

# Rui Li

## List of Publications by Year in descending order

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Version: 2024-02-01

15  
papers

1,584  
citations

759233

12  
h-index

940533

16  
g-index

16  
all docs

16  
docs citations

16  
times ranked

3514  
citing authors

#	ARTICLE	IF	CITATIONS
1	Paired Transcriptomic and Proteomic Analysis Implicates IL-1 $\beta$ in the Pathogenesis of Papulopustular Rosacea Explants. <i>Journal of Investigative Dermatology</i> , 2021, 141, 800-809.	0.7	12
2	ecDNA hubs drive cooperative intermolecular oncogene expression. <i>Nature</i> , 2021, 600, 731-736.	27.8	123
3	Alterations of Immune and Keratinization Gene Expression in Papulopustular Rosacea by Whole Transcriptome Analysis. <i>Journal of Investigative Dermatology</i> , 2020, 140, 1100-1103.e4.	0.7	10
4	Chromatin Landscape Underpinning Human Dendritic Cell Heterogeneity. <i>Cell Reports</i> , 2020, 32, 108180.	6.4	18
5	Chromatin accessibility landscapes of skin cells in systemic sclerosis nominate dendritic cells in disease pathogenesis. <i>Nature Communications</i> , 2020, 11, 5843.	12.8	22
6	TFAP2C- and p63-Dependent Networks Sequentially Rearrange Chromatin Landscapes to Drive Human Epidermal Lineage Commitment. <i>Cell Stem Cell</i> , 2019, 24, 271-284.e8.	11.1	76
7	PIRCh-seq: functional classification of non-coding RNAs associated with distinct histone modifications. <i>Genome Biology</i> , 2019, 20, 292.	8.8	20
8	Transcript-indexed ATAC-seq for precision immune profiling. <i>Nature Medicine</i> , 2018, 24, 580-590.	30.7	124
9	Chromatin Accessibility Landscape of Cutaneous T Cell Lymphoma and Dynamic Response to HDAC Inhibitors. <i>Cancer Cell</i> , 2017, 32, 27-41.e4.	16.8	136
10	Gpr124 is essential for blood-brain barrier integrity in central nervous system disease. <i>Nature Medicine</i> , 2017, 23, 450-460.	30.7	177
11	Enhancer connectome in primary human cells identifies target genes of disease-associated DNA elements. <i>Nature Genetics</i> , 2017, 49, 1602-1612.	21.4	419
12	Novel Gene Expression Profile of Women with Intrinsic Skin Youthfulness by Whole Transcriptome Sequencing. <i>PLoS ONE</i> , 2016, 11, e0165913.	2.5	11
13	Assessment of the Genetic Basis of Rosacea by Genome-Wide Association Study. <i>Journal of Investigative Dermatology</i> , 2015, 135, 1548-1555.	0.7	129
14	Leukemia-Associated Cohesin Mutants Dominantly Enforce Stem Cell Programs and Impair Human Hematopoietic Progenitor Differentiation. <i>Cell Stem Cell</i> , 2015, 17, 675-688.	11.1	177
15	Individuality and Variation of Personal Regulomes in Primary Human T Cells. <i>Cell Systems</i> , 2015, 1, 51-61.	6.2	128