.3	582
4	Mechanical regulation of transcription controls Polycomb-mediated gene silencing during lineage commitment. <i>Nature Cell Biology</i> , 2016, 18, 864-875.	4.6	364
5	Specific identification and quantification of circular RNAs from sequencing data. <i>Bioinformatics</i> , 2016, 32, 1094-1096.	1.8	325
6	The <i>Pristionchus pacificus</i> genome provides a unique perspective on nematode lifestyle and parasitism. <i>Nature Genetics</i> , 2008, 40, 1193-1198.	9.4	310
7	Mitofusin 2 is required to maintain mitochondrial coenzyme Q levels. <i>Journal of Cell Biology</i> , 2015, 208, 429-442.	2.3	180
8	doRiNA: a database of RNA interactions in post-transcriptional regulation. <i>Nucleic Acids Research</i> , 2012, 40, D180-D186.	6.5	177
9	Clinical genetics and outcome of left ventricular non-compaction cardiomyopathy. <i>European Heart Journal</i> , 2017, 38, 3449-3460.	1.0	168
10	Disorder and residual helicity alter p53-Mdm2 binding affinity and signaling in cells. <i>Nature Chemical Biology</i> , 2014, 10, 1000-1002.	3.9	167
11	MOV10 Is a 5' to 3' RNA Helicase Contributing to UPF1 mRNA Target Degradation by Translocation along 3' UTRs. <i>Molecular Cell</i> , 2014, 54, 573-585.	4.5	159
12	Proteogenomics of <i>Pristionchus pacificus</i> reveals distinct proteome structure of nematode models. <i>Genome Research</i> , 2010, 20, 837-846.	2.4	155
13	Flexbar 3.0—SIMD and multicore parallelization. <i>Bioinformatics</i> , 2017, 33, 2941-2942.	1.8	150
14	The SRF Target Gene Fhl2 Antagonizes RhoA/MAL-Dependent Activation of SRF. <i>Molecular Cell</i> , 2004, 16, 867-880.	4.5	137
15	DoRiNA 2.0—upgrading the doRiNA database of RNA interactions in post-transcriptional regulation. <i>Nucleic Acids Research</i> , 2015, 43, D160-D167.	6.5	136
16	Detection of active transcription factor binding sites with the combination of DNase hypersensitivity and histone modifications. <i>Bioinformatics</i> , 2014, 30, 3143-3151.	1.8	109
17	A spatially resolved brain region- and cell type-specific isoform atlas of the postnatal mouse brain. <i>Nature Communications</i> , 2021, 12, 463.	5.8	109
18	m ⁶ A-mRNA methylation regulates cardiac gene expression and cellular growth. <i>Life Science Alliance</i> , 2019, 2, e201800233.	1.3	109

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19	De novo assembly and validation of planaria transcriptome by massive parallel sequencing and shotgun proteomics. <i>Genome Research</i> , 2011, 21, 1193-1200.	2.4	100
20	How to become a parasite – lessons from the genomes of nematodes. <i>Trends in Genetics</i> , 2009, 25, 203-209.	2.9	99
21	A coding-independent function of an alternative Ube3a transcript during neuronal development. <i>Nature Neuroscience</i> , 2015, 18, 666-673.	7.1	95
22	Identification of circular RNAs with host gene-independent expression in human model systems for cardiac differentiation and disease. <i>Journal of Molecular and Cellular Cardiology</i> , 2017, 109, 48-56.	0.9	93
23	Isolation of naturally associated bacteria of necromenic <i>Pristionchus</i> nematodes and fitness consequences. <i>Journal of Experimental Biology</i> , 2008, 211, 1927-1936.	0.8	92
24	Sex-Biased Gene Expression and Evolution of the X Chromosome in Nematodes. <i>Genetics</i> , 2014, 197, 865-883.	1.2	92
25	Serum microRNAs in patients with genetic amyotrophic lateral sclerosis and pre-manifest mutation carriers. <i>Brain</i> , 2014, 137, 2938-2950.	3.7	91
26	A microRNA-miR-129a-5p/Rbfox crosstalk coordinates homeostatic downscaling of excitatory synapses. <i>EMBO Journal</i> , 2017, 36, 1770-1787.	3.5	85
