Jing-Dong J Han

List of Publications by Year
in descending order

105 papers	10,621 citations	61857 43 h-index	33814 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. Nature, 2004, 430, 88-93.	13.7	1,683
2	A Map of the Interactome Network of the Metazoan C. elegans. Science, 2004, 303, 540-543.	6.0	1,587
3	Network modeling links breast cancer susceptibility and centrosome dysfunction. Nature Genetics, 2007, 39, 1338-1349.	9.4	602
4	Annotation Transfer Between Genomes: Protein-Protein Interologs and Protein-DNA Regulogs. Genome Research, 2004, 14, 1107-1118.	2.4	516
5	Individual variation of the SARS–CoV–2 receptor ACE2 gene expression and regulation. Aging Cell, 2020, 19, e13168.	3.0	343
6	Effect of sampling on topology predictions of protein-protein interaction networks. Nature Biotechnology, 2005, 23, 839-844.	9.4	302
7	The metabolic ER stress sensor IRE1α suppresses alternative activation of macrophages and impairs energy expenditure in obesity. Nature Immunology, 2017, 18, 519-529.	7.0	279
8	Predictive models of molecular machines involved in Caenorhabditis elegans early embryogenesis. Nature, 2005, 436, 861-865.	13.7	260
9	Direct reprogramming of fibroblasts into endothelial cells capable of angiogenesis and reendothelialization in tissue-engineered vessels. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 13793-13798.	3.3	235
10	Spatial transcriptomic analysis of cryosectioned tissue samples with Geo-seq. Nature Protocols, 2017, 12, 566-580.	5.5	213
11	Histone Demethylase UTX-1 Regulates C.Âelegans Life Span by Targeting the Insulin/IGF-1 Signaling Pathway. Cell Metabolism, 2011, 14, 161-172.	7.2	206
12	Spatial Transcriptome for the Molecular Annotation of Lineage Fates and Cell Identity in Mid-gastrula Mouse Embryo. Developmental Cell, 2016, 36, 681-697.	3.1	201
13	MicroRNA miR-24 inhibits erythropoiesis by targeting activin type I receptor ALK4. Blood, 2008, 111, 588-595.	0.6	195
14	Aging and Alzheimer's disease: Comparison and associations from molecular to system level. Aging Cell, 2018, 17, e12802.	3.0	180
15	A human circulating immune cell landscape in aging and COVID-19. Protein and Cell, 2020, 11, 740-770.	4.8	179
16	Molecular architecture of lineage allocation and tissue organization in early mouse embryo. Nature, 2019, 572, 528-532.	13.7	163
17	A modular network model of aging. Molecular Systems Biology, 2007, 3, 147.	3.2	151
18	Molecular mechanisms underlying genotype‐dependent responses to dietary restriction. Aging Cell, 2013, 12, 1050-1061.	3.0	137

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19	BMP4 Signaling Acts via Dual-Specificity Phosphatase 9 to Control ERK Activity in Mouse Embryonic Stem Cells. Cell Stem Cell, 2012, 10, 171-182.	5.2	134
20	Evolution of Alu Elements toward Enhancers. Cell Reports, 2014, 7, 376-385.	2.9	134
21	Systematic Prediction of Pharmacodynamic Drug-Drug Interactions through Protein-Protein-Interaction Network. PLoS Computational Biology, 2013, 9, e1002998.	1.5	130
22	Inferring causal relationships among different histone modifications and gene expression. Genome Research, 2008, 18, 1314-1324.	2.4	116
23	Genome-wide mapping of SMAD target genes reveals the role of BMP signaling in embryonic stem cell fate determination. Genome Research, 2010, 20, 36-44.	2.4	108
24	Three-dimensional human facial morphologies as robust aging markers. Cell Research, 2015, 25, 574-587.	5.7	97
25	Dissecting the precise role of H3K9 methylation in crosstalk with DNA maintenance methylation in mammals. Nature Communications, 2016, 7, 12464.	5.8	94
26	Identification of the Proliferation/Differentiation Switch in the Cellular Network of Multicellular Organisms. PLoS Computational Biology, 2006, 2, e145.	1.5	91
27	WormFarm: a quantitative control and measurement device toward automated *Caenorhabditis elegans* aging analysis. Aging Cell, 2013, 12, 398-409.	3.0	90
28	Confirmation of Organized Modularity in the Yeast Interactome. PLoS Biology, 2007, 5, e153.	2.6	86
29	Smooth Muscle Cells Differentiated From Reprogrammed Embryonic Lung Fibroblasts Through DKK3 Signaling Are Potent for Tissue Engineering of Vascular Grafts. Circulation Research, 2013, 112, 1433-1443.	2.0	83
30	PKA phosphorylation couples hepatic inositol-requiring enzyme 1α to glucagon signaling in glucose metabolism. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 15852-15857.	3.3	76
31	Distinct biological ages of organs and systems identified from a multi-omics study. Cell Reports, 2022, 38, 110459.	2.9	74
32	IntNetDB v1.0: an integrated protein-protein interaction network database generated by a probabilistic model. BMC Bioinformatics, 2006, 7, 508.	1.2	73
33	Ribosome 18S m6A Methyltransferase METTL5 Promotes Translation Initiation and Breast Cancer Cell Growth. Cell Reports, 2020, 33, 108544.	2.9	71
34	A Systems Approach to Reverse Engineer Lifespan Extension by Dietary Restriction. Cell Metabolism, 2016, 23, 529-540.	7.2	67
35	Smad2 mediates Activin/Nodal signaling in mesendoderm differentiation of mouse embryonic stem cells. Cell Research, 2010, 20, 1306-1318.	5.7	62
36	The strand-biased mitochondrial DNA methylome and its regulation by DNMT3A. Genome Research, 2019, 29, 1622-1634.	2.4	62

