

Jing-Dong J Han

List of Publications by Year in descending order

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Version: 2024-02-01

105
papers

10,621
citations

61984

43
h-index

33894

99
g-index

112
all docs

112
docs citations

112
times ranked

15362
citing authors

#	ARTICLE	IF	CITATIONS
1	Evidence for dynamically organized modularity in the yeast protein-protein interaction network. <i>Nature</i> , 2004, 430, 88-93.	27.8	1,683
2	A Map of the Interactome Network of the Metazoan <i>C. elegans</i> . <i>Science</i> , 2004, 303, 540-543.	12.6	1,587
3	Network modeling links breast cancer susceptibility and centrosome dysfunction. <i>Nature Genetics</i> , 2007, 39, 1338-1349.	21.4	602
4	Annotation Transfer Between Genomes: Protein-Protein Interologs and Protein-DNA Regulogs. <i>Genome Research</i> , 2004, 14, 1107-1118.	5.5	516
5	Individual variation of the SARS-CoV-2 receptor ACE2 gene expression and regulation. <i>Aging Cell</i> , 2020, 19, e13168.	6.7	343
6	Effect of sampling on topology predictions of protein-protein interaction networks. <i>Nature Biotechnology</i> , 2005, 23, 839-844.	17.5	302
7	The metabolic ER stress sensor IRE1 α suppresses alternative activation of macrophages and impairs energy expenditure in obesity. <i>Nature Immunology</i> , 2017, 18, 519-529.	14.5	279
8	Predictive models of molecular machines involved in <i>Caenorhabditis elegans</i> early embryogenesis. <i>Nature</i> , 2005, 436, 861-865.	27.8	260
9	Direct reprogramming of fibroblasts into endothelial cells capable of angiogenesis and reendothelialization in tissue-engineered vessels. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13793-13798.	7.1	235
10	Spatial transcriptomic analysis of cryosectioned tissue samples with Geo-seq. <i>Nature Protocols</i> , 2017, 12, 566-580.	12.0	213
11	Histone Demethylase UTX-1 Regulates <i>C. elegans</i> Life Span by Targeting the Insulin/IGF-1 Signaling Pathway. <i>Cell Metabolism</i> , 2011, 14, 161-172.	16.2	206
12	Spatial Transcriptome for the Molecular Annotation of Lineage Fates and Cell Identity in Mid-gastrula Mouse Embryo. <i>Developmental Cell</i> , 2016, 36, 681-697.	7.0	201
13	MicroRNA miR-24 inhibits erythropoiesis by targeting activin type I receptor ALK4. <i>Blood</i> , 2008, 111, 588-595.	1.4	195
14	Aging and Alzheimer's disease: Comparison and associations from molecular to system level. <i>Aging Cell</i> , 2018, 17, e12802.	6.7	180
15	A human circulating immune cell landscape in aging and COVID-19. <i>Protein and Cell</i> , 2020, 11, 740-770.	11.0	179
16	Molecular architecture of lineage allocation and tissue organization in early mouse embryo. <i>Nature</i> , 2019, 572, 528-532.	27.8	163
17	A modular network model of aging. <i>Molecular Systems Biology</i> , 2007, 3, 147.	7.2	151
18	Molecular mechanisms underlying genotype-dependent responses to dietary restriction. <i>Aging Cell</i> , 2013, 12, 1050-1061.	6.7	137

