

Junhyong Kim

List of Publications by Year in descending order

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Version: 2024-02-01

75
papers

6,900
citations

94433

37
h-index

85541

71
g-index

84
all docs

84
docs citations

84
times ranked

11838
citing authors

#	ARTICLE	IF	CITATIONS
1	Single-cell analysis identifies the interaction of altered renal tubules with basophils orchestrating kidney fibrosis. <i>Nature Immunology</i> , 2022, 23, 947-959.	14.5	37
2	The Nuclear Receptor ESRRB Protects from Kidney Disease by Coupling Metabolism and Differentiation. <i>Cell Metabolism</i> , 2021, 33, 379-394.e8.	16.2	93
3	Single cell regulatory landscape of the mouse kidney highlights cellular differentiation programs and disease targets. <i>Nature Communications</i> , 2021, 12, 2277.	12.8	122
4	Multi-omics integration in the age of million single-cell data. <i>Nature Reviews Nephrology</i> , 2021, 17, 710-724.	9.6	97
5	Parallel pathways for recruiting effector proteins determine centromere drive and suppression. <i>Cell</i> , 2021, 184, 4904-4918.e11.	28.9	40
6	A Novel FBXO45-Gef-H1 Axis Controls Oncogenic Signaling in B-Cell Lymphoma. <i>Blood</i> , 2021, 138, 711-711.	1.4	1
7	A subspace clustering method for satisfying stoichiometric constraints in scRNA-seq. , 2021, , .		0
8	Multi-Dimensional Mapping of Brain-Derived Extracellular Vesicle MicroRNA Biomarker for Traumatic Brain Injury Diagnostics. <i>Journal of Neurotrauma</i> , 2020, 37, 2424-2434.	3.4	50
9	Photoactivated Selective Release of Droplets from Microwell Arrays. <i>ACS Applied Materials & Interfaces</i> , 2020, 12, 3936-3944.	8.0	7
10	Static array of droplets and on-demand recovery for biological assays. <i>Biomicrofluidics</i> , 2020, 14, 051302.	2.4	6
11	Insertion variants missing in the human reference genome are widespread among human populations. <i>BMC Biology</i> , 2020, 18, 167.	3.8	7
12	Lamin B2 Levels Regulate Polyploidization of Cardiomyocyte Nuclei and Myocardial Regeneration. <i>Developmental Cell</i> , 2020, 53, 42-59.e11.	7.0	57
13	IgSF11 regulates osteoclast differentiation through association with the scaffold protein PSD-95. <i>Bone Research</i> , 2020, 8, 5.	11.4	16
14	Understanding the kidney one cell at a time. <i>Kidney International</i> , 2019, 96, 862-870.	5.2	45
15	Control of cytokinesis by β_2 -adrenergic receptors indicates an approach for regulating cardiomyocyte endowment. <i>Science Translational Medicine</i> , 2019, 11, .	12.4	73
16	Single-Cell Profiling Reveals Sex, Lineage, and Regional Diversity in the Mouse Kidney. <i>Developmental Cell</i> , 2019, 51, 399-413.e7.	7.0	266
17	A lineage-resolved molecular atlas of <i>C. elegans</i> embryogenesis at single-cell resolution. <i>Science</i> , 2019, 365, .	12.6	354
18	Comprehensive catalog of dendritically localized mRNA isoforms from sub-cellular sequencing of single mouse neurons. <i>BMC Biology</i> , 2019, 17, 5.	3.8	50

