

Silva Kasela

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

23
papers

2,191
citations

15
h-index

27
g-index

27
ext. papers

3,606
ext. citations

23.1
avg. IF

4.1
L-index

#	Paper	IF	Citations
23	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. <i>Nature</i> , 2017 , 541, 81-86	50.4	511
22	The transcriptional landscape of age in human peripheral blood. <i>Nature Communications</i> , 2015 , 6, 8570	17.4	335
21	Identification of Required Host Factors for SARS-CoV-2 Infection in Human Cells. <i>Cell</i> , 2021 , 184, 92-105.e16	41.6	240
20	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. <i>Nature Genetics</i> , 2015 , 47, 1282-1293	36.3	223
19	Unraveling the polygenic architecture of complex traits using blood eQTL metaanalysis		175
18	The impact of sex on gene expression across human tissues. <i>Science</i> , 2020 , 369,	33.3	100
17	Cell Specific eQTL Analysis without Sorting Cells. <i>PLoS Genetics</i> , 2015 , 11, e1005223	6	81
16	Age-related profiling of DNA methylation in CD8+ T cells reveals changes in immune response and transcriptional regulator genes. <i>Scientific Reports</i> , 2015 , 5, 13107	4.9	81
15	The GTEx Consortium atlas of genetic regulatory effects across human tissues		81
14	Pathogenic implications for autoimmune mechanisms derived by comparative eQTL analysis of CD4+ versus CD8+ T cells. <i>PLoS Genetics</i> , 2017 , 13, e1006643	6	75
13	A Quantitative Proteome Map of the Human Body. <i>Cell</i> , 2020 , 183, 269-283.e19	56.2	73
12	Cell type-specific genetic regulation of gene expression across human tissues. <i>Science</i> , 2020 , 369,	33.3	68
11	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. <i>Nature Genetics</i> , 2021 , 53, 1300-1310	36.3	60
10	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021 , 53, 1311-1321	36.3	27
9	A vast resource of allelic expression data spanning human tissues. <i>Genome Biology</i> , 2020 , 21, 234	18.3	18
8	Imprinted genes and imprinting control regions show predominant intermediate methylation in adult somatic tissues. <i>Epigenomics</i> , 2016 , 8, 789-99	4.4	14
7	Integrative approach identifies SLC6A20 and CXCR6 as putative causal genes for the COVID-19 GWAS signal in the 3p21.31 locus. <i>Genome Biology</i> , 2021 , 22, 242	18.3	11

6	Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. <i>Nature Communications</i> , 2020 , 11, 5182	17.4	6
5	Genetic and non-genetic factors affecting the expression of COVID-19-relevant genes in the large airway epithelium. <i>Genome Medicine</i> , 2021 , 13, 66	14.4	6
4	Integrative approach identifies and as putative causal genes for the COVID-19 GWAS signal in the 3p21.31 locus 2021 ,		3
3	Transcription factor regulation of eQTL activity across individuals and tissues.. <i>PLoS Genetics</i> , 2022 , 18, e1009719	6	1
2	Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus. <i>Nature Communications</i> , 2021 , 12, 7173	17.4	1
1	Meta-analyses identify DNA methylation associated with kidney function and damage. <i>Nature Communications</i> , 2021 , 12, 7174	17.4	0