

Akul Singhanian

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

1,507
citations

393982

19
h-index

454577

30
g-index

36
all docs

36
docs citations

36
times ranked

3382
citing authors

#	ARTICLE	IF	CITATIONS
1	An In-Depth Comparison of Latent HIV-1 Reactivation in Multiple Cell Model Systems and Resting CD4+ T Cells from Aviremic Patients. <i>PLoS Pathogens</i> , 2013, 9, e1003834.	2.1	360
2	A modular transcriptional signature identifies phenotypic heterogeneity of human tuberculosis infection. <i>Nature Communications</i> , 2018, 9, 2308.	5.8	142
3	Epithelial IL-6 trans-signaling defines a new asthma phenotype with increased airway inflammation. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 143, 577-590.	1.5	140
4	The value of transcriptomics in advancing knowledge of the immune response and diagnosis in tuberculosis. <i>Nature Immunology</i> , 2018, 19, 1159-1168.	7.0	88
5	Multitissue Transcriptomics Delineates the Diversity of Airway T Cell Functions in Asthma. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2018, 58, 261-270.	1.4	82
6	Mouse transcriptome reveals potential signatures of protection and pathogenesis in human tuberculosis. <i>Nature Immunology</i> , 2020, 21, 464-476.	7.0	71
7	Transcriptional profiling unveils type I and II interferon networks in blood and tissues across diseases. <i>Nature Communications</i> , 2019, 10, 2887.	5.8	65
8	Whole Serum 3D LC-nESI-FTMS Quantitative Proteomics Reveals Sexual Dimorphism in the Microenvironment of Overweight and Obese Adults. <i>Journal of Proteome Research</i> , 2014, 13, 5094-5105.	1.8	49
9	Altered Epithelial Gene Expression in Peripheral Airways of Severe Asthma. <i>PLoS ONE</i> , 2017, 12, e0168680.	1.1	48
10	Systemic delivery of E6/7 siRNA using novel lipidic particles and its application with cisplatin in cervical cancer mouse models. <i>Gene Therapy</i> , 2011, 18, 14-22.	2.3	44
11	Blood transcriptomics reveal the evolution and resolution of the immune response in tuberculosis. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	36
12	HLA-DR Marks Recently Divided Antigen-Specific Effector CD4 T Cells in Active Tuberculosis Patients. <i>Journal of Immunology</i> , 2021, 207, 523-533.	0.4	33
13	Differential gene expression in HIV-infected individuals following ART. <i>Antiviral Research</i> , 2013, 100, 420-428.	1.9	32
14	Gene expression in human fungal pathogen <i>Coccidioides immitis</i> changes as arthroconidia differentiate into spherules and mature. <i>BMC Microbiology</i> , 2013, 13, 121.	1.3	31
15	Gender-Dependent Differences in Plasma Matrix Metalloproteinase-8 Elevated in Pulmonary Tuberculosis. <i>PLoS ONE</i> , 2015, 10, e0117605.	1.1	30
16	OnPLS-Based Multi-Block Data Integration: A Multivariate Approach to Interrogating Biological Interactions in Asthma. <i>Analytical Chemistry</i> , 2018, 90, 13400-13408.	3.2	27
17	The Utility of Gene Expression in Blood Cells for Diagnosing Neuropsychiatric Disorders. <i>International Review of Neurobiology</i> , 2011, 101, 41-63.	0.9	26
18	The TCR repertoire of α -synuclein-specific T cells in Parkinson's disease is surprisingly diverse. <i>Scientific Reports</i> , 2021, 11, 302.	1.6	26

#	ARTICLE	IF	CITATIONS
19	Vitamin D Metabolites Inhibit Hepatitis C Virus and Modulate Cellular Gene Expression. <i>Journal of Virology & Antiviral Research</i> , 2014, 03, .	0.1	25
20	Suberoylanilide hydroxamic acid induces limited changes in the transcriptome of primary CD4+ T cells. <i>Aids</i> , 2013, 27, 29-37.	1.0	23
21	Dose-responsive gene expression in suberoylanilide hydroxamic acid-treated resting CD4+ T cells. <i>Aids</i> , 2015, 29, 2235-2244.	1.0	18
22	Factors regulated by interferon gamma and hypoxia-inducible factor 1A contribute to responses that protect mice from <i>Coccidioides immitis</i> infection. <i>BMC Microbiology</i> , 2012, 12, 218.	1.3	17
23	IFN- γ Influences Epithelial Antiviral Responses via Histone Methylation of the RIG-I Promoter. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2017, 57, 428-438.	1.4	17
24	Quantitative and qualitative iNKT repertoire associations with disease susceptibility and outcome in macaque tuberculosis infection. <i>Tuberculosis</i> , 2017, 105, 86-95.	0.8	16
25	Are you also what your mother eats? Distinct proteomic portrait as a result of maternal high-fat diet in the cerebral cortex of the adult mouse. <i>International Journal of Obesity</i> , 2015, 39, 1325-1328.	1.6	13
26	Distinct blood transcriptomic signature of treatment in latent tuberculosis infected individuals at risk of developing active disease. <i>Tuberculosis</i> , 2021, 131, 102127.	0.8	13
27	Effective Delivery of PEGylated siRNA-Containing Lipoplexes to Extraperitoneal Tumours following Intraperitoneal Administration. <i>Journal of Drug Delivery</i> , 2011, 2011, 1-7.	2.5	12
28	CD4+CCR6+ T cells dominate the BCG-induced transcriptional signature. <i>EBioMedicine</i> , 2021, 74, 103746.	2.7	11
29	Upregulation of epithelial metallothioneins by metal-rich ultrafine particulate matter from an underground railway. <i>Metallomics</i> , 2020, 12, 1070-1082.	1.0	6
30	A metric for evaluating biological information in gene sets and its application to identify co-expressed gene clusters in PBMC. <i>PLoS Computational Biology</i> , 2021, 17, e1009459.	1.5	2
31	IFN- γ influences bronchial epithelial anti-viral immune responses via inducible epigenetic control of histone methylation of the RIG-I promoter. , 2015, , .		0
32	LSC Abstract " Unsupervised gene co-expression analysis identifies a novel endotype in severe asthma. , 2016, , .		0
33	Transcriptional Signature Identifies Phenotypic Heterogeneity of Human Tuberculosis Infection. , 2018, , .		0
34	LSC - 2019 - Novel cellular effects of ultrafine particulate matter from an underground railway station uncovered through RNAseq. , 2019, , .		0