

Carsten O Daub

List of Publications by Year in descending order

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Version: 2024-02-01

92
papers

14,475
citations

57758

44
h-index

42399

92
g-index

98
all docs

98
docs citations

98
times ranked

25139
citing authors

#	ARTICLE	IF	CITATIONS
1	Sequence determinants of human gene regulatory elements. <i>Nature Genetics</i> , 2022, 54, 283-294.	21.4	87
2	Multiomic atlas with functional stratification and developmental dynamics of zebrafish cis-regulatory elements. <i>Nature Genetics</i> , 2022, 54, 1037-1050.	21.4	26
3	Human White Adipose Tissue Displays Selective Insulin Resistance in the Obese State. <i>Diabetes</i> , 2021, 70, 1486-1497.	0.6	16
4	Micro-biopsy for detection of gene expression changes in ischemic swine myocardium: A pilot study. <i>PLoS ONE</i> , 2021, 16, e0250582.	2.5	1
5	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , 2021, 12, 3297.	12.8	11
6	Generation of RNA sequencing libraries for transcriptome analysis of globin-rich tissues of the domestic dog. <i>STAR Protocols</i> , 2021, 2, 100995.	1.2	6
7	Ten simple rules for annotating sequencing experiments. <i>PLoS Computational Biology</i> , 2020, 16, e1008260.	3.2	12
8	Myocardial micro-biopsy procedure for molecular characterization with increased precision and reduced trauma. <i>Scientific Reports</i> , 2020, 10, 8029.	3.3	11
9	*-DCC: A platform to collect, annotate, and explore a large variety of sequencing experiments. <i>GigaScience</i> , 2020, 9, .	6.4	7
10	A putative silencer variant in a spontaneous canine model of retinitis pigmentosa. <i>PLoS Genetics</i> , 2020, 16, e1008659.	3.5	9
11	Identification and transfer of spatial transcriptomics signatures for cancer diagnosis. <i>Breast Cancer Research</i> , 2020, 22, 6.	5.0	54
12	Identification of novel cerebellar developmental transcriptional regulators with motif activity analysis. <i>BMC Genomics</i> , 2019, 20, 718.	2.8	11
13	Long-Term Improvement in Aortic Pulse Wave Velocity After Weight Loss Can Be Predicted by White Adipose Tissue Factors. <i>American Journal of Hypertension</i> , 2018, 31, 450-457.	2.0	12
14	Discovery of Transcription Factors Novel to Mouse Cerebellar Granule Cell Development Through Laser-Capture Microdissection. <i>Cerebellum</i> , 2018, 17, 308-325.	2.5	6
15	Characterization of the human RFX transcription factor family by regulatory and target gene analysis. <i>BMC Genomics</i> , 2018, 19, 181.	2.8	73
16	Conserved temporal ordering of promoter activation implicates common mechanisms governing the immediate early response across cell types and stimuli. <i>Open Biology</i> , 2018, 8, 180011.	3.6	13
17	Promoter Usage and Dynamics in Vascular Smooth Muscle Cells Exposed to Fibroblast Growth Factor-2 or Interleukin-1 β . <i>Scientific Reports</i> , 2018, 8, 13164.	3.3	10
18	Shared activity patterns arising at genetic susceptibility loci reveal underlying genomic and cellular architecture of human disease. <i>PLoS Computational Biology</i> , 2018, 14, e1005934.	3.2	17

