

# Silva Kasela

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9270049/publications.pdf>

Version: 2024-02-01

21  
papers

4,737  
citations

471509

17  
h-index

713466

21  
g-index

27  
all docs

27  
docs citations

27  
times ranked

11239  
citing authors

#	ARTICLE	IF	CITATIONS
1	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. <i>Nature</i> , 2017, 541, 81-86.	27.8	743
2	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.	21.4	590
3	The transcriptional landscape of age in human peripheral blood. <i>Nature Communications</i> , 2015, 6, 8570.	12.8	533
4	Identification of Required Host Factors for SARS-CoV-2 Infection in Human Cells. <i>Cell</i> , 2021, 184, 92-105.e16.	28.9	480
5	The impact of sex on gene expression across human tissues. <i>Science</i> , 2020, 369, .	12.6	329
6	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.	21.4	294
7	A Quantitative Proteome Map of the Human Body. <i>Cell</i> , 2020, 183, 269-283.e19.	28.9	243
8	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	21.4	218
9	Cell type-specific genetic regulation of gene expression across human tissues. <i>Science</i> , 2020, 369, .	12.6	210
10	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.	3.3	148
11	Cell Specific eQTL Analysis without Sorting Cells. <i>PLoS Genetics</i> , 2015, 11, e1005223.	3.5	115
12	Pathogenic implications for autoimmune mechanisms derived by comparative eQTL analysis of CD4+ versus CD8+ T cells. <i>PLoS Genetics</i> , 2017, 13, e1006643.	3.5	110
13	A vast resource of allelic expression data spanning human tissues. <i>Genome Biology</i> , 2020, 21, 234.	8.8	68
14	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.	8.8	40
15	Imprinted genes and imprinting control regions show predominant intermediate methylation in adult somatic tissues. <i>Epigenomics</i> , 2016, 8, 789-799.	2.1	35
16	Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. <i>Nature Communications</i> , 2020, 11, 5182.	12.8	32
17	Meta-analyses identify DNA methylation associated with kidney function and damage. <i>Nature Communications</i> , 2021, 12, 7174.	12.8	30
18	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.	8.2	21

#	ARTICLE	IF	CITATIONS
19	Arsenic Exposure, Blood DNA Methylation, and Cardiovascular Disease. Circulation Research, 2022, 131, .	4.5	20
20	Transcription factor regulation of eQTL activity across individuals and tissues. PLoS Genetics, 2022, 18, e1009719.	3.5	14
21	Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus. Nature Communications, 2021, 12, 7173.	12.8	8