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19	BMP4 Signaling Acts via Dual-Specificity Phosphatase 9 to Control ERK Activity in Mouse Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2012, 10, 171-182.	11.1	134
20	Evolution of Alu Elements toward Enhancers. <i>Cell Reports</i> , 2014, 7, 376-385.	6.4	134
21	Systematic Prediction of Pharmacodynamic Drug-Drug Interactions through Protein-Protein-Interaction Network. <i>PLoS Computational Biology</i> , 2013, 9, e1002998.	3.2	130
22	Inferring causal relationships among different histone modifications and gene expression. <i>Genome Research</i> , 2008, 18, 1314-1324.	5.5	116
23	Genome-wide mapping of SMAD target genes reveals the role of BMP signaling in embryonic stem cell fate determination. <i>Genome Research</i> , 2010, 20, 36-44.	5.5	108
24	Three-dimensional human facial morphologies as robust aging markers. <i>Cell Research</i> , 2015, 25, 574-587.	12.0	97
25	Dissecting the precise role of H3K9 methylation in crosstalk with DNA maintenance methylation in mammals. <i>Nature Communications</i> , 2016, 7, 12464.	12.8	94
26	Identification of the Proliferation/Differentiation Switch in the Cellular Network of Multicellular Organisms. <i>PLoS Computational Biology</i> , 2006, 2, e145.	3.2	91
27	WormFarm: a quantitative control and measurement device toward automated <i>Caenorhabditis elegans</i> aging analysis. <i>Aging Cell</i> , 2013, 12, 398-409.	6.7	90
28	Confirmation of Organized Modularity in the Yeast Interactome. <i>PLoS Biology</i> , 2007, 5, e153.	5.6	86
29	Smooth Muscle Cells Differentiated From Reprogrammed Embryonic Lung Fibroblasts Through DKK3 Signaling Are Potent for Tissue Engineering of Vascular Grafts. <i>Circulation Research</i> , 2013, 112, 1433-1443.	4.5	83
30	PKA phosphorylation couples hepatic inositol-requiring enzyme 1 α to glucagon signaling in glucose metabolism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 15852-15857.	7.1	76
31	Distinct biological ages of organs and systems identified from a multi-omics study. <i>Cell Reports</i> , 2022, 38, 110459.	6.4	74
32	IntNetDB v1.0: an integrated protein-protein interaction network database generated by a probabilistic model. <i>BMC Bioinformatics</i> , 2006, 7, 508.	2.6	73
33	Ribosome 18S m6A Methyltransferase METTL5 Promotes Translation Initiation and Breast Cancer Cell Growth. <i>Cell Reports</i> , 2020, 33, 108544.	6.4	71
34	A Systems Approach to Reverse Engineer Lifespan Extension by Dietary Restriction. <i>Cell Metabolism</i> , 2016, 23, 529-540.	16.2	67
35	Smad2 mediates Activin/Nodal signaling in mesendoderm differentiation of mouse embryonic stem cells. <i>Cell Research</i> , 2010, 20, 1306-1318.	12.0	62
36	The strand-biased mitochondrial DNA methylome and its regulation by DNMT3A. <i>Genome Research</i> , 2019, 29, 1622-1634.	5.5	62

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37	Apoptosin is a Novel Pro-Apoptotic Protein and Mediates Cell Death in Neurodegeneration. Journal of Neuroscience, 2012, 32, 15565-15576.	3.6	58
38	HER2/EGFR- AKT Signaling Switches $\text{TGF}\beta^2$ from Inhibiting Cell Proliferation to Promoting Cell Migration in Breast Cancer. Cancer Research, 2018, 78, 6073-6085.	0.9	58
39	Midlife gene expressions identify modulators of aging through dietary interventions. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1201-9.	7.1	57
40	Repression of human and mouse brain inflammaging transcriptome by broad gene-body histone hyperacetylation. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 7611-7616.	7.1	55
41	Transcriptome analyses of rhesus monkey preimplantation embryos reveal a reduced capacity for DNA double-strand break repair in primate oocytes and early embryos. Genome Research, 2017, 27, 567-579.	5.5	54
42	Epigenomics and the regulation of aging. Epigenomics, 2013, 5, 205-227.	2.1	52
43	The effects of graded levels of calorie restriction: III. Impact of short term calorie and protein restriction on mean daily body temperature and torpor use in the C57BL/6 mouse. Oncotarget, 2015, 6, 18314-18337.	1.8	51
44	Cross-species metabolomic analysis identifies uridine as a potent regeneration promoting factor. Cell Discovery, 2022, 8, 6.	6.7	50
45	The effects of graded levels of calorie restriction: IX. Global metabolomic screen reveals modulation of carnitines, sphingolipids and bile acids in the liver of C57BL/6 mice. Aging Cell, 2017, 16, 529-540.	6.7	48
46	Accurate loop calling for 3D genomic data with cLoops. Bioinformatics, 2020, 36, 666-675.	4.1	47
47	A 3D Atlas of Hematopoietic Stem and Progenitor Cell Expansion by Multi-dimensional RNA-Seq Analysis. Cell Reports, 2019, 27, 1567-1578.e5.	6.4	45
48	Widespread roles of enhancer-like transposable elements in cell identity and long-range genomic interactions. Genome Research, 2019, 29, 40-52.	5.5	45
49	Three-dimensional facial-image analysis to predict heterogeneity of the human ageing rate and the impact of lifestyle. Nature Metabolism, 2020, 2, 946-957.	11.9	45
50	Stress-associated H^3K^4 methylation accumulates during postnatal development and aging of rhesus macaque brain. Aging Cell, 2012, 11, 1055-1064.	6.7	44
51	Impacts of protein-protein interaction domains on organism and network complexity. Genome Research, 2008, 18, 1500-1508.	5.5	42
52	Impact of Dietary Interventions on Noncoding RNA Networks and mRNAs Encoding Chromatin-Related Factors. Cell Reports, 2017, 18, 2957-2968.	6.4	42
53	The effects of graded levels of calorie restriction: V. Impact of short term calorie and protein restriction on physical activity in the C57BL/6 mouse. Oncotarget, 2016, 7, 19147-19170.	1.8	37
54	CoCiter: An Efficient Tool to Infer Gene Function by Assessing the Significance of Literature Co-Citation. PLoS ONE, 2013, 8, e74074.	2.5	36