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19	An atlas of human long non-coding RNAs with accurate 5' ends. <i>Nature</i> , 2017, 543, 199-204.	27.8	898
20	Transcriptome Analysis Uncovers a Growth-Promoting Activity of Orosomucoid-1 on Hepatocytes. <i>EBioMedicine</i> , 2017, 24, 257-266.	6.1	24
21	An integrated expression atlas of miRNAs and their promoters in human and mouse. <i>Nature Biotechnology</i> , 2017, 35, 872-878.	17.5	456
22	FANTOM5 CAGE profiles of human and mouse samples. <i>Scientific Data</i> , 2017, 4, 170112.	5.3	195
23	Acute doses of caffeine shift nervous system cell expression profiles toward promotion of neuronal projection growth. <i>Scientific Reports</i> , 2017, 7, 11458.	3.3	14
24	Transcriptional Dynamics During Human Adipogenesis and Its Link to Adipose Morphology and Distribution. <i>Diabetes</i> , 2017, 66, 218-230.	0.6	27
25	Analysis of the human monocyte-derived macrophage transcriptome and response to lipopolysaccharide provides new insights into genetic aetiology of inflammatory bowel disease. <i>PLoS Genetics</i> , 2017, 13, e1006641.	3.5	161
26	DeepCAGE transcriptomics identify HOXD10 as transcription factor regulating lymphatic endothelial responses to VEGF-C. <i>Journal of Cell Science</i> , 2016, 129, 2573-85.	2.0	15
27	The Adipose Transcriptional Response to Insulin Is Determined by Obesity, Not Insulin Sensitivity. <i>Cell Reports</i> , 2016, 16, 2317-2326.	6.4	35
28	A predictive computational framework for direct reprogramming between human cell types. <i>Nature Genetics</i> , 2016, 48, 331-335.	21.4	263
29	Promoter-level expression clustering identifies time development of transcriptional regulatory cascades initiated by ErbB receptors in breast cancer cells. <i>Scientific Reports</i> , 2015, 5, 11999.	3.3	30
30	System-wide analysis of the transcriptional network of human myelomonocytic leukemia cells predicts attractor structure and phorbol-ester-induced differentiation and dedifferentiation transitions. <i>Scientific Reports</i> , 2015, 5, 8283.	3.3	3
31	DeepCAGE Transcriptomics Reveal an Important Role of the Transcription Factor MAFB in the Lymphatic Endothelium. <i>Cell Reports</i> , 2015, 13, 1493-1504.	6.4	46
32	Application of Gene Expression Trajectories Initiated from ErbB Receptor Activation Highlights the Dynamics of Divergent Promoter Usage. <i>PLoS ONE</i> , 2015, 10, e0144176.	2.5	1
33	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. <i>Science</i> , 2015, 347, 1010-1014.	12.6	517
34	Gateways to the FANTOM5 promoter level mammalian expression atlas. <i>Genome Biology</i> , 2015, 16, 22.	8.8	687
35	Telomerase Reverse Transcriptase Regulates microRNAs. <i>International Journal of Molecular Sciences</i> , 2015, 16, 1192-1208.	4.1	22
36	Transcriptional Dynamics Reveal Critical Roles for Non-coding RNAs in the Immediate-Early Response. <i>PLoS Computational Biology</i> , 2015, 11, e1004217.	3.2	22

