

# Jong Kyoung Kim

## List of Publications by Year in descending order

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Version: 2024-02-01

37  
papers

4,509  
citations

331670

21  
h-index

330143

37  
g-index

43  
all docs

43  
docs citations

43  
times ranked

7622  
citing authors

#	ARTICLE	IF	CITATIONS
1	Distinct properties of adipose stem cell subpopulations determine fat depot-specific characteristics. <i>Cell Metabolism</i> , 2022, 34, 458-472.e6.	16.2	56
2	Dissecting chicken germ cell dynamics by combining a germ cell tracing transgenic chicken model with single-cell RNA sequencing. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 1654-1669.	4.1	13
3	Homeostatic serum IgE is secreted by plasma cells in the thymus and enhances mast cell survival. <i>Nature Communications</i> , 2022, 13, 1418.	12.8	11
4	Distinct Properties of Adipose Stem Cell Subpopulations Determine Fat Depot-Specific Characteristics. <i>FASEB Journal</i> , 2022, 36, .	0.5	0
5	p57Kip2 imposes the reserve stem cell state of gastric chief cells. <i>Cell Stem Cell</i> , 2022, 29, 826-839.e9.	11.1	17
6	Identification of Adipose-Specific iNKT Cell Subpopulation through Single-Cell RNA Sequencing. <i>FASEB Journal</i> , 2022, 36, .	0.5	0
7	Characterization of Adipose Stem Cells through Single Cell RNA-sequencing Analysis. <i>FASEB Journal</i> , 2021, 35, .	0.5	0
8	Tracing oncogene-driven remodelling of the intestinal stem cell niche. <i>Nature</i> , 2021, 594, 442-447.	27.8	56
9	Soft windowing application to improve analysis of high-throughput phenotyping data. <i>Bioinformatics</i> , 2020, 36, 1492-1500.	4.1	9
10	PiggyBac mutagenesis and exome sequencing identify genetic driver landscapes and potential therapeutic targets of EGFR-mutant gliomas. <i>Genome Biology</i> , 2020, 21, 181.	8.8	18
11	Single-cell RNA sequencing identifies shared differentiation paths of mouse thymic innate T cells. <i>Nature Communications</i> , 2020, 11, 4367.	12.8	56
12	Discovery of new epigenomics-based biomarkers and the early diagnosis of neurodegenerative diseases. <i>Ageing Research Reviews</i> , 2020, 61, 101069.	10.9	7
13	Dopaminergic Regulation of Nucleus Accumbens Cholinergic Interneurons Demarcates Susceptibility to Cocaine Addiction. <i>Biological Psychiatry</i> , 2020, 88, 746-757.	1.3	30
14	Defining the Identity and Dynamics of Adult Gastric Isthmus Stem Cells. <i>Cell Stem Cell</i> , 2019, 25, 342-356.e7.	11.1	97
15	Analysis of Technical and Biological Variability in Single-Cell RNA Sequencing. <i>Methods in Molecular Biology</i> , 2019, 1935, 25-43.	0.9	2
16	A Genome-Wide Knockout Screen in Human Macrophages Identified Host Factors Modulating <i>Salmonella</i> Infection. <i>MBio</i> , 2019, 10, .	4.1	42
17	Wnt3a disrupts GR-TEAD4-PPAR $\beta$ positive circuits and cytoskeletal rearrangement in a $\beta$ -catenin-dependent manner during early adipogenesis. <i>Cell Death and Disease</i> , 2019, 10, 16.	6.3	13
18	Dissecting Cellular Heterogeneity Using Single-Cell RNA Sequencing. <i>Molecules and Cells</i> , 2019, 42, 189-199.	2.6	45

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19	The International Mouse Phenotyping Consortium (IMPC): a functional catalogue of the mammalian genome that informs conservation. <i>Conservation Genetics</i> , 2018, 19, 995-1005.	1.5	82
20	Flipping between Polycomb repressed and active transcriptional states introduces noise in gene expression. <i>Nature Communications</i> , 2017, 8, 36.	12.8	62
21	Stella modulates transcriptional and endogenous retrovirus programs during maternal-to-zygotic transition. <i>ELife</i> , 2017, 6, .	6.0	92
22	Classification of low quality cells from single-cell RNA-seq data. <i>Genome Biology</i> , 2016, 17, 29.	8.8	572
23	The Technology and Biology of Single-Cell RNA Sequencing. <i>Molecular Cell</i> , 2015, 58, 610-620.	9.7	1,014
24	Characterizing noise structure in single-cell RNA-seq distinguishes genuine from technical stochastic allelic expression. <i>Nature Communications</i> , 2015, 6, 8687.	12.8	213
25	Single Cell RNA-Sequencing of Pluripotent States Unlocks Modular Transcriptional Variation. <i>Cell Stem Cell</i> , 2015, 17, 471-485.	11.1	505
26	Genome-wide Bisulfite Sequencing in Zygotes Identifies Demethylation Targets and Maps the Contribution of TET3 Oxidation. <i>Cell Reports</i> , 2014, 9, 1990-2000.	6.4	116
27	NF $\kappa$ B and STAT3 synergistically activate the expression of FAT10, a gene counteracting the tumor suppressor p53. <i>Molecular Oncology</i> , 2014, 8, 642-655.	4.6	51
28	Inferring the kinetics of stochastic gene expression from single-cell RNA-sequencing data. <i>Genome Biology</i> , 2013, 14, R7.	9.6	180
29	Accounting for technical noise in single-cell RNA-seq experiments. <i>Nature Methods</i> , 2013, 10, 1093-1095.	19.0	929
30	Identification of co-occurring transcription factor binding sites from DNA sequence using clustered position weight matrices. <i>Nucleic Acids Research</i> , 2012, 40, e38-e38.	14.5	18
31	Probabilistic Models for Semisupervised Discriminative Motif Discovery in DNA Sequences. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 1309-1317.	3.0	8
32	Prediction and Experimental Validation of Novel STAT3 Target Genes in Human Cancer Cells. <i>PLoS ONE</i> , 2009, 4, e6911.	2.5	27
33	Clustering with $\gamma$ -regular graphs. <i>Pattern Recognition</i> , 2009, 42, 2020-2028.	8.1	5
34	<i>Arabidopsis</i> Nuclear-Encoded Plastid Transit Peptides Contain Multiple Sequence Subgroups with Distinctive Chloroplast-Targeting Sequence Motifs. <i>Plant Cell</i> , 2008, 20, 1603-1622.	6.6	117
35	Independent arrays or independent time courses for gene expression time series data analysis. <i>Neurocomputing</i> , 2008, 71, 2377-2387.	5.9	4
36	Sequence-driven features for prediction of subcellular localization of proteins. <i>Pattern Recognition</i> , 2006, 39, 2301-2311.	8.1	8

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37	Prediction of subcellular localization of proteins using pairwise sequence alignment and support vector machine. Pattern Recognition Letters, 2006, 27, 996-1001.	4.2	25