

# Itoshi Nikaido

## List of Publications by Year in descending order

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43  
papers

4,986  
citations

257450

24  
h-index

265206

42  
g-index

54  
all docs

54  
docs citations

54  
times ranked

7399  
citing authors

#	ARTICLE	IF	CITATIONS
1	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. <i>Nature</i> , 2002, 420, 563-573.	27.8	1,548
2	Functional annotation of a full-length mouse cDNA collection. <i>Nature</i> , 2001, 409, 685-690.	27.8	653
3	Quartz-Seq: a highly reproducible and sensitive single-cell RNA sequencing method, reveals non-genetic gene-expression heterogeneity. <i>Genome Biology</i> , 2013, 14, R31.	8.8	378
4	Benchmarking single-cell RNA-sequencing protocols for cell atlas projects. <i>Nature Biotechnology</i> , 2020, 38, 747-755.	17.5	313
5	SCODE: an efficient regulatory network inference algorithm from single-cell RNA-Seq during differentiation. <i>Bioinformatics</i> , 2017, 33, 2314-2321.	4.1	297
6	Single-cell full-length total RNA sequencing uncovers dynamics of recursive splicing and enhancer RNAs. <i>Nature Communications</i> , 2018, 9, 619.	12.8	192
7	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.	3.4	150
8	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.	2.1	126
9	Context-Dependent Wiring of Sox2 Regulatory Networks for Self-Renewal of Embryonic and Trophoblast Stem Cells. <i>Molecular Cell</i> , 2013, 52, 380-392.	9.7	122
10	Quartz-Seq2: a high-throughput single-cell RNA-sequencing method that effectively uses limited sequence reads. <i>Genome Biology</i> , 2018, 19, 29.	8.8	101
11	Discovery of Imprinted Transcripts in the Mouse Transcriptome Using Large-Scale Expression Profiling. <i>Genome Research</i> , 2003, 13, 1402-1409.	5.5	96
12	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.	7.9	73
13	Benchmarking principal component analysis for large-scale single-cell RNA-sequencing. <i>Genome Biology</i> , 2020, 21, 9.	8.8	71
14	Systematic Expression Profiling of the Mouse Transcriptome Using RIKEN cDNA Microarrays. <i>Genome Research</i> , 2003, 13, 1318-1323.	5.5	69
15	Id4, a New Candidate Gene for Senile Osteoporosis, Acts as a Molecular Switch Promoting Osteoblast Differentiation. <i>PLoS Genetics</i> , 2010, 6, e1001019.	3.5	67
16	An automated system for high-throughput single cell-based breeding. <i>Scientific Reports</i> , 2013, 3, 1191.	3.3	66
17	Genome-wide kinetic properties of transcriptional bursting in mouse embryonic stem cells. <i>Science Advances</i> , 2020, 6, eaaz6699.	10.3	66
18	Tracing the origin of hair follicle stem cells. <i>Nature</i> , 2021, 594, 547-552.	27.8	62

#	ARTICLE	IF	CITATIONS
19	Quantitative Expression Profile of Distinct Functional Regions in the Adult Mouse Brain. PLoS ONE, 2011, 6, e23228.	2.5	60
20	Identification of novel PPAR $\beta$ 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.	2.1	52
21	MeSH ORA framework: R/Bioconductor packages to support MeSH over-representation analysis. BMC Bioinformatics, 2015, 16, 45.	2.6	40
22	Development and Evaluation of an Automated Annotation Pipeline and cDNA Annotation System. Genome Research, 2003, 13, 1542-1551.	5.5	34
23	Chromatin remodeler CHD7 regulates the stem cell identity of human neural progenitors. Genes and Development, 2018, 32, 165-180.	5.9	28
24	Comprehensive Analysis of the Mouse Metabolome Based on the Transcriptome. Genome Research, 2003, 13, 1345-1349.	5.5	27
25	An application of MeSH enrichment analysis in livestock. Animal Genetics, 2015, 46, 381-387.	1.7	26
26	The Number of Transcription Factors at an Enhancer Determines Switch-like Gene Expression. Cell Reports, 2020, 31, 107724.	6.4	25
27	CellFishing.jl: an ultrafast and scalable cell search method for single-cell RNA sequencing. Genome Biology, 2019, 20, 31.	8.8	22
28	Single-oocyte transcriptome analysis reveals aging-associated effects influenced by life stage and calorie restriction. Aging Cell, 2021, 20, e13428.	6.7	22
29	Local states of chromatin compaction at transcription start sites control transcription levels. Nucleic Acids Research, 2021, 49, 8007-8023.	14.5	18
30	EICO (Expression-based Imprint Candidate Organizer): finding disease-related imprinted genes. Nucleic Acids Research, 2004, 32, 548D-551.	14.5	17
31	Transcriptome Tomography for Brain Analysis in the Web-Accessible Anatomical Space. PLoS ONE, 2012, 7, e45373.	2.5	17
32	Primed to Naive-Like Conversion of the Common Marmoset Embryonic Stem Cells. Stem Cells and Development, 2020, 29, 761-773.	2.1	14
33	Polysaccharide hydrolase of the hadal zone amphipods <i>Hirondellea gigas</i> . Bioscience, Biotechnology and Biochemistry, 2018, 82, 1123-1133.	1.3	10
34	Cell type-specific transcriptome analysis unveils secreted signaling molecule genes expressed in apical epithelial cap during appendage regeneration. Development Growth and Differentiation, 2019, 61, 447-456.	1.5	9
35	Enhanced transcriptional heterogeneity mediated by NF- $\kappa$ B super-enhancers. PLoS Genetics, 2022, 18, e1010235.	3.5	7
36	Strategies for Converting RNA to Amplifiable cDNA for Single-Cell RNA Sequencing Methods. Advances in Experimental Medicine and Biology, 2019, 1129, 1-17.	1.6	6

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37	Integration of exogenous DNA into mouse embryonic stem cell chromosomes shows preference into genes and frequent modification at junctions. <i>Chromosome Research</i> , 2010, 18, 191-201.	2.2	5
38	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.	3.2	5
39	Millefy: visualizing cell-to-cell heterogeneity in read coverage of single-cell RNA sequencing datasets. <i>BMC Genomics</i> , 2020, 21, 177.	2.8	5
40	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.	4.1	5
41	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.	7.9	4
42	Comprehensive Quantification of Gene Expression Fluctuation by Single-cell RNA-seq. <i>Seibutsu Butsuri</i> , 2016, 56, 330-333.	0.1	0
43	Improved MeSH analysis software tools for farm animals. <i>Animal Genetics</i> , 2022, 53, 171-172.	1.7	0