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19	Avian Primordial Germ Cells Contribute to and Interact With the Extracellular Matrix During Early Migration. <i>Frontiers in Cell and Developmental Biology</i> , 2019, 7, 35.	3.7	19
20	Genomic evidence for shared common ancestry of East African hunting-gathering populations and insights into local adaptation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 4166-4175.	7.1	40
21	Moldable Perfluoropolyetherâ€“Polyethylene Glycol Networks with Tunable Wettability and Solvent Resistance for Rapid Prototyping of Droplet Microfluidics. <i>Chemistry of Materials</i> , 2018, 30, 2583-2588.	6.7	13
22	Rare Cell Detection by Single-Cell RNA Sequencing as Guided by Single-Molecule RNA FISH. <i>Cell Systems</i> , 2018, 6, 171-179.e5.	6.2	111
23	PIVOT: platform for interactive analysis and visualization of transcriptomics data. <i>BMC Bioinformatics</i> , 2018, 19, 6.	2.6	55
24	miRNA Profiling of Magnetic Nanoporeâ€“Isolated Extracellular Vesicles for the Diagnosis of Pancreatic Cancer. <i>Cancer Research</i> , 2018, 78, 3688-3697.	0.9	63
25	Exosomal PD-L1 contributes to immunosuppression and is associated with anti-PD-1 response. <i>Nature</i> , 2018, 560, 382-386.	27.8	1,836
26	Coordination of olfactory receptor choice with guidance receptor expression and function in olfactory sensory neurons. <i>PLoS Genetics</i> , 2018, 14, e1007164.	3.5	18
27	Primary Cell Culture of Live Neurosurgically Resected Aged Adult Human Brain Cells and Single Cell Transcriptomics. <i>Cell Reports</i> , 2017, 18, 791-803.	6.4	60
28	CYCLOPS reveals human transcriptional rhythms in health and disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 5312-5317.	7.1	184
29	The purinergic receptor P2X5 regulates inflammasome activity and hyper-multinucleation of murine osteoclasts. <i>Scientific Reports</i> , 2017, 7, 196.	3.3	41
30	Accounting for technical noise in differential expression analysis of single-cell RNA sequencing data. <i>Nucleic Acids Research</i> , 2017, 45, 10978-10988.	14.5	73
31	Single cell transcriptomics of noncoding <sc>RNAs</sc> and their cellâ€“specificity. <i>Wiley Interdisciplinary Reviews RNA</i> , 2017, 8, e1433.	6.4	23
32	Pervasive within-Mitochondrion Single-Nucleotide Variant Heteroplasmy as Revealed by Single-Mitochondrion Sequencing. <i>Cell Reports</i> , 2017, 21, 2706-2713.	6.4	48
33	Complete fold annotation of the human proteome using a novel structural feature space. <i>Scientific Reports</i> , 2017, 7, 46321.	3.3	4
34	Challenges and emerging directions in single-cell analysis. <i>Genome Biology</i> , 2017, 18, 84.	8.8	258
35	Assessing characteristics of RNA amplification methods for single cell RNA sequencing. <i>BMC Genomics</i> , 2016, 17, 966.	2.8	34
36	Variation is function: Are single cell differences functionally important?. <i>BioEssays</i> , 2016, 38, 172-180.	2.5	66

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37	Single-cell transcriptomics and functional target validation of brown adipocytes show their complex roles in metabolic homeostasis. <i>FASEB Journal</i> , 2016, 30, 81-92.	0.5	39
38	Single-cell mRNA sequencing identifies subclonal heterogeneity in anti-cancer drug responses of lung adenocarcinoma cells. <i>Genome Biology</i> , 2015, 16, 127.	9.6	228
39	Deep sequencing reveals cell-type-specific patterns of single-cell transcriptome variation. <i>Genome Biology</i> , 2015, 16, 122.	9.6	95
40	Can one hear the shape of a population history?. <i>Theoretical Population Biology</i> , 2015, 100, 26-38.	1.1	26
41	Cellular Deconstruction: Finding Meaning in Individual Cell Variation. <i>Trends in Cell Biology</i> , 2015, 25, 569-578.	7.9	28
42	Divergence of RNA localization between rat and mouse neurons reveals the potential for rapid brain evolution. <i>BMC Genomics</i> , 2014, 15, 883.	2.8	22
43	Machine Learning Helps Identify CHRONO as a Circadian Clock Component. <i>PLoS Biology</i> , 2014, 12, e1001840.	5.6	109
44	The promise of single-cell sequencing. <i>Nature Methods</i> , 2014, 11, 25-27.	19.0	262
45	Transcriptome in vivo analysis (TIVA) of spatially defined single cells in live tissue. <i>Nature Methods</i> , 2014, 11, 190-196.	19.0	235
46	Serotonergic neuron regulation informed by in vivo single-cell transcriptomics. <i>FASEB Journal</i> , 2014, 28, 771-780.	0.5	55
47	NoFold: RNA structure clustering without folding or alignment. <i>Rna</i> , 2014, 20, 1671-1683.	3.5	16
48	IVT-seq reveals extreme bias in RNA sequencing. <i>Genome Biology</i> , 2014, 15, R86.	9.6	134
49	Pervasive Antisense Transcription Is Evolutionarily Conserved in Budding Yeast. <i>Molecular Biology and Evolution</i> , 2013, 30, 409-421.	8.9	22
50	Subcellular RNA Sequencing Reveals Broad Presence of Cytoplasmic Intron-Sequence Retaining Transcripts in Mouse and Rat Neurons. <i>PLoS ONE</i> , 2013, 8, e76194.	2.5	35
51	Quantitative biology of single neurons. <i>Journal of the Royal Society Interface</i> , 2012, 9, 3165-3183.	3.4	18
52	Cytoplasmic Intron Sequence-Retaining Transcripts Can Be Dendritically Targeted via ID Element Retrotransposons. <i>Neuron</i> , 2011, 69, 877-884.	8.1	148
53	Transcriptome transfer provides a model for understanding the phenotype of cardiomyocytes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11918-11923.	7.1	31
54	RNA: state memory and mediator of cellular phenotype. <i>Trends in Cell Biology</i> , 2010, 20, 311-318.	7.9	62

