

Long Gao

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3655801/publications.pdf>

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18
papers

1,469
citations

567281

15
h-index

839539

18
g-index

22
all docs

22
docs citations

22
times ranked

3733
citing authors

#	ARTICLE	IF	CITATIONS
1	Discovery of 318 new risk loci for type 2 diabetes and related vascular outcomes among 1.4 million participants in a multi-ancestry meta-analysis. <i>Nature Genetics</i> , 2020, 52, 680-691.	21.4	445
2	Runx1 Deficiency Decreases Ribosome Biogenesis and Confers Stress Resistance to Hematopoietic Stem and Progenitor Cells. <i>Cell Stem Cell</i> , 2015, 17, 165-177.	11.1	195
3	The effect of smoking on DNA methylation of peripheral blood mononuclear cells from African American women. <i>BMC Genomics</i> , 2014, 15, 151.	2.8	193
4	Multiplexed In Situ Imaging Mass Cytometry Analysis of the Human Endocrine Pancreas and Immune System in Type 1 Diabetes. <i>Cell Metabolism</i> , 2019, 29, 769-783.e4.	16.2	151
5	RUNX1 and the endothelial origin of blood. <i>Experimental Hematology</i> , 2018, 68, 2-9.	0.4	68
6	Single-cell transcriptomics of human islet ontogeny defines the molecular basis of β^2 -cell dedifferentiation in T2D. <i>Molecular Metabolism</i> , 2020, 42, 101057.	6.5	63
7	Modeling disease progression using dynamics of pathway connectivity. <i>Bioinformatics</i> , 2014, 30, 2343-2350.	4.1	56
8	Revealing Pathway Dynamics in Heart Diseases by Analyzing Multiple Differential Networks. <i>PLoS Computational Biology</i> , 2015, 11, e1004332.	3.2	43
9	Collapse of the hepatic gene regulatory network in the absence of FoxA factors. <i>Genes and Development</i> , 2020, 34, 1039-1050.	5.9	36
10	Identifying noncoding risk variants using disease-relevant gene regulatory networks. <i>Nature Communications</i> , 2018, 9, 702.	12.8	35
11	Transcriptional regulatory network controlling the ontogeny of hematopoietic stem cells. <i>Genes and Development</i> , 2020, 34, 950-964.	5.9	33
12	FoxA-dependent demethylation of DNA initiates epigenetic memory of cellular identity. <i>Developmental Cell</i> , 2021, 56, 602-612.e4.	7.0	30
13	Multi-Analyte Network Markers for Tumor Prognosis. <i>PLoS ONE</i> , 2012, 7, e52973.	2.5	22
14	Maturation of hematopoietic stem cells from prehematopoietic stem cells is accompanied by up-regulation of PD-L1. <i>Journal of Experimental Medicine</i> , 2018, 215, 645-659.	8.5	19
15	Discover context-specific combinatorial transcription factor interactions by integrating diverse ChIP-Seq data sets. <i>Nucleic Acids Research</i> , 2014, 42, e24-e24.	14.5	18
16	CD27 marks murine embryonic hematopoietic stem cells and type II prehematopoietic stem cells. <i>Blood</i> , 2017, 130, 372-376.	1.4	18
17	CHD7 and Runx1 interaction provides a braking mechanism for hematopoietic differentiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 23626-23635.	7.1	18
18	Analysis of multiple gene co-expression networks to discover interactions favoring CFTR biogenesis and β^2 F508-CFTR rescue. <i>BMC Medical Genomics</i> , 2021, 14, 258.	1.5	2