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37	Appoptosin is a Novel Pro-Apoptotic Protein and Mediates Cell Death in Neurodegeneration. Journal of Neuroscience, 2012, 32, 15565-15576.	1.7	58
38	HER2/EGFRâ€"AKT Signaling Switches TGFÎ² from Inhibiting Cell Proliferation to Promoting Cell Migration in Breast Cancer. Cancer Research, 2018, 78, 6073-6085.	0.4	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.	3.3	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.	3.3	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.	2.4	54
42	Epigenomics and the regulation of aging. Epigenomics, 2013, 5, 205-227.	1.0	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.	0.8	51
44	Cross-species metabolomic analysis identifies uridine as a potent regeneration promoting factor. Cell Discovery, 2022, 8, 6.	3.1	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.	3.0	48
46	Accurate loop calling for 3D genomic data with cLoops. Bioinformatics, 2020, 36, 666-675.	1.8	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.	2.9	45
48	Widespread roles of enhancer-like transposable elements in cell identity and long-range genomic interactions. Genome Research, 2019, 29, 40-52.	2.4	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.	5.1	45
50	Stressâ€associated <scp>H</scp>3<scp>K</scp>4 methylation accumulates during postnatal development and aging of rhesus macaque brain. Aging Cell, 2012, 11, 1055-1064.	3.0	44
51	Impacts of proteinâ€"protein interaction domains on organism and network complexity. Genome Research, 2008, 18, 1500-1508.	2.4	42
52	Impact of Dietary Interventions on Noncoding RNA Networks and mRNAs Encoding Chromatin-Related Factors. Cell Reports, 2017, 18, 2957-2968.	2.9	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.	0.8	37
54	CoCiter: An Efficient Tool to Infer Gene Function by Assessing the Significance of Literature Co-Citation. PLoS ONE, 2013, 8, e74074.	1.1	36

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55	A single-cell resolution developmental atlas of hematopoietic stem and progenitor cell expansion in zebrafish. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	34
56	CXXC5 suppresses hepatocellular carcinoma by promoting TGF-Î²-induced cell cycle arrest and apoptosis. Journal of Molecular Cell Biology, 2018, 10, 48-59.	1.5	33
57	Inference of differentiation time for single cell transcriptomes using cell population reference data. Nature Communications, 2017, 8, 1856.	5.8	30
58	Epigenetic regulation by nuclear receptors. Epigenomics, 2011, 3, 59-72.	1.0	29
59	Transcriptome analysis reveals determinant stages controlling human embryonic stem cell commitment to neuronal cells. Journal of Biological Chemistry, 2017, 292, 19590-19604.	1.6	29
60	Immune Cell Types and Secreted Factors Contributing to Inflammation-to-Cancer Transition and Immune Therapy Response. Cell Reports, 2019, 26, 1965-1977.e4.	2.9	28
61	Activin/Smad2-induced Histone H3 Lys-27 Trimethylation (H3K27me3) Reduction Is Crucial to Initiate Mesendoderm Differentiation of Human Embryonic Stem Cells. Journal of Biological Chemistry, 2017, 292, 1339-1350.	1.6	26
62	Histone deacetylation promotes mouse neural induction by restricting Nodal-dependent mesendoderm fate. Nature Communications, 2015, 6, 6830.	5.8	25
63	Single-cell RNA-sequencing reveals the existence of naive and primed pluripotency in pre-implantation rhesus monkey embryos. Genome Research, 2018, 28, 1481-1493.	2.4	25
64	De novo generation of macrophage from placenta-derived hemogenic endothelium. Developmental Cell, 2021, 56, 2121-2133.e6.	3.1	25
65	BACH1 recruits NANOG and histone H3 lysine 4 methyltransferase MLL/SET1 complexes to regulate enhancerâ€"promoter activity and maintains pluripotency. Nucleic Acids Research, 2021, 49, 1972-1986.	6.5	24
66	Assessing the rate of aging to monitor aging itself. Ageing Research Reviews, 2021, 69, 101350.	5.0	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. Aging, 2016, 8, 642-661.	1.4	24
68	Ageing induces tissueâ€specific transcriptomic changes in <i>Caenorhabditis elegans</i>. EMBO Journal, 2022, 41, e109633.	3.5	22
69	A novel Bayesian network inference algorithm for integrative analysis of heterogeneous deep sequencing data. Cell Research, 2013, 23, 440-443.	5.7	20
70	Ab initio identification of transcription start sites in the Rhesus macaque genome by histone modification and RNA-Seq. Nucleic Acids Research, 2011, 39, 1408-1418.	6.5	19
71	The precursor of PI(3,4,5)P3 alleviates aging by activating daf-18(Pten) and independent of daf-16. Nature Communications, 2020, 11, 4496.	5.8	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. Aging Cell, 2017, 16, 113-124.	3.0	18

