

Itoshi Nikaido

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

4,986
citations

257101

24
h-index

264894

42
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54
all docs

54
docs citations

54
times ranked

7399
citing authors

#	ARTICLE	IF	CITATIONS
1	Improved MeSH analysis software tools for farm animals. <i>Animal Genetics</i> , 2022, 53, 171-172.	0.6	0
2	A common epigenetic mechanism across different cellular origins underlies systemic immune dysregulation in an idiopathic autism mouse model. <i>Molecular Psychiatry</i> , 2022, 27, 3343-3354.	4.1	4
3	Enhanced transcriptional heterogeneity mediated by NF- κ B super-enhancers. <i>PLoS Genetics</i> , 2022, 18, e1010235.	1.5	7
4	Derepression of inflammation-related genes link to microglia activation and neural maturation defect in a mouse model of Kleefstra syndrome. <i>IScience</i> , 2021, 24, 102741.	1.9	5
5	Tracing the origin of hair follicle stem cells. <i>Nature</i> , 2021, 594, 547-552.	13.7	62
6	Single- α oocyte transcriptome analysis reveals aging-associated effects influenced by life stage and calorie restriction. <i>Aging Cell</i> , 2021, 20, e13428.	3.0	22
7	Local states of chromatin compaction at transcription start sites control transcription levels. <i>Nucleic Acids Research</i> , 2021, 49, 8007-8023.	6.5	18
8	Developmental excitation-inhibition imbalance underlying psychoses revealed by single-cell analyses of discordant twins-derived cerebral organoids. <i>Molecular Psychiatry</i> , 2020, 25, 2695-2711.	4.1	73
9	The Number of Transcription Factors at an Enhancer Determines Switch-like Gene Expression. <i>Cell Reports</i> , 2020, 31, 107724.	2.9	25
10	Genome-wide kinetic properties of transcriptional bursting in mouse embryonic stem cells. <i>Science Advances</i> , 2020, 6, eaaz6699.	4.7	66
11	An NMF-based approach to discover overlooked differentially expressed gene regions from single-cell RNA-seq data. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqz020.	1.5	5
12	Primed to Naive-Like Conversion of the Common Marmoset Embryonic Stem Cells. <i>Stem Cells and Development</i> , 2020, 29, 761-773.	1.1	14
13	Milleyfy: visualizing cell-to-cell heterogeneity in read coverage of single-cell RNA sequencing datasets. <i>BMC Genomics</i> , 2020, 21, 177.	1.2	5
14	Benchmarking single-cell RNA-sequencing protocols for cell atlas projects. <i>Nature Biotechnology</i> , 2020, 38, 747-755.	9.4	313
15	Benchmarking principal component analysis for large-scale single-cell RNA-sequencing. <i>Genome Biology</i> , 2020, 21, 9.	3.8	71
16	Strategies for Converting RNA to Amplifiable cDNA for Single-Cell RNA Sequencing Methods. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1129, 1-17.	0.8	6
17	CellFishing.jl: an ultrafast and scalable cell search method for single-cell RNA sequencing. <i>Genome Biology</i> , 2019, 20, 31.	3.8	22
18	Cell type-specific transcriptome analysis unveils secreted signaling molecule genes expressed in apical epithelial cap during appendage regeneration. <i>Development Growth and Differentiation</i> , 2019, 61, 447-456.	0.6	9

