Pelin Sahlén

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/12202563/publications.pdf

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		1040056	1281871
11	2,244	9	11
papers	citations	h-index	g-index
11	11	11	4075
11	11	11	4073
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Chromatin interactions in differentiating keratinocytes reveal novel atopic dermatitis– and psoriasis-associated genes. Journal of Allergy and Clinical Immunology, 2021, 147, 1742-1752.	2.9	18
2	Variants That Differentiate Wolf and Dog Populations Are Enriched in Regulatory Elements. Genome Biology and Evolution, $2021,13,\ldots$	2.5	4
3	Whole-genome sequencing and gene network modules predict gemcitabine/carboplatin-induced myelosuppression in non-small cell lung cancer patients. Npj Systems Biology and Applications, 2020, 6, 25.	3.0	9
4	A Multi-Omics Approach to Liver Diseases: Integration of Single Nuclei Transcriptomics with Proteomics and HiCap Bulk Data in Human Liver. OMICS A Journal of Integrative Biology, 2020, 24, 180-194.	2.0	26
5	Promoter anchored interaction landscape of THP-1 macrophages captures early immune response processes. Cellular Immunology, 2020, 355, 104148.	3.0	9
6	High-Resolution Regulatory Maps Connect Vascular Risk Variants to Disease-Related Pathways. Circulation Genomic and Precision Medicine, 2019, 12, e002353.	3.6	13
7	Allele specific chromatin signals, 3D interactions, and motif predictions for immune and B cell related diseases. Scientific Reports, 2019, 9, 2695.	3.3	24
8	The BAF and PRC2 Complex Subunits Dpf2 and Eed Antagonistically Converge on Tbx3 to Control ESC Differentiation. Cell Stem Cell, 2019, 24, 138-152.e8.	11.1	30
9	HiCapTools: a software suite for probe design and proximity detection for targeted chromosome conformation capture applications. Bioinformatics, 2018, 34, 675-677.	4.1	20
10	Visualization and analysis of gene expression in tissue sections by spatial transcriptomics. Science, 2016, 353, 78-82.	12.6	1,983
11	Genome-wide mapping of promoter-anchored interactions with close to single-enhancer resolution. Genome Biology, 2015, 16, 156.	8.8	108