27	Integrin-linked kinase regulates the niche of quiescent epidermal stem cells. <i>Nature Communications</i> , 2015, 6, 8198.	5.8	83
28	Somatic increase of CCT8 mimics proteostasis of human pluripotent stem cells and extends <i>C. elegans</i> lifespan. <i>Nature Communications</i> , 2016, 7, 13649.	5.8	81
29	ATF6 Regulates Cardiac Hypertrophy by Transcriptional Induction of the mTORC1 Activator, Rheb. <i>Circulation Research</i> , 2019, 124, 79-93.	2.0	80
30	mGene: Accurate SVM-based gene finding with an application to nematode genomes. <i>Genome Research</i> , 2009, 19, 2133-2143.	2.4	79
31	Characterization of Genetic Diversity in the Nematode <i>Pristionchus pacificus</i> from Population-Scale Resequencing Data. <i>Genetics</i> , 2014, 196, 1153-1165.	1.2	79
32	Profiling and Validation of the Circular RNA Repertoire in Adult Murine Hearts. <i>Genomics, Proteomics and Bioinformatics</i> , 2016, 14, 216-223.	3.0	79
33	An Insulin-Sensitive Circular RNA that Regulates Lifespan in <i>Drosophila</i> . <i>Molecular Cell</i> , 2020, 79, 268-279.e5.	4.5	77
34	JACUSA: site-specific identification of RNA editing events from replicate sequencing data. <i>BMC Bioinformatics</i> , 2017, 18, 7.	1.2	76
35	Mondo complexes regulate TFEB via TOR inhibition to promote longevity in response to gonadal signals. <i>Nature Communications</i> , 2016, 7, 10944.	5.8	71
36	Bayesian prediction of RNA translation from ribosome profiling. <i>Nucleic Acids Research</i> , 2017, 45, gkw1350.	6.5	64

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37	A <i>Grhl2</i> -dependent gene network controls trophoblast branching morphogenesis. <i>Development</i> (Cambridge), 2015, 142, 1125-1136.	1.2	61
38	Exon Junction Complexes Suppress Spurious Splice Sites to Safeguard Transcriptome Integrity. <i>Molecular Cell</i> , 2018, 72, 482-495.e7.	4.5	61
39	Evolution of a Core Gene Network for Skeletogenesis in Chordates. <i>PLoS Genetics</i> , 2008, 4, e1000025.	1.5	59
40	A post-transcriptional program coordinated by CSDE1 prevents intrinsic neural differentiation of human embryonic stem cells. <i>Nature Communications</i> , 2017, 8, 1456.	5.8	59
41	Deregulated Splicing Is a Major Mechanism of RNA-Induced Toxicity in Huntington's Disease. <i>Journal of Molecular Biology</i> , 2019, 431, 1869-1877.	2.0	57
42	CYNTENATOR: Progressive Gene Order Alignment of 17 Vertebrate Genomes. <i>PLoS ONE</i> , 2010, 5, e8861.	1.1	56
43	Monitoring Cell-Type-Specific Gene Expression Using Ribosome Profiling In Vivo During Cardiac Hemodynamic Stress. <i>Circulation Research</i> , 2019, 125, 431-448.	2.0	56
44	Ythdf is a N ⁶ -methyladenosine reader that modulates Fmr1 target mRNA selection and restricts axonal growth in <i>Drosophila</i> . <i>EMBO Journal</i> , 2021, 40, e104975.	3.5	56
45	Global profiling of miRNAs and the hairpin precursors: insights into miRNA processing and novel miRNA discovery. <i>Nucleic Acids Research</i> , 2013, 41, 3619-3634.	6.5	55
46	The cardiac microenvironment uses non-canonical WNT signaling to activate monocytes after myocardial infarction. <i>EMBO Molecular Medicine</i> , 2017, 9, 1279-1293.	3.3	55
47	SMG5-SMG7 authorize nonsense-mediated mRNA decay by enabling SMG6 endonucleolytic activity. <i>Nature Communications</i> , 2021, 12, 3965.	5.8	54
48	Computational approaches for circular RNA analysis. <i>Wiley Interdisciplinary Reviews RNA</i> , 2019, 10, e1528.	3.2	52