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55	A single-cell resolution developmental atlas of hematopoietic stem and progenitor cell expansion in zebrafish. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	34
56	CXXC5 suppresses hepatocellular carcinoma by promoting TGF- β -induced cell cycle arrest and apoptosis. <i>Journal of Molecular Cell Biology</i> , 2018, 10, 48-59.	3.3	33
57	Inference of differentiation time for single cell transcriptomes using cell population reference data. <i>Nature Communications</i> , 2017, 8, 1856.	12.8	30
58	Epigenetic regulation by nuclear receptors. <i>Epigenomics</i> , 2011, 3, 59-72.	2.1	29
59	Transcriptome analysis reveals determinant stages controlling human embryonic stem cell commitment to neuronal cells. <i>Journal of Biological Chemistry</i> , 2017, 292, 19590-19604.	3.4	29
60	Immune Cell Types and Secreted Factors Contributing to Inflammation-to-Cancer Transition and Immune Therapy Response. <i>Cell Reports</i> , 2019, 26, 1965-1977.e4.	6.4	28
61	Activin/Smad2-induced Histone H3 Lys-27 Trimethylation (H3K27me3) Reduction Is Crucial to Initiate Mesendoderm Differentiation of Human Embryonic Stem Cells. <i>Journal of Biological Chemistry</i> , 2017, 292, 1339-1350.	3.4	26
62	Histone deacetylation promotes mouse neural induction by restricting Nodal-dependent mesendoderm fate. <i>Nature Communications</i> , 2015, 6, 6830.	12.8	25
63	Single-cell RNA-sequencing reveals the existence of naive and primed pluripotency in pre-implantation rhesus monkey embryos. <i>Genome Research</i> , 2018, 28, 1481-1493.	5.5	25
64	De novo generation of macrophage from placenta-derived hemogenic endothelium. <i>Developmental Cell</i> , 2021, 56, 2121-2133.e6.	7.0	25
65	BACH1 recruits NANOG and histone H3 lysine 4 methyltransferase MLL/SET1 complexes to regulate enhancerâ€“promoter activity and maintains pluripotency. <i>Nucleic Acids Research</i> , 2021, 49, 1972-1986.	14.5	24
66	Assessing the rate of aging to monitor aging itself. <i>Ageing Research Reviews</i> , 2021, 69, 101350.	10.9	24
67	The effects of graded levels of calorie restriction: VI. Impact of short-term graded calorie restriction on transcriptomic responses of the hypothalamic hunger and circadian signaling pathways. <i>Aging</i> , 2016, 8, 642-661.	3.1	24
68	Ageing induces tissueâ€“specific transcriptomic changes in <i>Caenorhabditis elegans</i> . <i>EMBO Journal</i> , 2022, 41, e109633.	7.8	22
69	A novel Bayesian network inference algorithm for integrative analysis of heterogeneous deep sequencing data. <i>Cell Research</i> , 2013, 23, 440-443.	12.0	20
70	Ab initio identification of transcription start sites in the Rhesus macaque genome by histone modification and RNA-Seq. <i>Nucleic Acids Research</i> , 2011, 39, 1408-1418.	14.5	19
71	The precursor of PI(3,4,5)P3 alleviates aging by activating daf-18(Pten) and independent of daf-16. <i>Nature Communications</i> , 2020, 11, 4496.	12.8	19
72	LINâ€“28 balances longevity and germline stem cell number in <i>Caenorhabditis elegans</i> through letâ€“7<i>/i>-AKT<i>/i>-DAFâ€“16 axis. <i>Aging Cell</i> , 2017, 16, 113-124.	6.7	18