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19	Polysaccharide hydrolase of the hadal zone amphipods <i>Hirondellea gigas</i> . Bioscience, Biotechnology and Biochemistry, 2018, 82, 1123-1133.	0.6	10
20	Single-cell full-length total RNA sequencing uncovers dynamics of recursive splicing and enhancer RNAs. Nature Communications, 2018, 9, 619.	5.8	192
21	Chromatin remodeler CHD7 regulates the stem cell identity of human neural progenitors. Genes and Development, 2018, 32, 165-180.	2.7	28
22	Quartz-Seq2: a high-throughput single-cell RNA-sequencing method that effectively uses limited sequence reads. Genome Biology, 2018, 19, 29.	3.8	101
23	SCODE: an efficient regulatory network inference algorithm from single-cell RNA-Seq during differentiation. Bioinformatics, 2017, 33, 2314-2321.	1.8	297
24	Comprehensive Quantification of Gene Expression Fluctuation by Single-cell RNA-seq. Seibutsu Butsurei, 2016, 56, 330-333.	0.0	0
25	An application of MeSH enrichment analysis in livestock. Animal Genetics, 2015, 46, 381-387.	0.6	26
26	MeSH ORA framework: R/Bioconductor packages to support MeSH over-representation analysis. BMC Bioinformatics, 2015, 16, 45.	1.2	40
27	Quartz-Seq: a highly reproducible and sensitive single-cell RNA sequencing method, reveals non-genetic gene-expression heterogeneity. Genome Biology, 2013, 14, R31.	3.8	378
28	Context-Dependent Wiring of Sox2 Regulatory Networks for Self-Renewal of Embryonic and Trophoblast Stem Cells. Molecular Cell, 2013, 52, 380-392.	4.5	122
29	An automated system for high-throughput single cell-based breeding. Scientific Reports, 2013, 3, 1191.	1.6	66
30	Transcriptome Tomography for Brain Analysis in the Web-Accessible Anatomical Space. PLoS ONE, 2012, 7, e45373.	1.1	17
31	Quantitative Expression Profile of Distinct Functional Regions in the Adult Mouse Brain. PLoS ONE, 2011, 6, e23228.	1.1	60
32	Integration of exogenous DNA into mouse embryonic stem cell chromosomes shows preference into genes and frequent modification at junctions. Chromosome Research, 2010, 18, 191-201.	1.0	5
33	Id4, a New Candidate Gene for Senile Osteoporosis, Acts as a Molecular Switch Promoting Osteoblast Differentiation. PLoS Genetics, 2010, 6, e1001019.	1.5	67
34	Identification of novel PPAR γ target genes by integrated analysis of CHIP-on-chip and microarray expression data during adipocyte differentiation. Biochemical and Biophysical Research Communications, 2008, 372, 362-366.	1.0	52
35	EICO (Expression-based Imprint Candidate Organizer): finding disease-related imprinted genes. Nucleic Acids Research, 2004, 32, 548D-551.	6.5	17
36	Development and Evaluation of an Automated Annotation Pipeline and cDNA Annotation System. Genome Research, 2003, 13, 1542-1551.	2.4	34

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37	Systematic Expression Profiling of the Mouse Transcriptome Using RIKEN cDNA Microarrays. <i>Genome Research</i> , 2003, 13, 1318-1323.	2.4	69
38	Discovery of Imprinted Transcripts in the Mouse Transcriptome Using Large-Scale Expression Profiling. <i>Genome Research</i> , 2003, 13, 1402-1409.	2.4	96
39	Comprehensive Analysis of the Mouse Metabolome Based on the Transcriptome. <i>Genome Research</i> , 2003, 13, 1345-1349.	2.4	27
40	Asb4, Ata3, and Dcn Are Novel Imprinted Genes Identified by High-Throughput Screening Using RIKEN cDNA Microarray. <i>Biochemical and Biophysical Research Communications</i> , 2002, 290, 1499-1505.	1.0	126
41	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. <i>Nature</i> , 2002, 420, 563-573.	13.7	1,548
42	Functional annotation of a full-length mouse cDNA collection. <i>Nature</i> , 2001, 409, 685-690.	13.7	653
43	Generation of 10,154 Expressed Sequence Tags from a Leafy Gametophyte of a Marine Red Alga, <i>Porphyra yezoensis</i> . <i>DNA Research</i> , 2000, 7, 223-227.	1.5	150