49	Deep and accurate detection of m6A RNA modifications using miCLIP2 and m6Aboost machine learning. <i>Nucleic Acids Research</i> , 2021, 49, e92-e92.	6.5	50
50	Reducing RBM20 activity improves diastolic dysfunction and cardiac atrophy. <i>Journal of Molecular Medicine</i> , 2016, 94, 1349-1358.	1.7	48
51	circTools: a one-stop software solution for circular RNA research. <i>Bioinformatics</i> , 2019, 35, 2326-2328.	1.8	46
52	The genome of <i>Eimeria falciformis</i> - reduction and specialization in a single host apicomplexan parasite. <i>BMC Genomics</i> , 2014, 15, 696.	1.2	44
53	Insights into the ubiquitin-proteasome system of human embryonic stem cells. <i>Scientific Reports</i> , 2018, 8, 4092.	1.6	44
54	A Vastly Increased Chemical Variety of RNA Modifications Containing a Thioacetal Structure. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 7893-7897.	7.2	44

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55	A proteomic atlas of insulin signalling reveals tissue-specific mechanisms of longevity assurance. <i>Molecular Systems Biology</i> , 2017, 13, 939.	3.2	42
56	The lipid-droplet-associated protein ABHD5 protects the heart through proteolysis of HDAC4. <i>Nature Metabolism</i> , 2019, 1, 1157-1167.	5.1	42
57	Single-cell transcriptomics defines heterogeneity of epicardial cells and fibroblasts within the infarcted murine heart. <i>ELife</i> , 2021, 10, .	2.8	42
58	A secreted microRNA disrupts autophagy in distinct tissues of <i>Caenorhabditis elegans</i> upon ageing. <i>Nature Communications</i> , 2019, 10, 4827.	5.8	40
59	Circular RNAs in the cardiovascular system. <i>Non-coding RNA Research</i> , 2018, 3, 1-11.	2.4	36
60	Transcriptome-wide measurement of ribosomal occupancy by ribosome profiling. <i>Methods</i> , 2015, 85, 75-89.	1.9	35
61	A placental mammal-specific microRNA cluster acts as a natural brake for sociability in mice. <i>EMBO Reports</i> , 2019, 20, .	2.0	35
62	CASC3 promotes transcriptome-wide activation of nonsense-mediated decay by the exon junction complex. <i>Nucleic Acids Research</i> , 2020, 48, 8626-8644.	6.5	35
63	Label-Free Protein-RNA Interactome Analysis Identifies Khgrp Signaling Downstream of the p38/Mk2 Kinase Complex as a Critical Modulator of Cell Cycle Progression. <i>PLoS ONE</i> , 2015, 10, e0125745.	1.1	32
64	ADAR-deficiency perturbs the global splicing landscape in mouse tissues. <i>Genome Research</i> , 2020, 30, 1107-1118.	2.4	32
65	Conserved miRNAs Are Candidate Post-Transcriptional Regulators of Developmental Arrest in Free-Living and Parasitic Nematodes. <i>Genome Biology and Evolution</i> , 2013, 5, 1246-1260.	1.1	31
66	A MAFG-lncRNA axis links systemic nutrient abundance to hepatic glucose metabolism. <i>Nature Communications</i> , 2020, 11, 644.	5.8	29
67	A host beetle pheromone regulates development and behavior in the nematode <i>Pristionchus pacificus</i> . <i>ELife</i> , 2014, 3, .	2.8	29
68	CWC22-dependent pre-mRNA splicing and eIF4A3 binding enables global deposition of exon junction complexes. <i>Nucleic Acids Research</i> , 2015, 43, 4687-4700.	6.5	28
69	Identification and regulation of the long non-coding RNA Heat2 in heart failure. <i>Journal of Molecular and Cellular Cardiology</i> , 2019, 126, 13-22.	0.9	27
70	Loss of genomic integrity induced by lysosphingolipid imbalance drives ageing in the heart. <i>EMBO Reports</i> , 2019, 20, .	2.0	26
71	RNA modification mapping with JACUSA2. <i>Genome Biology</i> , 2022, 23, 115.	3.8	25
72	Prognostic Relevance of Tumor Purity and Interaction with MGMT Methylation in Glioblastoma. <i>Molecular Cancer Research</i> , 2017, 15, 532-540.	1.5	23

