# Jong Kyoung Kim

List of Publications by Year
in descending order

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|---|---|---|---|
| 37 papers | 4,509 citations | 331259<br>21 h-index | 329751<br>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. Cell Metabolism, 2022, 34, 458-472.e6. | 7.2 | 56 |
| 2 | Dissecting chicken germ cell dynamics by combining a germ cell tracing transgenic chicken model with single-cell RNA sequencing. Computational and Structural Biotechnology Journal, 2022, 20, 1654-1669. | 1.9 | 13 |
| 3 | Homeostatic serum IgE is secreted by plasma cells in the thymus and enhances mast cell survival. Nature Communications, 2022, 13, 1418. | 5.8 | 11 |
| 4 | Distinct Properties of Adipose Stem Cell Subpopulations Determine Fat Depot–Specific Characteristics. FASEB Journal, 2022, 36, . | 0.2 | 0 |
| 5 | p57Kip2 imposes the reserve stem cell state of gastric chief cells. Cell Stem Cell, 2022, 29, 826-839.e9. | 5.2 | 17 |
| 6 | Identification of Adipose–Specific iNKT Cell Subpopulation through Single–Cell RNA Sequencing. FASEB Journal, 2022, 36, . | 0.2 | 0 |
| 7 | Characterization of Adipose Stem Cells through Single Cell RNA–sequencing Analysis. FASEB Journal, 2021, 35, . | 0.2 | 0 |
| 8 | Tracing oncogene-driven remodelling of the intestinal stem cell niche. Nature, 2021, 594, 442-447. | 13.7 | 56 |
| 9 | Soft windowing application to improve analysis of high-throughput phenotyping data. Bioinformatics, 2020, 36, 1492-1500. | 1.8 | 9 |
| 10 | PiggyBac mutagenesis and exome sequencing identify genetic driver landscapes and potential therapeutic targets of EGFR-mutant gliomas. Genome Biology, 2020, 21, 181. | 3.8 | 18 |
| 11 | Single-cell RNA sequencing identifies shared differentiation paths of mouse thymic innate T cells. Nature Communications, 2020, 11, 4367. | 5.8 | 56 |
| 12 | Discovery of new epigenomics-based biomarkers and the early diagnosis of neurodegenerative diseases. Ageing Research Reviews, 2020, 61, 101069. | 5.0 | 7 |
| 13 | Dopaminergic Regulation of Nucleus Accumbens Cholinergic Interneurons Demarcates Susceptibility to Cocaine Addiction. Biological Psychiatry, 2020, 88, 746-757. | 0.7 | 30 |
| 14 | Defining the Identity and Dynamics of Adult Gastric Isthmus Stem Cells. Cell Stem Cell, 2019, 25, 342-356.e7. | 5.2 | 97 |
| 15 | Analysis of Technical and Biological Variability in Single-Cell RNA Sequencing. Methods in Molecular Biology, 2019, 1935, 25-43. | 0.4 | 2 |
| 16 | A Genome-Wide Knockout Screen in Human Macrophages Identified Host Factors Modulating <i>Salmonella</i> Infection. MBio, 2019, 10, . | 1.8 | 42 |
| 17 | Wnt3a disrupts GR-TEAD4-PPARÎ³2 positive circuits and cytoskeletal rearrangement in a Î²-catenin-dependent manner during early adipogenesis. Cell Death and Disease, 2019, 10, 16. | 2.7 | 13 |
| 18 | Dissecting Cellular Heterogeneity Using Single-Cell RNA Sequencing. Molecules and Cells, 2019, 42, 189-199. | 1.0 | 45 |

| # | ARTICLE | IF | CITATIONS |
|---|---------|-----|-----------|
| 19 | The International Mouse Phenotyping Consortium (IMPC): a functional catalogue of the mammalian genome that informs conservation. Conservation Genetics, 2018, 19, 995-1005. | 0.8 | 82 |
| 20 | Flipping between Polycomb repressed and active transcriptional states introduces noise in gene expression. Nature Communications, 2017, 8, 36. | 5.8 | 62 |
| 21 | Stella modulates transcriptional and endogenous retrovirus programs during maternal-to-zygotic transition. ELife, 2017, 6, . | 2.8 | 92 |
| 22 | Classification of low quality cells from single-cell RNA-seq data. Genome Biology, 2016, 17, 29. | 3.8 | 572 |
| 23 | The Technology and Biology of Single-Cell RNA Sequencing. Molecular Cell, 2015, 58, 610-620. | 4.5 | 1,014 |
| 24 | Characterizing noise structure in single-cell RNA-seq distinguishes genuine from technical stochastic allelic expression. Nature Communications, 2015, 6, 8687. | 5.8 | 213 |
| 25 | Single Cell RNA-Sequencing of Pluripotent States Unlocks Modular Transcriptional Variation. Cell Stem Cell, 2015, 17, 471-485. | 5.2 | 505 |
| 26 | Genome-wide Bisulfite Sequencing in Zygotes Identifies Demethylation Targets and Maps the Contribution of TET3 Oxidation. Cell Reports, 2014, 9, 1990-2000. | 2.9 | 116 |
| 27 | NFÎºB and STAT3 synergistically activate the expression of FAT10, a gene counteracting the tumor suppressor p53. Molecular Oncology, 2014, 8, 642-655. | 2.1 | 51 |
| 28 | Inferring the kinetics of stochastic gene expression from single-cell RNA-sequencing data. Genome Biology, 2013, 14, R7. | 13.9 | 180 |
| 29 | Accounting for technical noise in single-cell RNA-seq experiments. Nature Methods, 2013, 10, 1093-1095. | 9.0 | 929 |
| 30 | Identification of co-occurring transcription factor binding sites from DNA sequence using clustered position weight matrices. Nucleic Acids Research, 2012, 40, e38-e38. | 6.5 | 18 |
| 31 | Probabilistic Models for Semisupervised Discriminative Motif Discovery in DNA Sequences. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 1309-1317. | 1.9 | 8 |
| 32 | Prediction and Experimental Validation of Novel STAT3 Target Genes in Human Cancer Cells. PLoS ONE, 2009, 4, e6911. | 1.1 | 27 |
| 33 | Clustering with -regular graphs. Pattern Recognition, 2009, 42, 2020-2028. | 5.1 | 5 |
| 34 | <i>Arabidopsis</i>Nuclear-Encoded Plastid Transit Peptides Contain Multiple Sequence Subgroups with Distinctive Chloroplast-Targeting Sequence Motifs. Plant Cell, 2008, 20, 1603-1622. | 3.1 | 117 |
| 35 | Independent arrays or independent time courses for gene expression time series data analysis. Neurocomputing, 2008, 71, 2377-2387. | 3.5 | 4 |
| 36 | Sequence-driven features for prediction of subcellular localization of proteins. Pattern Recognition, 2006, 39, 2301-2311. | 5.1 | 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. | 2.6 | 25 |