

Silva Kasela

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/9270049/silva-kasela-publications-by-year.pdf>

Version: 2024-04-19

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	Transcription factor regulation of eQTL activity across individuals and tissues.. <i>PLoS Genetics</i> , 2022 , 18, e1009719	6	1
22	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
21	Integrative approach identifies and as putative causal genes for the COVID-19 GWAS signal in the 3p21.31 locus 2021 ,		3
20	Identification of Required Host Factors for SARS-CoV-2 Infection in Human Cells. <i>Cell</i> , 2021 , 184, 92-105.e16	36.6	240
19	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
18	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021 , 53, 1311-1321	36.3	27
17	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
16	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
15	Meta-analyses identify DNA methylation associated with kidney function and damage. <i>Nature Communications</i> , 2021 , 12, 7174	17.4	0
14	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
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	The impact of sex on gene expression across human tissues. <i>Science</i> , 2020 , 369,	33.3	100
10	A vast resource of allelic expression data spanning human tissues. <i>Genome Biology</i> , 2020 , 21, 234	18.3	18
9	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. <i>Nature</i> , 2017 , 541, 81-86	50.4	511
8	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
7	Imprinted genes and imprinting control regions show predominant intermediate methylation in adult somatic tissues. <i>Epigenomics</i> , 2016 , 8, 789-99	4.4	14

6	Cell Specific eQTL Analysis without Sorting Cells. <i>PLoS Genetics</i> , 2015 , 11, e1005223	6	81
5	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
4	The transcriptional landscape of age in human peripheral blood. <i>Nature Communications</i> , 2015 , 6, 8570	17.4	335
3	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
2	Unraveling the polygenic architecture of complex traits using blood eQTL metaanalysis		175
1	The GTEx Consortium atlas of genetic regulatory effects across human tissues		81