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73	Deep Characterization of Circular RNAs from Human Cardiovascular Cell Models and Cardiac Tissue. <i>Cells</i> , 2020, 9, 1616.	1.8	22
74	Ageing induces tissue-specific transcriptomic changes in <i>Caenorhabditis elegans</i> . <i>EMBO Journal</i> , 2022, 41, e109633.	3.5	22
75	Human UPF3A and UPF3B enable fault-tolerant activation of nonsense-mediated mRNA decay. <i>EMBO Journal</i> , 2022, 41, e109191.	3.5	21
76	Dual RNA-seq reveals no plastic transcriptional response of the coccidian parasite <i>Eimeria falciformis</i> to host immune defenses. <i>BMC Genomics</i> , 2017, 18, 686.	1.2	20
77	The E3 ubiquitin ligase UBR5 interacts with the H/ACA ribonucleoprotein complex and regulates ribosomal RNA biogenesis in embryonic stem cells. <i>FEBS Letters</i> , 2020, 594, 175-188.	1.3	19
78	Rapid-CNS2: rapid comprehensive adaptive nanopore-sequencing of CNS tumors, a proof-of-concept study. <i>Acta Neuropathologica</i> , 2022, 143, 609-612.	3.9	19
79	A Single Transcriptome of a Green Toad (<i>Bufo viridis</i>) Yields Candidate Genes for Sex Determination and -Differentiation and Non-Anonymous Population Genetic Markers. <i>PLoS ONE</i> , 2016, 11, e0156419.	1.1	18
80	Deep Computational Circular RNA Analytics from RNA-seq Data. <i>Methods in Molecular Biology</i> , 2018, 1724, 9-25.	0.4	18
81	Validation strategies for antibodies targeting modified ribonucleotides. <i>Rna</i> , 2020, 26, 1489-1506.	1.6	18
82	pulseR: Versatile computational analysis of RNA turnover from metabolic labeling experiments. <i>Bioinformatics</i> , 2017, 33, 3305-3307.	1.8	16
83	On the optimal design of metabolic RNA labeling experiments. <i>PLoS Computational Biology</i> , 2019, 15, e1007252.	1.5	16
84	The RNA-Protein Interactome of Differentiated Kidney Tubular Epithelial Cells. <i>Journal of the American Society of Nephrology: JASN</i> , 2019, 30, 564-576.	3.0	16
85	Updated and enhanced pig cardiac transcriptome based on long-read RNA sequencing and proteomics. <i>Journal of Molecular and Cellular Cardiology</i> , 2021, 150, 23-31.	0.9	16
86	Therapeutic inhibition of RBM20 improves diastolic function in a murine heart failure model and human engineered heart tissue. <i>Science Translational Medicine</i> , 2021, 13, eabe8952.	5.8	14
87	MicroRNA-138 controls hippocampal interneuron function and short-term memory in mice. <i>ELife</i> , 2022, 11, .	2.8	14
88	Pervasive compartment-specific regulation of gene expression during homeostatic synaptic scaling. <i>EMBO Reports</i> , 2021, 22, e52094.	2.0	13
89	Muscle-specific Cand2 is translationally upregulated by mTORC1 and promotes adverse cardiac remodeling. <i>EMBO Reports</i> , 2021, 22, e52170.	2.0	13
90	Genome-wide analysis of trans-splicing in the nematode <i>Pristionchus pacificus</i> unravels conserved gene functions for germline and dauer development in divergent operons. <i>Rna</i> , 2014, 20, 1386-1397.	1.6	12

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91	Single-cell transcriptome sequencing on the Nanopore platform with ScNapBar. <i>Rna</i> , 2021, 27, 763-770.	1.6	12
92	A comparison of metabolic labeling and statistical methods to infer genome-wide dynamics of RNA turnover. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	11
93	Cellular heterogeneity contributes to subtype-specific expression of ZEB1 in human glioblastoma. <i>PLoS ONE</i> , 2017, 12, e0185376.	1.1	10