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73	Classification and prediction of toxicity of chemicals using an automated phenotypic profiling of Caenorhabditis elegans. BMC Pharmacology & Toxicology, 2018, 19, 18.	1.0	18
74	Dynamics of Wnt activity on the acquisition of ectoderm potency in epiblast stem cells. Development (Cambridge), 2019, 146, .	1.2	18
75	Integrative genomic analysis of early neurogenesis reveals a temporal genetic program for differentiation and specification of preplate and Cajal-Retzius neurons. PLoS Genetics, 2021, 17, e1009355.	1.5	15
76	Aging-associated lncRNAs are evolutionarily conserved and participate in NFÎºB signaling. Nature Aging, 2021, 1, 438-453.	5.3	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. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2019, 74, 16-26.	1.7	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. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2020, 75, 218-229.	1.7	14
79	H3K14me3 genomic distributions and its regulation by KDM4 family demethylases. Cell Research, 2018, 28, 1118-1120.	5.7	13
80	An advanced fragment analysis-based individualized subtype classification of pediatric acute lymphoblastic leukemia. Scientific Reports, 2015, 5, 12435.	1.6	12
81	Bioimaging for quantitative phenotype analysis. Methods, 2016, 102, 20-25.	1.9	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. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2021, 76, 601-610.	1.7	8
83	Functional Dissection of Regulatory Models Using Gene Expression Data of Deletion Mutants. PLoS Genetics, 2013, 9, e1003757.	1.5	7
84	Characterization of functional transposable element enhancers in acute myeloid leukemia. Science China Life Sciences, 2020, 63, 675-687.	2.3	7
85	Single-cell-level spatial gene expression in the embryonic neural differentiation niche. Genome Research, 2015, 25, 570-581.	2.4	6
86	Mouse gastrulation: Attributes of transcription factor regulatory network for epiblast patterning. Development Growth and Differentiation, 2018, 60, 463-472.	0.6	6
87	A gene regulatory network anchored by LIM homeobox 1 for embryonic head development. Genesis, 2018, 56, e23246.	0.8	6
88	Comparing the biological coherence of network clusters identified by different detection algorithms. Science Bulletin, 2007, 52, 2938-2944.	1.7	5
89	Application of Bayesian networks on large-scale biological data. Frontiers in Biology, 2010, 5, 98-104.	0.7	5
90	Understanding super-enhancers. Science China Life Sciences, 2016, 59, 277-280.	2.3	5

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91	A High-throughput Assay for the Prediction of Chemical Toxicity by Automated Phenotypic Profiling of Caenorhabditis elegans. Journal of Visualized Experiments, 2019, , .	0.2	5
92	Regulatory network characterization in development: challenges and opportunities. F1000Research, 2018, 7, 1477.	0.8	4
93	Understanding human diseases with high-throughput quantitative measurement and analysis of molecular signatures. Science China Life Sciences, 2013, 56, 213-219.	2.3	3
94	Inter-nucleosomal communication between histone modifications for nucleosome phasing. PLoS Computational Biology, 2018, 14, e1006416.	1.5	3
95	The system capacity view of aging and longevity. Quantitative Biology, 2017, 5, 251-259.	0.3	2
96	Aging phenomics enabled by quantitative imaging analysis. Oncotarget, 2015, 6, 16794-16795.	0.8	2
97	Reply to Toward the complete interactome. Nature Biotechnology, 2006, 24, 615-615.	9.4	1
98	Approaches to uncovering cancer diagnostic and prognostic molecular signatures. Molecular and Cellular Oncology, 2014, 1, e957981.	0.3	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.	0.8	1
101	Targeting Ageing to Decrease Complex Non-Communicable Human Diseases. Journal of Genetics and Genomics, 2014, 41, 457-458.	1.7	0
102	A digitized catalog of COVIDâ€19 epidemiology data. Quantitative Biology, 2021, 9, 23-46.	0.3	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 Drosophila melanogaster. Phenomics, 0, , 1.	0.9	0