

Charles G Danko

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

5,520
citations

201575

27
h-index

161767

54
g-index

85
all docs

85
docs citations

85
times ranked

8225
citing authors

#	ARTICLE	IF	CITATIONS
1	Darwinian genomics and diversity in the tree of life. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	19
2	E-Protein Inhibition in ILC2 Development Shapes the Function of Mature ILC2s during Allergic Airway Inflammation. Journal of Immunology, 2022, 208, 1007-1020.	0.4	2
3	Prediction of histone post-translational modification patterns based on nascent transcription data. Nature Genetics, 2022, 54, 295-305.	9.4	53
4	Cell type and gene expression deconvolution with BayesPrism enables Bayesian integrative analysis across bulk and single-cell RNA sequencing in oncology. Nature Cancer, 2022, 3, 505-517.	5.7	119
5	Deconvolution of expression for nascent RNA-sequencing data (DENR) highlights pre-RNA isoform diversity in human cells. Bioinformatics, 2021, 37, 4727-4736.	1.8	4
6	GLP-1 receptor signaling increases PCSK1 and \hat{I}^2 cell features in human \hat{I}^{\pm} cells. JCI Insight, 2021, 6, .	2.3	24
7	Characterizing RNA stability genome-wide through combined analysis of PRO-seq and RNA-seq data. BMC Biology, 2021, 19, 30.	1.7	38
8	Uncovering transcriptional dark matter via gene annotation independent single-cell RNA sequencing analysis. Nature Communications, 2021, 12, 2158.	5.8	9
9	The <i>Dryas iulia</i> Genome Supports Multiple Gains of a W Chromosome from a B Chromosome in Butterflies. Genome Biology and Evolution, 2021, 13, .	1.1	24
10	Chromosome Fusion Affects Genetic Diversity and Evolutionary Turnover of Functional Loci but Consistently Depends on Chromosome Size. Molecular Biology and Evolution, 2021, 38, 4449-4462.	3.5	51
11	Identification and prediction of developmental enhancers in sea urchin embryos. BMC Genomics, 2021, 22, 751.	1.2	9
12	Multiple stages of evolutionary change in anthrax toxin receptor expression in humans. Nature Communications, 2021, 12, 6590.	5.8	2
13	Many functionally connected loci foster adaptive diversification along a neotropical hybrid zone. Science Advances, 2020, 6, .	4.7	18
14	Chromatin run-on sequencing analysis finds that ECM remodeling plays an important role in canine hemangiosarcoma pathogenesis. BMC Veterinary Research, 2020, 16, 206.	0.7	4
15	The H2BG53D oncohistone directly upregulates ANXA3 transcription and enhances cell migration in pancreatic ductal adenocarcinoma. Signal Transduction and Targeted Therapy, 2020, 5, 106.	7.1	12
16	Elevated circulating Th2 but not group 2 innate lymphoid cell responses characterize canine atopic dermatitis. Veterinary Immunology and Immunopathology, 2020, 221, 110015.	0.5	6
17	Hotspots of Aberrant Enhancer Activity in Fibrolamellar Carcinoma Reveal Candidate Oncogenic Pathways and Therapeutic Vulnerabilities. Cell Reports, 2020, 31, 107509.	2.9	28
18	Physical confinement induces malignant transformation in mammary epithelial cells. Biomaterials, 2019, 217, 119307.	5.7	13

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19	Chromatin conformation remains stable upon extensive transcriptional changes driven by heat shock. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 19431-19439.	3.3	87
20	The Notch signaling pathway promotes basophil responses during helminth-induced type 2 inflammation. <i>Journal of Experimental Medicine</i> , 2019, 216, 1268-1279.	4.2	26
21	AlleleHMM: a data-driven method to identify allele specific differences in distributed functional genomic marks. <i>Nucleic Acids Research</i> , 2019, 47, e64-e64.	6.5	2
22	Parallel evolution of ancient, pleiotropic enhancers underlies butterfly wing pattern mimicry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24174-24183.	3.3	102
23	Simultaneous multiplexed amplicon sequencing and transcriptome profiling in single cells. <i>Nature Methods</i> , 2019, 16, 59-62.	9.0	68
24	Identification of regulatory elements from nascent transcription using dREG. <i>Genome Research</i> , 2019, 29, 293-303.	2.4	85
25	Discovering Transcriptional Regulatory Elements From Run-On and Sequencing Data Using the Web-Based dREG Gateway. <i>Current Protocols in Bioinformatics</i> , 2019, 66, e70.	25.8	27
26	Dynamic evolution of regulatory element ensembles in primate CD4+ T cells. <i>Nature Ecology and Evolution</i> , 2018, 2, 537-548.	3.4	65
27	Herpes Simplex Virus 1 Dramatically Alters Loading and Positioning of RNA Polymerase II on Host Genes Early in Infection. <i>Journal of Virology</i> , 2018, 92, .	1.5	51
28	Building a Science Gateway For Processing and Modeling Sequencing Data Via Apache Airavata. , 2018, 2018, .		4
29	Chromatin run-on and sequencing maps the transcriptional regulatory landscape of glioblastoma multiforme. <i>Nature Genetics</i> , 2018, 50, 1553-1564.	9.4	108
30	A bi-stable feedback loop between GDNF, EGR1, and ER α contribute to endocrine resistant breast cancer. <i>PLoS ONE</i> , 2018, 13, e0194522.	1.1	5
31	ER-positive breast cancer cells are poised for RET-mediated endocrine resistance. <i>PLoS ONE</i> , 2018, 13, e0194023.	1.1	19
32	A common pattern of DNase I footprinting throughout the human mtDNA unveils clues for a chromatin-like organization. <i>Genome Research</i> , 2018, 28, 1158-1168.	2.4	15
33	Initiation of mtDNA transcription is followed by pausing, and diverges across human cell types and during evolution. <i>Genome Research</i> , 2017, 27, 362-373.	2.4	41
34	Nascent RNA sequencing reveals a dynamic global transcriptional response at genes and enhancers to the natural medicinal compound celastrol. <i>Genome Research</i> , 2017, 27, 1816-1829.	2.4	31
35	Transcriptional response to stress is pre-wired by promoter and enhancer architecture. <i>Nature Communications</i> , 2017, 8, 255.	5.8	136
36	XX Disorder of Sex Development is associated with an insertion on chromosome 9 and downregulation of RSPO1 in dogs (<i>Canis lupus familiaris</i>). <i>PLoS ONE</i> , 2017, 12, e0186331.	1.1	12