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55	Dissecting the molecular mechanism of drosophila odorant receptors through activity modeling and comparative analysis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 381-399.	2.6	24
56	Transcriptome transfer produces a predictable cellular phenotype. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 7624-7629.	7.1	86
57	Mutational robustness and geometrical form in protein structures. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2008, 310B, 216-226.	1.3	6
58	Translation of Sensory Input into Behavioral Output via an Olfactory System. <i>Neuron</i> , 2008, 59, 110-124.	8.1	258
59	Self Containment, a Property of Modular RNA Structures, Distinguishes microRNAs. <i>PLoS Computational Biology</i> , 2008, 4, e1000150.	3.2	17
60	Penalized Likelihood Phylogenetic Inference: Bridging the Parsimony-Likelihood Gap. <i>Systematic Biology</i> , 2008, 57, 665-674.	5.6	55
61	Molecular Evolution of Drosophila Odorant Receptor Genes. <i>Molecular Biology and Evolution</i> , 2007, 24, 1198-1207.	8.9	125
62	Transcriptional Target Prediction Using Qualitative Reasoning. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society</i> , 2006, , .	0.5	0
63	The Cobweb of Life Revealed by Genome-Scale Estimates of Horizontal Gene Transfer. <i>PLoS Biology</i> , 2005, 3, e316.	5.6	113
64	Guest Editorial: WABI Special Section Part II. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2005, 2, 1-2.	3.0	3
65	Guest Editorial: WABI Special Section Part 1. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2004, 1, 137-138.	3.0	1
66	Estimating genomic coexpression networks using first-order conditional independence. <i>Genome Biology</i> , 2004, 5, R100.	9.6	115
67	Reconstructing the temporal ordering of biological samples using microarray data. <i>Bioinformatics</i> , 2003, 19, 842-850.	4.1	96
68	Gene discovery by e-genetics: Drosophila odor and taste receptors. <i>Journal of Cell Science</i> , 2002, 115, 1107-12.	2.0	18
69	Descartes' fly: the geometry of genomic annotation. <i>Functional and Integrative Genomics</i> , 2001, 1, 241-249.	3.5	2
70	Macro-evolution of the hairy enhancer in Drosophila species. <i>The Journal of Experimental Zoology</i> , 2001, 291, 175-185.	1.4	15
71	Phylogeny of Holothuroidea (Echinodermata) inferred from morphology. <i>Zoological Journal of the Linnean Society</i> , 2001, 133, 63-81.	2.3	57
72	AFTER THE MOLECULAR EVOLUTION REVOLUTION. <i>Evolution; International Journal of Organic Evolution</i> , 2001, 55, 2620-2622.	2.3	2

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73	Constraint structure analysis of gene expression. <i>Functional and Integrative Genomics</i> , 2000, 1, 174-185.	3.5	8
74	A TREE OBSCURED BY VINES: HORIZONTAL GENE TRANSFER AND THE MEDIAN TREE METHOD OF ESTIMATING SPECIES PHYLOGENY. , 2000, , 571-82.		5
75	Bi-penta-bi-decaradial symmetry: A review of evolutionary and developmental trends in holothuroidea (echinodermata). , 1999, 285, 93-103.		21