

Sanghyuk Lee

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10509040/publications.pdf>

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	A p53/miRNA-34 axis regulates Snail1-dependent cancer cell epithelialâ€mesenchymal transition. <i>Journal of Cell Biology</i> , 2011, 195, 417-433.	5.2	390
2	A recurrent inactivating mutation in RHOA GTPase in angioimmunoblastic T cell lymphoma. <i>Nature Genetics</i> , 2014, 46, 371-375.	21.4	326
3	p53 and MicroRNA-34 Are Suppressors of Canonical Wnt Signaling. <i>Science Signaling</i> , 2011, 4, ra71.	3.6	272
4	MRP8, A New Member of ABC Transporter Superfamily, Identified by EST Database Mining and Gene Prediction Program, Is Highly Expressed in Breast Cancer. <i>Molecular Medicine</i> , 2001, 7, 509-516.	4.4	170
5	Programming of Plant Leaf Senescence with Temporal and Inter-Organellar Coordination of Transcriptome in Arabidopsis1 Å. <i>Plant Physiology</i> , 2016, 171, 452-467.	4.8	121
6	MRP9, an unusual truncated member of the ABC transporter superfamily, is highly expressed in breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 6997-7002.	7.1	116
7	Accurate quantification of transcriptome from RNA-Seq data by effective length normalization. <i>Nucleic Acids Research</i> , 2011, 39, e9-e9.	14.5	101
8	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
9	ECgene: Genome-based EST clustering and gene modeling for alternative splicing. <i>Genome Research</i> , 2005, 15, 566-576.	5.5	86
10	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
11	Frequent CTLA4-CD28 gene fusion in diverse types of T-cell lymphoma. <i>Haematologica</i> , 2016, 101, 757-763.	3.5	75
12	A High-Dimensional, Deep-Sequencing Study of Lung Adenocarcinoma in Female Never-Smokers. <i>PLoS ONE</i> , 2013, 8, e55596.	2.5	70
13	ECgene: genome annotation for alternative splicing. <i>Nucleic Acids Research</i> , 2004, 33, D75-D79.	14.5	52
14	A highly recurrent novel missense mutation in CD28 among angioimmunoblastic T-cell lymphoma patients. <i>Haematologica</i> , 2015, 100, e505-e507.	3.5	43
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	EMSAR: estimation of transcript abundance from RNA-seq data by mappability-based segmentation and reclustering. <i>BMC Bioinformatics</i> , 2015, 16, 278.	2.6	18
18	ASmodeler: gene modeling of alternative splicing from genomic alignment of mRNA, EST and protein sequences. <i>Nucleic Acids Research</i> , 2004, 32, W181-W186.	14.5	17

#	ARTICLE	IF	CITATIONS
19	ASePCR: alternative splicing electronic RT-PCR in multiple tissues and organs. <i>Nucleic Acids Research</i> , 2005, 33, W681-W685.	14.5	9
20	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
21	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
22	Bayesian Hierarchical Models for Serial Analysis of Gene Expression. <i>Lecture Notes in Computer Science</i> , 2006, , 29-39.	1.3	0
23	A p53/miRNA-34 axis regulates Snail1-dependent cancer cell epithelialâ€mesenchymal transition. <i>Journal of Experimental Medicine</i> , 2011, 208, i32-i32.	8.5	0