

Sanghyuk Lee

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

2,112
citations

471509

17
h-index

713466

21
g-index

23
all docs

23
docs citations

23
times ranked

3897
citing authors

#	ARTICLE	IF	CITATIONS
1	Mice transgenic for human <i>CTLA4-CD28</i> fusion gene show proliferation and transformation of ATLL-like and AITL-like T cells. <i>Oncolmmunology</i> , 2022, 11, 2015170.	4.6	2
2	Angioimmunoblastic T-cell lymphoma-like lymphadenopathy in mice transgenic for human <i>RHOA</i> with p.Gly17Val mutation. <i>Oncolmmunology</i> , 2020, 9, 1746553.	4.6	5
3	Frequent <i>CTLA4-CD28</i> gene fusion in diverse types of T-cell lymphoma. <i>Haematologica</i> , 2016, 101, 757-763.	3.5	75
4	Programming of Plant Leaf Senescence with Temporal and Inter-Organellar Coordination of Transcriptome in <i>Arabidopsis1</i> . <i>Plant Physiology</i> , 2016, 171, 452-467.	4.8	121
5	A highly recurrent novel missense mutation in <i>CD28</i> among angioimmunoblastic T-cell lymphoma patients. <i>Haematologica</i> , 2015, 100, e505-e507.	3.5	43
6	EMSA: estimation of transcript abundance from RNA-seq data by mappability-based segmentation and reclustering. <i>BMC Bioinformatics</i> , 2015, 16, 278.	2.6	18
7	A recurrent inactivating mutation in <i>RHOA</i> GTPase in angioimmunoblastic T cell lymphoma. <i>Nature Genetics</i> , 2014, 46, 371-375.	21.4	326
8	A High-Dimensional, Deep-Sequencing Study of Lung Adenocarcinoma in Female Never-Smokers. <i>PLoS ONE</i> , 2013, 8, e55596.	2.5	70
9	Clinical Validation of Colorectal Cancer Biomarkers Identified from Bioinformatics Analysis of Public Expression Data. <i>Clinical Cancer Research</i> , 2011, 17, 700-709.	7.0	80
10	Accurate quantification of transcriptome from RNA-Seq data by effective length normalization. <i>Nucleic Acids Research</i> , 2011, 39, e9-e9.	14.5	101
11	A p53/miRNA-34 axis regulates Snail1-dependent cancer cell epithelial→mesenchymal transition. <i>Journal of Cell Biology</i> , 2011, 195, 417-433.	5.2	390
12	p53 and MicroRNA-34 Are Suppressors of Canonical Wnt Signaling. <i>Science Signaling</i> , 2011, 4, ra71.	3.6	272
13	A p53/miRNA-34 axis regulates Snail1-dependent cancer cell epithelial→mesenchymal transition. <i>Journal of Experimental Medicine</i> , 2011, 208, i32-i32.	8.5	0
14	Clinical Validity of the Lung Cancer Biomarkers Identified by Bioinformatics Analysis of Public Expression Data. <i>Cancer Research</i> , 2007, 67, 7431-7438.	0.9	90
15	ECgene: an alternative splicing database update. <i>Nucleic Acids Research</i> , 2007, 35, D99-D103.	14.5	35
16	ChimerDB--a knowledgebase for fusion sequences. <i>Nucleic Acids Research</i> , 2006, 34, D21-D24.	14.5	34
17	Bayesian Hierarchical Models for Serial Analysis of Gene Expression. <i>Lecture Notes in Computer Science</i> , 2006, , 29-39.	1.3	0
18	ECgene: Genome-based EST clustering and gene modeling for alternative splicing. <i>Genome Research</i> , 2005, 15, 566-576.	5.5	86

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19	ASePCR: alternative splicing electronic RT-PCR in multiple tissues and organs. Nucleic Acids Research, 2005, 33, W681-W685.	14.5	9
20	ASmodeler: gene modeling of alternative splicing from genomic alignment of mRNA, EST and protein sequences. Nucleic Acids Research, 2004, 32, W181-W186.	14.5	17
21	ECgene: genome annotation for alternative splicing. Nucleic Acids Research, 2004, 33, D75-D79.	14.5	52
22	MRP9, an unusual truncated member of the ABC transporter superfamily, is highly expressed in breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 6997-7002.	7.1	116
23	MRP8, A New Member of ABC Transporter Superfamily, Identified by EST Database Mining and Gene Prediction Program, Is Highly Expressed in Breast Cancer. Molecular Medicine, 2001, 7, 509-516.	4.4	170