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37	Transcriptome analysis of controlled and therapy-resistant childhood asthma reveals distinct gene expression profiles. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 136, 638-648.	2.9	59
38	Complementing tissue characterization by integrating transcriptome profiling from the Human Protein Atlas and from the FANTOM5 consortium. <i>Nucleic Acids Research</i> , 2015, 43, 6787-6798.	14.5	94
39	Ceruloplasmin Is a Novel Adipokine Which Is Overexpressed in Adipose Tissue of Obese Subjects and in Obesity-Associated Cancer Cells. <i>PLoS ONE</i> , 2014, 9, e80274.	2.5	50
40	NanoCAGE analysis of the mouse olfactory epithelium identifies the expression of vomeronasal receptors and of proximal LINE elements. <i>Frontiers in Cellular Neuroscience</i> , 2014, 8, 41.	3.7	11
41	Additive Effects of MicroRNAs and Transcription Factors on CCL2 Production in Human White Adipose Tissue. <i>Diabetes</i> , 2014, 63, 1248-1258.	0.6	38
42	A simple metric of promoter architecture robustly predicts expression breadth of human genes suggesting that most transcription factors are positive regulators. <i>Genome Biology</i> , 2014, 15, 413.	8.8	20
43	Differential roles of epigenetic changes and Foxp3 expression in regulatory T cell-specific transcriptional regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5289-5294.	7.1	111
44	Interactive visualization and analysis of large-scale sequencing datasets using ZENBU. <i>Nature Biotechnology</i> , 2014, 32, 217-219.	17.5	163
45	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	27.8	1,838
46	An atlas of active enhancers across human cell types and tissues. <i>Nature</i> , 2014, 507, 455-461.	27.8	2,269
47	MOIRAI: a compact workflow system for CAGE analysis. <i>BMC Bioinformatics</i> , 2014, 15, 144.	2.6	66
48	Chromatin states reveal functional associations for globally defined transcription start sites in four human cell lines. <i>BMC Genomics</i> , 2014, 15, 120.	2.8	17
49	High-throughput transcription profiling identifies putative epigenetic regulators of hematopoiesis. <i>Blood</i> , 2014, 123, e46-e57.	1.4	21
50	Early B Cell Factor 1 Regulates Adipocyte Morphology and Lipolysis in White Adipose Tissue. <i>Cell Metabolism</i> , 2014, 19, 981-992.	16.2	90
51	Molecular Networks of DYX1C1 Gene Show Connection to Neuronal Migration Genes and Cytoskeletal Proteins. <i>Biological Psychiatry</i> , 2013, 73, 583-590.	1.3	38
52	Regional differences in gene expression and promoter usage in aged human brains. <i>Neurobiology of Aging</i> , 2013, 34, 1825-1836.	3.1	30
53	<i>Glycyrrhiza uralensis</i> Transcriptome Landscape and Study of Phytochemicals. <i>Plant and Cell Physiology</i> , 2013, 54, 697-710.	3.1	80
54	A comprehensive promoter landscape identifies a novel promoter for CD133 in restricted tissues, cancers, and stem cells. <i>Frontiers in Genetics</i> , 2013, 4, 209.	2.3	10

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55	Promoter architecture of mouse olfactory receptor genes. <i>Genome Research</i> , 2012, 22, 486-497.	5.5	52
56	pre-miRNA profiles obtained through application of locked nucleic acids and deep sequencing reveals complex 5' arm variation including concomitant cleavage and polyuridylation patterns. <i>Nucleic Acids Research</i> , 2012, 40, 1424-1437.	14.5	30
57	Nonimmunoglobulin target loci of activation-induced cytidine deaminase (AID) share unique features with immunoglobulin genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 2479-2484.	7.1	64
58	Adipose Tissue MicroRNAs as Regulators of CCL2 Production in Human Obesity. <i>Diabetes</i> , 2012, 61, 1986-1993.	0.6	263
59	Conservation and divergence in Toll-like receptor 4-regulated gene expression in primary human versus mouse macrophages. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E944-53.	7.1	332
60	Unamplified cap analysis of gene expression on a single-molecule sequencer. <i>Genome Research</i> , 2011, 21, 1150-1159.	5.5	172
61	Optimization of turn-back primers in isothermal amplification. <i>Nucleic Acids Research</i> , 2011, 39, e59-e59.	14.5	66
62	Profiling transcription initiation in human aged brain using deep-CAGE. <i>BMC Bioinformatics</i> , 2011, 12, .	2.6	3
63	SAMStat: monitoring biases in next generation sequencing data. <i>Bioinformatics</i> , 2011, 27, 130-131.	4.1	175
64	Update of the FANTOM web resource: from mammalian transcriptional landscape to its dynamic regulation. <i>Nucleic Acids Research</i> , 2011, 39, D856-D860.	14.5	49
65	The Short Non-Coding Transcriptome of the Protozoan Parasite <i>Trypanosoma cruzi</i> . <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1283.	3.0	35
66	Core promoter structure and genomic context reflect histone 3 lysine 9 acetylation patterns. <i>BMC Genomics</i> , 2010, 11, 257.	2.8	34
67	Linking promoters to functional transcripts in small samples with nanoCAGE and CAGEscan. <i>Nature Methods</i> , 2010, 7, 528-534.	19.0	152
68	Building promoter aware transcriptional regulatory networks using siRNA perturbation and deepCAGE. <i>Nucleic Acids Research</i> , 2010, 38, 8141-8148.	14.5	17
69	NGSView: an extensible open source editor for next-generation sequencing data. <i>Bioinformatics</i> , 2010, 26, 125-126.	4.1	8
70	Cross-mapping and the identification of editing sites in mature microRNAs in high-throughput sequencing libraries. <i>Genome Research</i> , 2010, 20, 257-264.	5.5	126
71	A comprehensive survey of animal miRNA modification events and a possible role for adenylation in modulating miRNA targeting effectiveness. <i>Genome Research</i> , 2010, 20, 1398-1410.	5.5	309
72	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. <i>Cell</i> , 2010, 140, 744-752.	28.9	667

