Sarah Kim-Hellmuth

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1816788/publications.pdf

Version: 2024-02-01

25 papers 12,077 citations

394286 19 h-index 25 g-index

31 all docs

31 docs citations

31 times ranked

25024 citing authors

#	Article	IF	Citations
1	Genetic effects on gene expression across human tissues. Nature, 2017, 550, 204-213.	13.7	3,500
2	The GTEx Consortium atlas of genetic regulatory effects across human tissues. Science, 2020, 369, 1318-1330.	6.0	2,385
3	5'-Triphosphate RNA Is the Ligand for RIG-I. Science, 2006, 314, 994-997.	6.0	2,094
4	Severe COVID-19 Is Marked by a Dysregulated Myeloid Cell Compartment. Cell, 2020, 182, 1419-1440.e23.	13.5	1,162
5	Swarm Learning for decentralized and confidential clinical machine learning. Nature, 2021, 594, 265-270.	13.7	375
6	The impact of sex on gene expression across human tissues. Science, 2020, 369, .	6.0	329
7	Inflammasomes: current understanding and open questions. Cellular and Molecular Life Sciences, 2011, 68, 765-783.	2.4	316
8	Determinants of telomere length across human tissues. Science, 2020, 369, .	6.0	257
9	A Quantitative Proteome Map of the Human Body. Cell, 2020, 183, 269-283.e19.	13.5	243
10	<i>Listeria monocytogenes</i> is sensed by the NLRP3 and AIM2 inflammasome. European Journal of Immunology, 2010, 40, 1545-1551.	1.6	221
11	Cell type–specific genetic regulation of gene expression across human tissues. Science, 2020, 369, .	6.0	210
12	Genetic regulatory effects modified by immune activation contribute to autoimmune disease associations. Nature Communications, 2017, 8, 266.	5.8	157
13	Exploiting the GTEx resources to decipher the mechanisms at GWAS loci. Genome Biology, 2021, 22, 49.	3.8	150
14	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. Cell, 2021, 184, 2633-2648.e19.	13.5	94
15	Selection of Molecular Structure and Delivery of RNA Oligonucleotides to Activate TLR7 versus TLR8 and to Induce High Amounts of IL-12p70 in Primary Human Monocytes. Journal of Immunology, 2009, 182, 6824-6833.	0.4	90
16	A vast resource of allelic expression data spanning human tissues. Genome Biology, 2020, 21, 234.	3.8	68
17	Selfâ€priming determines high type I <scp>IFN</scp> production by plasmacytoid dendritic cells. European Journal of Immunology, 2014, 44, 807-818.	1.6	63
18	Characterizing the genetic basis of innate immune response in TLR4-activated human monocytes. Nature Communications, 2014, 5, 5236.	5.8	61

#	Article	IF	CITATION
19	De novo nonsense and frameshift variants of TCF20 in individuals with intellectual disability and postnatal overgrowth. European Journal of Human Genetics, 2016, 24, 1739-1745.	1.4	28
20	Whole exome sequencing and arrayâ€based molecular karyotyping as aids to prenatal diagnosis in fetuses with suspected Simpson–Golabi–Behmel syndrome. Prenatal Diagnosis, 2016, 36, 961-965.	1.1	19
21	An autoimmune disease risk variant: A trans master regulatory effect mediated by IRF1 under immune stimulation?. PLoS Genetics, 2021, 17, e1009684.	1.5	17
22	Transcription factor regulation of eQTL activity across individuals and tissues. PLoS Genetics, 2022, 18, e1009719.	1.5	14
23	An unexpected role for RNA in the recognition of DNA by the innate immune system. RNA Biology, 2010, 7, 151-157.	1.5	11
24	SARS-CoV-2 Triggering Severe Acute Respiratory Distress Syndrome and Secondary Hemophagocytic Lymphohistiocytosis in a 3-Year-Old Child With Down Syndrome. Journal of the Pediatric Infectious Diseases Society, 2021, 10, 543-546.	0.6	11
25	Concerted Genetic Function in Blood Traits. Cell, 2016, 167, 1167-1169.	13.5	4