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73	Classification and prediction of toxicity of chemicals using an automated phenotypic profiling of <i>Caenorhabditis elegans</i> . <i>BMC Pharmacology & Toxicology</i> , 2018, 19, 18.	2.4	18
74	Dynamics of Wnt activity on the acquisition of ectoderm potency in epiblast stem cells. <i>Development</i> (Cambridge), 2019, 146, .	2.5	18
75	Integrative genomic analysis of early neurogenesis reveals a temporal genetic program for differentiation and specification of preplate and Cajal-Retzius neurons. <i>PLoS Genetics</i> , 2021, 17, e1009355.	3.5	15
76	Aging-associated lncRNAs are evolutionarily conserved and participate in NF- κ B signaling. <i>Nature Aging</i> , 2021, 1, 438-453.	11.6	15
77	The Effects of Graded Levels of Calorie Restriction: XIII. Global Metabolomics Screen Reveals Graded Changes in Circulating Amino Acids, Vitamins, and Bile Acids in the Plasma of C57BL/6 Mice. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2019, 74, 16-26.	3.6	14
78	The Effects of Graded Levels of Calorie Restriction: XIV. Global Metabolomics Screen Reveals Brown Adipose Tissue Changes in Amino Acids, Catecholamines, and Antioxidants After Short-Term Restriction in C57BL/6 Mice. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2020, 75, 218-229.	3.6	14
79	H3K14me3 genomic distributions and its regulation by KDM4 family demethylases. <i>Cell Research</i> , 2018, 28, 1118-1120.	12.0	13
80	An advanced fragment analysis-based individualized subtype classification of pediatric acute lymphoblastic leukemia. <i>Scientific Reports</i> , 2015, 5, 12435.	3.3	12
81	Bioimaging for quantitative phenotype analysis. <i>Methods</i> , 2016, 102, 20-25.	3.8	12
82	The Effects of Graded Levels of Calorie Restriction: XVI. Metabolomic Changes in the Cerebellum Indicate Activation of Hypothalamocerebellar Connections Driven by Hunger Responses. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2021, 76, 601-610.	3.6	8
83	Functional Dissection of Regulatory Models Using Gene Expression Data of Deletion Mutants. <i>PLoS Genetics</i> , 2013, 9, e1003757.	3.5	7
84	Characterization of functional transposable element enhancers in acute myeloid leukemia. <i>Science China Life Sciences</i> , 2020, 63, 675-687.	4.9	7
85	Single-cell-level spatial gene expression in the embryonic neural differentiation niche. <i>Genome Research</i> , 2015, 25, 570-581.	5.5	6
86	Mouse gastrulation: Attributes of transcription factor regulatory network for epiblast patterning. <i>Development Growth and Differentiation</i> , 2018, 60, 463-472.	1.5	6
87	A gene regulatory network anchored by LIM homeobox 1 for embryonic head development. <i>Genesis</i> , 2018, 56, e23246.	1.6	6
88	Comparing the biological coherence of network clusters identified by different detection algorithms. <i>Science Bulletin</i> , 2007, 52, 2938-2944.	1.7	5
89	Application of Bayesian networks on large-scale biological data. <i>Frontiers in Biology</i> , 2010, 5, 98-104.	0.7	5
90	Understanding super-enhancers. <i>Science China Life Sciences</i> , 2016, 59, 277-280.	4.9	5

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91	A High-throughput Assay for the Prediction of Chemical Toxicity by Automated Phenotypic Profiling of <i>Caenorhabditis elegans</i> . Journal of Visualized Experiments, 2019, , .	0.3	5
92	Regulatory network characterization in development: challenges and opportunities. F1000Research, 2018, 7, 1477.	1.6	4
93	Understanding human diseases with high-throughput quantitative measurement and analysis of molecular signatures. Science China Life Sciences, 2013, 56, 213-219.	4.9	3
94	Inter-nucleosomal communication between histone modifications for nucleosome phasing. PLoS Computational Biology, 2018, 14, e1006416.	3.2	3
95	The system capacity view of aging and longevity. Quantitative Biology, 2017, 5, 251-259.	0.5	2
96	Aging phenomics enabled by quantitative imaging analysis. Oncotarget, 2015, 6, 16794-16795.	1.8	2
97	Reply to Toward the complete interactome. Nature Biotechnology, 2006, 24, 615-615.	17.5	1
98	Approaches to uncovering cancer diagnostic and prognostic molecular signatures. Molecular and Cellular Oncology, 2014, 1, e957981.	0.7	1
99	Systems Approaches to Understanding Aging. , 2016, , 241-261.		1
100	Systems Biology in Aging Research. Advances in Experimental Medicine and Biology, 2018, 1086, 1-15.	1.6	1
101	Targeting Ageing to Decrease Complex Non-Communicable Human Diseases. Journal of Genetics and Genomics, 2014, 41, 457-458.	3.9	0
102	A digitized catalog of COVID-19 epidemiology data. Quantitative Biology, 2021, 9, 23-46.	0.5	0
103	Epigenomic, Transcriptome and Image-Based Biomarkers of Aging. Healthy Ageing and Longevity, 2019, , 47-66.	0.2	0
104	A 3D Atlas of Hematopoietic Stem and Progenitor Cell Expansion by Multi-Dimensional RNA-Seq Analysis. SSRN Electronic Journal, 0, , .	0.4	0
105	Immunosuppression Induced by Brain-Specific HDAC6 Knockdown Improves Aging Performance in <i>Drosophila melanogaster</i> . Phenomics, 0, , 1.	2.9	0