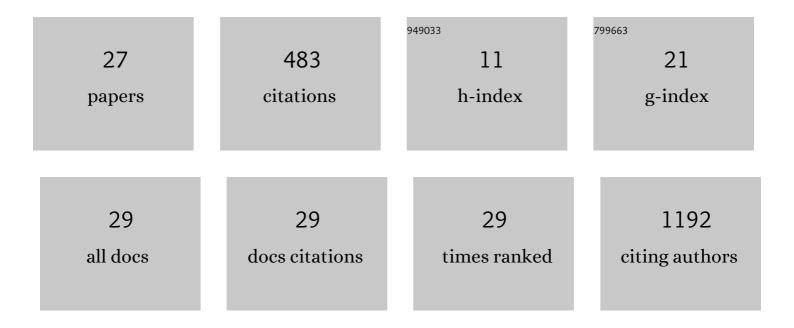
Sung-Joon Park

List of Publications by Year in descending order

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| # | Article | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Generation of 3D lacrimal gland organoids from human pluripotent stem cells. Nature, 2022, 605, 126-131. | 13.7 | 18 |
| 2 | Signaling Pathway of Taurine-Induced Upregulation of TXNIP. Metabolites, 2022, 12, 636. | 1.3 | 2 |
| 3 | OpenContami: a web-based application for detecting microbial contaminants in next-generation sequencing data. Bioinformatics, 2021, 37, 3021-3022. | 1.8 | 4 |
| 4 | Characterizing Promoter and Enhancer Sequences by a Deep Learning Method. Frontiers in Genetics, 2021, 12, 681259. | 1.1 | 2 |
| 5 | Existence and possible roles of independent non-CpG methylation in the mammalian brain. DNA Research, 2020, 27, . | 1.5 | 10 |
| 6 | HHEX promotes myeloid transformation in cooperation with mutant ASXL1. Blood, 2020, 136, 1670-1684. | 0.6 | 11 |
| 7 | RNA-sequencing reveals positional memory of multipotent mesenchymal stromal cells from oral and maxillofacial tissue transcriptomes. BMC Genomics, 2020, 21, 417. | 1.2 | 11 |
| 8 | Broad Heterochromatic Domains Open in Gonocyte Development Prior to De Novo DNA Methylation. Developmental Cell, 2019, 51, 21-34.e5. | 3.1 | 26 |
| 9 | A systematic sequencing-based approach for microbial contaminant detection and functional inference. BMC Biology, 2019, 17, 72. | 1.7 | 13 |
| 10 | Analyzing the 3D chromatin organization coordinating with gene expression regulation in B-cell lymphoma. BMC Medical Genomics, 2019, 11, 127. | 0.7 | 13 |
| 11 | Homeobox Transcription Factor Hhex Promotes Myeloid Leukemia in Cooperation with Mutant ASXL1. Blood, 2019, 134, 2525-2525. | 0.6 | 0 |
| 12 | Differential landscape of non-CpG methylation in embryonic stem cells and neurons caused by DNMT3s. Scientific Reports, 2017, 7, 11295. | 1.6 | 59 |
| 13 | Multidisciplinary insight into clonal expansion of HTLV-1–infected cells in adult T-cell leukemia via modeling by deterministic finite automata coupled with high-throughput sequencing. BMC Medical Genomics, 2017, 10, 4. | 0.7 | 10 |
| 14 | ZBTB16 as a Downstream Target Gene of Osterix Regulates Osteoblastogenesis of Human Multipotent Mesenchymal Stromal Cells. Journal of Cellular Biochemistry, 2016, 117, 2423-2434. | 1.2 | 27 |
| 15 | Transcriptional regulation of a horizontally transferred gene from bacterium to chordate. Proceedings of the Royal Society B: Biological Sciences, 2016, 283, 20161712. | 1.2 | 20 |
| 16 | Advances, practice, and clinical perspectives in highâ€ŧhroughput sequencing. Oral Diseases, 2016, 22, 353-364. | 1.5 | 11 |
| 17 | PAX6 Isoforms, along with Reprogramming Factors, Differentially Regulate the Induction of Cornea-specific Genes. Scientific Reports, 2016, 6, 20807. | 1.6 | 39 |
| 18 | OpenTein: a database of digital whole-slide images of stem cell-derived teratomas. Nucleic Acids Research. 2016. 44. D1000-D1004. | 6.5 | 3 |

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| # | Article | IF | CITATIONS |
|----|---|-----|-----------|
| 19 | An integrative approach for efficient analysis of whole genome bisulfite sequencing data. BMC Genomics, 2015, 16, S14. | 1.2 | 9 |
| 20 | DBTMEE: a database of transcriptome in mouse early embryos. Nucleic Acids Research, 2015, 43, D771-D776. | 6.5 | 71 |
| 21 | Computational Promoter Modeling Identifies the Modes of Transcriptional Regulation in Hematopoietic Stem Cells. PLoS ONE, 2014, 9, e93853. | 1.1 | 8 |
| 22 | Inferring the choreography of parental genomes during fertilization from ultralarge-scale whole-transcriptome analysis. Genes and Development, 2013, 27, 2736-2748. | 2.7 | 86 |
| 23 | A regression analysis of gene expression in ES cells reveals two gene classes that are significantly different in epigenetic patterns. BMC Bioinformatics, 2011, 12, S50. | 1.2 | 18 |
| 24 | Predicting promoter activities of primary human DNA sequences. Nucleic Acids Research, 2011, 39, e75-e75. | 6.5 | 10 |
| 25 | GA-based generic method for protein structure comparison. , 0, , . | | 1 |
| 26 | Two-layer protein structure comparison. , 0, , . | | 1 |
| 27 | Computational Inference of Gene Regulation from Whole-Transcriptome Analysis of Early Embryos. Advances in Medical Technologies and Clinical Practice Book Series, 0, , 241-279. | 0.3 | 0 |