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73	Beyond the FANTOM4. <i>Genome Biology</i> , 2010, 11, O11.	9.6	0
74	Genome-wide detection and analysis of hippocampus core promoters using DeepCAGE. <i>Genome Research</i> , 2009, 19, 255-265.	5.5	128
75	MiR-107 and MiR-185 Can Induce Cell Cycle Arrest in Human Non Small Cell Lung Cancer Cell Lines. <i>PLoS ONE</i> , 2009, 4, e6677.	2.5	200
76	Probabilistic resolution of multi-mapping reads in massively parallel sequencing data using MuMRescueLite. <i>Bioinformatics</i> , 2009, 25, 2613-2614.	4.1	41
77	TagDust—a program to eliminate artifacts from next generation sequencing data. <i>Bioinformatics</i> , 2009, 25, 2839-2840.	4.1	210
78	SDRF2GRAPH—a visualization tool of a spreadsheet-based description of experimental processes. <i>BMC Bioinformatics</i> , 2009, 10, 133.	2.6	3
79	Tiny RNAs associated with transcription start sites in animals. <i>Nature Genetics</i> , 2009, 41, 572-578.	21.4	327
80	The regulated retrotransposon transcriptome of mammalian cells. <i>Nature Genetics</i> , 2009, 41, 563-571.	21.4	731
81	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009, 41, 553-562.	21.4	408
82	Methods for analyzing deep sequencing expression data: constructing the human and mouse promoterome with deepCAGE data. <i>Genome Biology</i> , 2009, 10, R79.	9.6	131
83	FANTOM4 EdgeExpressDB: an integrated database of promoters, genes, microRNAs, expression dynamics and regulatory interactions. <i>Genome Biology</i> , 2009, 10, R39.	9.6	67
84	The FANTOM web resource: from mammalian transcriptional landscape to its dynamic regulation. <i>Genome Biology</i> , 2009, 10, R40.	9.6	73
85	Transcriptional features of genomic regulatory blocks. <i>Genome Biology</i> , 2009, 10, R38.	9.6	90
86	Hidden layers of human small RNAs. <i>BMC Genomics</i> , 2008, 9, 157.	2.8	255
87	Employing conservation of co-expression to improve functional inference. <i>BMC Systems Biology</i> , 2008, 2, 81.	3.0	5
88	Prediction of Function Divergence in Protein Families Using the Substitution Rate Variation Parameter Alpha. <i>Molecular Biology and Evolution</i> , 2006, 23, 1406-1413.	8.9	12
89	Integrative gene-metabolite network with implemented causality deciphers informational fluxes of sulphur stress response. <i>Journal of Experimental Botany</i> , 2005, 56, 1887-1896.	4.8	129
90	Measuring Distances Between Variables by Mutual Information. , 2005, , 81-90.		6

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91	Estimating mutual information using B-spline functions—an improved similarity measure for analysing gene expression data. BMC Bioinformatics, 2004, 5, 118.	2.6	228
92	MetaGeneAlyse: analysis of integrated transcriptional and metabolite data. Bioinformatics, 2003, 19, 2332-2333.	4.1	60