94	Exon junction complex-associated multi-adaptor RNPS1 nucleates splicing regulatory complexes to maintain transcriptome surveillance. <i>Nucleic Acids Research</i> , 2022, 50, 5899-5918.	6.5	9
95	Identification of Methylated Transcripts Using the TRIBE Approach. <i>Methods in Molecular Biology</i> , 2019, 1870, 89-106.	0.4	8
96	Analysis of myocardial cellular gene expression during pressure overload reveals matrix based functional intercellular communication. <i>IScience</i> , 2022, 25, 103965.	1.9	8
97	A protocol for chemical mutagenesis in <i>Strongyloides ratti</i> . <i>Experimental Parasitology</i> , 2015, 158, 2-7.	0.5	6
98	The recurrent postzygotic pathogenic variant p.Glu47Lys in RHOA causes a novel recognizable neuroectodermal phenotype. <i>Human Mutation</i> , 2020, 41, 591-599.	1.1	6
99	Stable Redox-Cycling Nitroxide Tempol Has Antifungal and Immune-Modulatory Properties. <i>Frontiers in Microbiology</i> , 2019, 10, 1843.	1.5	5
100	Transcriptional signatures regulated by TRPC1/C4-mediated Background Ca ²⁺ entry after pressure-overload induced cardiac remodelling. <i>Progress in Biophysics and Molecular Biology</i> , 2021, 159, 86-104.	1.4	5
101	RN7SK small nuclear RNA controls bidirectional transcription of highly expressed gene pairs in skin. <i>Nature Communications</i> , 2021, 12, 5864.	5.8	5
102	SPIRE, a modular pipeline for eQTL analysis of RNA-Seq data, reveals a regulatory hotspot controlling miRNA expression in <i>C. elegans</i> . <i>Molecular BioSystems</i> , 2016, 12, 3447-3458.	2.9	4
103	Improved nanopore direct RNA sequencing of cardiac myocyte samples by selective mt-RNA depletion. <i>Journal of Molecular and Cellular Cardiology</i> , 2022, 163, 175-186.	0.9	4
104	A Multi-Network Comparative Analysis of Transcriptome and Translatome Identifies Novel Hub Genes in Cardiac Remodeling. <i>Frontiers in Genetics</i> , 2020, 11, 583124.	1.1	4
105	Targeted Analysis of circRNA Expression in Patient Samples by Lexo-circSeq. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	4
106	ACCUSA2: multi-purpose SNV calling enhanced by probabilistic integration of quality scores. <i>Bioinformatics</i> , 2013, 29, 1809-1810.	1.8	3
107	RNA modifications in cardiovascular disease—An experimental and computational perspective. , 2021, , 113-125.		3
108	New Tricks with Old Dogs: Computational Identification and Experimental Validation of New miRNA—mRNA Regulation in hiPSC-CMs. <i>Biomedicines</i> , 2022, 10, 391.	1.4	3

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109	Circular RNA circCCNT2 is upregulated in the anterior cingulate cortex of individuals with bipolar disorder. <i>Translational Psychiatry</i> , 2021, 11, 629.	2.4	3
110	RNA Modification Level Estimation with pulseR. <i>Genes</i> , 2018, 9, 619.	1.0	2
111	De-Identification of German Medical Admission Notes. <i>Studies in Health Technology and Informatics</i> , 2018, 253, 165-169.	0.2	2
112	Unsupervised Bayesian Prediction of RNA Translation from Ribosome Profiling Data. <i>Methods in Molecular Biology</i> , 2021, 2252, 295-312.	0.4	0
113	A04â€¦Circhtt, a circular rna from the huntingtonâ€™s disease gene locus: functional characterization and possible implications for disease modulation. , 2021, , .		0
114	PATH-48. RAPID-CNS2: RAPID COMPREHENSIVE ADAPTIVE NANOPORE-SEQUENCING OF CNS TUMORS, A PROOF OF CONCEPT STUDY. <i>Neuro-Oncology</i> , 2021, 23, vi126-vi126.	0.6	0
115	Structured, Harmonized, and Interoperable Integration of Clinical Routine Data to Compute Heart Failure Risk Scores. <i>Life</i> , 2022, 12, 749.	1.1	0