

Sung-Joon Park

List of Publications by Year in descending order

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Version: 2024-02-01

27
papers

483
citations

949033

11
h-index

799663

21
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29
all docs

29
docs citations

29
times ranked

1192
citing authors

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

#	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