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37	Base-pair-resolution genome-wide mapping of active RNA polymerases using precision nuclear run-on (PRO-seq). <i>Nature Protocols</i> , 2016, 11, 1455-1476.	5.5	392
38	Poised for development. <i>Nature Genetics</i> , 2016, 48, 822-823.	9.4	6
39	RTFBSDB: an integrated framework for transcription factor binding site analysis. <i>Bioinformatics</i> , 2016, 32, 3024-3026.	1.8	27
40	Mammalian Heat Shock Response and Mechanisms Underlying Its Genome-wide Transcriptional Regulation. <i>Molecular Cell</i> , 2016, 62, 63-78.	4.5	322
41	GAGA Factor Maintains Nucleosome-Free Regions and Has a Role in RNA Polymerase II Recruitment to Promoters. <i>PLoS Genetics</i> , 2015, 11, e1005108.	1.5	87
42	A unified architecture of transcriptional regulatory elements. <i>Trends in Genetics</i> , 2015, 31, 426-433.	2.9	173
43	Identification of active transcriptional regulatory elements from GRO-seq data. <i>Nature Methods</i> , 2015, 12, 433-438.	9.0	198
44	groHMM: a computational tool for identifying unannotated and cell type-specific transcription units from global run-on sequencing data. <i>BMC Bioinformatics</i> , 2015, 16, 222.	1.2	57
45	Analysis of nascent RNA identifies a unified architecture of initiation regions at mammalian promoters and enhancers. <i>Nature Genetics</i> , 2014, 46, 1311-1320.	9.4	572
46	Dynamic reorganization of the AC16 cardiomyocyte transcriptome in response to TNF α signaling revealed by integrated genomic analyses. <i>BMC Genomics</i> , 2014, 15, 155.	1.2	39
47	Signaling Pathways Differentially Affect RNA Polymerase II Initiation, Pausing, and Elongation Rate in Cells. <i>Molecular Cell</i> , 2013, 50, 212-222.	4.5	300
48	Enhancer transcripts mark active estrogen receptor binding sites. <i>Genome Research</i> , 2013, 23, 1210-1223.	2.4	410
49	Gene Regulation by CcpA and Catabolite Repression Explored by RNA-Seq in <i>Streptococcus mutans</i> . <i>PLoS ONE</i> , 2013, 8, e60465.	1.1	74
50	A Rapid, Extensive, and Transient Transcriptional Response to Estrogen Signaling in Breast Cancer Cells. <i>Cell</i> , 2011, 145, 622-634.	13.5	458
51	Bayesian inference of ancient human demography from individual genome sequences. <i>Nature Genetics</i> , 2011, 43, 1031-1034.	9.4	526
52	Ultrastructural changes in cardiac myocytes from Boxer dogs with arrhythmogenic right ventricular cardiomyopathy. <i>Journal of Veterinary Cardiology</i> , 2011, 13, 101-113.	0.3	41
53	Complete Khoisan and Bantu genomes from southern Africa. <i>Nature</i> , 2010, 463, 943-947.	13.7	400
54	Identification of gene co-regulatory modules and associated cis-elements involved in degenerative heart disease. <i>BMC Medical Genomics</i> , 2009, 2, 31.	0.7	7

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55	Bioinformatic identification of novel putative photoreceptor specific cis-elements. BMC Bioinformatics, 2007, 8, 407.	1.2	4
56	MeCP2 Expression in Human Cerebral Cortex and Lymphoid Cells: Immunochemical Characterization of a Novel Higher-Molecular-Weight Form. Journal of Child Neurology, 2003, 18, 675-682.	0.7	10
57	DART-seq. Protocol Exchange, 0, , .	0.3	1
58	Genetic dissection of the RNA polymerase II transcription cycle. ELife, 0, 11, .	2.8	9