

Xianjun Dong

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6249066/publications.pdf>

Version: 2024-02-01

38
papers

20,743
citations

279798

23
h-index

345221

36
g-index

44
all docs

44
docs citations

44
times ranked

40471
citing authors

#	ARTICLE	IF	CITATIONS
1	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012, 489, 57-74.	27.8	15,516
2	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). <i>PLoS Biology</i> , 2011, 9, e1001046.	5.6	1,257
3	Sequence features and chromatin structure around the genomic regions bound by 119 human transcription factors. <i>Genome Research</i> , 2012, 22, 1798-1812.	5.5	762
4	Mbd3/NURD Complex Regulates Expression of 5-Hydroxymethylcytosine Marked Genes in Embryonic Stem Cells. <i>Cell</i> , 2011, 147, 1498-1510.	28.9	424
5	Î²2-Adrenoreceptor is a regulator of the Î±-synuclein gene driving risk of Parkinson's disease. <i>Science</i> , 2017, 357, 891-898.	12.6	341
6	An Ancient Transcription Factor Initiates the Burst of piRNA Production during Early Meiosis in Mouse Testes. <i>Molecular Cell</i> , 2013, 50, 67-81.	9.7	322
7	Factorbook.org: a Wiki-based database for transcription factor-binding data generated by the ENCODE consortium. <i>Nucleic Acids Research</i> , 2013, 41, D171-D176.	14.5	274
8	Modeling gene expression using chromatin features in various cellular contexts. <i>Genome Biology</i> , 2012, 13, R53.	9.6	231
9	Two independent transcription initiation codes overlap on vertebrate core promoters. <i>Nature</i> , 2014, 507, 381-385.	27.8	182
10	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. <i>Genome Research</i> , 2012, 22, 1658-1667.	5.5	166
11	Exosome detection via the ultrafast-isolation system: EXODUS. <i>Nature Methods</i> , 2021, 18, 212-218.	19.0	157
12	The correlation between histone modifications and gene expression. <i>Epigenomics</i> , 2013, 5, 113-116.	2.1	154
13	MicroRNAs Located in the Hox Gene Clusters Are Implicated in Huntington's Disease Pathogenesis. <i>PLoS Genetics</i> , 2014, 10, e1004188.	3.5	97
14	Transcriptional features of genomic regulatory blocks. <i>Genome Biology</i> , 2009, 10, R38.	9.6	90
15	Genome-wide survival study identifies a novel synaptic locus and polygenic score for cognitive progression in Parkinson's disease. <i>Nature Genetics</i> , 2021, 53, 787-793.	21.4	82
16	Enhancers active in dopamine neurons are a primary link between genetic variation and neuropsychiatric disease. <i>Nature Neuroscience</i> , 2018, 21, 1482-1492.	14.8	79
17	Association between Î±-synuclein blood transcripts and early, neuroimaging-supported Parkinson's disease. <i>Brain</i> , 2015, 138, 2659-2671.	7.6	69
18	Epigenetic dysregulation of hairy and enhancer of split 4 (HES4) is associated with striatal degeneration in postmortem Huntington brains. <i>Human Molecular Genetics</i> , 2015, 24, 1441-1456.	2.9	67

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19	Differential Evolution of the 13 Atlantic Salmon Hox Clusters. <i>Molecular Biology and Evolution</i> , 2008, 25, 1333-1343.	8.9	66
20	Accelerating Medicines Partnership: Parkinson's Disease. <i>Genetic Resource. Movement Disorders</i> , 2021, 36, 1795-1804.	3.9	60
21	The genetic source tracking of human urinary exosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	49
22	The Role of H3K4me3 in Transcriptional Regulation Is Altered in Huntington's Disease. <i>PLoS ONE</i> , 2015, 10, e0144398.	2.5	47
23	Exonic remnants of whole-genome duplication reveal cis-regulatory function of coding exons. <i>Nucleic Acids Research</i> , 2010, 38, 1071-1085.	14.5	46
24	WebCSEA: web-based cell-type-specific enrichment analysis of genes. <i>Nucleic Acids Research</i> , 2022, 50, W782-W790.	14.5	29
25	A pipeline for RNA-seq based eQTL analysis with automated quality control procedures. <i>BMC Bioinformatics</i> , 2021, 22, 403.	2.6	27
26	Synorth: exploring the evolution of synteny and long-range regulatory interactions in vertebrate genomes. <i>Genome Biology</i> , 2009, 10, R86.	9.6	25
27	Genome-wide association meta-analysis identifies 29 new acne susceptibility loci. <i>Nature Communications</i> , 2022, 13, 702.	12.8	23
28	Review of multi-omics data resources and integrative analysis for human brain disorders. <i>Briefings in Functional Genomics</i> , 2021, 20, 223-234.	2.7	19
29	Genetic Modifiers of Age at Onset for Parkinson's Disease in Asians: A Genome-Wide Association Study. <i>Movement Disorders</i> , 2021, 36, 2077-2084.	3.9	15
30	Understanding the effect of smoking and drinking behavior on Parkinson's disease risk: a Mendelian randomization study. <i>Scientific Reports</i> , 2021, 11, 13980.	3.3	14
31	powerEQL: an R package and shiny application for sample size and power calculation of bulk tissue and single-cell eQTL analysis. <i>Bioinformatics</i> , 2021, 37, 4269-4271.	4.1	13
32	An automated quality control pipeline for eQTL analysis with RNA-seq data. , 2019, , .		8
33	High-resolution analysis of differential gene expression during skeletal muscle atrophy and programmed cell death. <i>Physiological Genomics</i> , 2020, 52, 492-511.	2.3	8
34	Signaling Pathway Analysis Combined With the Strength Variations of Interactions Between Genes Under Different Conditions. <i>IEEE Access</i> , 2020, 8, 138036-138045.	4.2	4
35	Making enhancers from spare parts of the genome. <i>Genome Biology</i> , 2011, 12, 138.	9.6	1
36	gWord: A Tool for Genome-Wide Word Search and Count. , 2007, , .		0

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37	The brainstorm [Essay]. IEEE Potentials, 2009, 28, 8-9.	0.3	0
38	Translog, a web browser for studying the expression divergence of homologous genes. BMC Bioinformatics, 2010, 11, S59.	2.6	0