

# Samuel W Lukowski

## List of Publications by Year in descending order

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Version: 2024-02-01

41  
papers

1,779  
citations

331538

21  
h-index

330025

37  
g-index

52  
all docs

52  
docs citations

52  
times ranked

3840  
citing authors

#	ARTICLE	IF	CITATIONS
1	Single-Cell Transcriptomic Analysis of Cardiac Differentiation from Human PSCs Reveals HOPX-Dependent Cardiomyocyte Maturation. <i>Cell Stem Cell</i> , 2018, 23, 586-598.e8.	5.2	215
2	A single-cell transcriptome atlas of the adult human retina. <i>EMBO Journal</i> , 2019, 38, e100811.	3.5	185
3	The Serum Resistome of a Globally Disseminated Multidrug Resistant Uropathogenic <i>Escherichia coli</i> Clone. <i>PLoS Genetics</i> , 2013, 9, e1003834.	1.5	146
4	Dynamics of human monocytes and airway macrophages during healthy aging and after transplant. <i>Journal of Experimental Medicine</i> , 2020, 217, .	4.2	113
5	Single-cell RNA-seq of human induced pluripotent stem cells reveals cellular heterogeneity and cell state transitions between subpopulations. <i>Genome Research</i> , 2018, 28, 1053-1066.	2.4	102
6	Single-Cell Transcriptional Profiling of Aortic Endothelium Identifies a Hierarchy from Endovascular Progenitors to Differentiated Cells. <i>Cell Reports</i> , 2019, 27, 2748-2758.e3.	2.9	96
7	Ferrets exclusively synthesize Neu5Ac and express naturally humanized influenza A virus receptors. <i>Nature Communications</i> , 2014, 5, 5750.	5.8	94
8	Transcriptomics and single-cell RNA-sequencing. <i>Respirology</i> , 2019, 24, 29-36.	1.3	77
9	Single cell eQTL analysis identifies cell type-specific genetic control of gene expression in fibroblasts and reprogrammed induced pluripotent stem cells. <i>Genome Biology</i> , 2021, 22, 76.	3.8	58
10	Single cell RNA sequencing of stem cell-derived retinal ganglion cells. <i>Scientific Data</i> , 2018, 5, 180013.	2.4	55
11	CR1g-expressing peritoneal macrophages are associated with disease severity in patients with cirrhosis and ascites. <i>JCI Insight</i> , 2016, 1, e86914.	2.3	53
12	Genetic regulation of disease risk and endometrial gene expression highlights potential target genes for endometriosis and polycystic ovarian syndrome. <i>Scientific Reports</i> , 2018, 8, 11424.	1.6	49
13	Tissue specific regulation of transcription in endometrium and association with disease. <i>Human Reproduction</i> , 2020, 35, 377-393.	0.4	43
14	Comparative performance of the BGI and Illumina sequencing technology for single-cell RNA-sequencing. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa034.	1.5	37
15	Slightly deleterious genomic variants and transcriptome perturbations in Down syndrome embryonic selection. <i>Genome Research</i> , 2018, 28, 1-10.	2.4	36
16	ascend: R package for analysis of single-cell RNA-seq data. <i>GigaScience</i> , 2019, 8, .	3.3	36
17	Gene Age Predicts the Strength of Purifying Selection Acting on Gene Expression Variation in Humans. <i>American Journal of Human Genetics</i> , 2014, 95, 660-674.	2.6	35
18	Hepatic expression profiling identifies steatosis-independent and steatosis-driven advanced fibrosis genes. <i>JCI Insight</i> , 2018, 3, .	2.3	35

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19	The genetic regulation of transcription in human endometrial tissue. <i>Human Reproduction</i> , 2017, 32, 893-904.	0.4	32
20	Genetic regulation of methylation in human endometrium and blood and gene targets for reproductive diseases. <i>Clinical Epigenetics</i> , 2019, 11, 49.	1.8	26
21	FGB mutations leading to congenital quantitative fibrinogen deficiencies: An update and report of four novel mutations. <i>Thrombosis Research</i> , 2014, 133, 868-874.	0.8	23
22	Genetic correlations reveal the shared genetic architecture of transcription in human peripheral blood. <i>Nature Communications</i> , 2017, 8, 483.	5.8	22
23	Detection of HPV E7 Transcription at Single-Cell Resolution in Epidermis. <i>Journal of Investigative Dermatology</i> , 2018, 138, 2558-2567.	0.3	19
24	Single-cell RNA sequencing reveals cell type-specific HPV expression in hyperplastic skin lesions. <i>Virology</i> , 2019, 537, 14-19.	1.1	19
25	Hypofibrinogenemia and liver disease: a new case of Aguadilla fibrinogen and review of the literature. <i>Haemophilia</i> , 2015, 21, 820-827.	1.0	18
26	Disrupted posttranscriptional regulation of the cystic fibrosis transmembrane conductance regulator (CFTR) by a 5' UTR mutation is associated with a cftr-related disease. <i>Human Mutation</i> , 2011, 32, E2266-E2282.	1.1	17
27	Absence of Batf3 reveals a new dimension of cell state heterogeneity within conventional dendritic cells. <i>IScience</i> , 2021, 24, 102402.	1.9	16
28	Longitudinal expression profiling of CD4+ and CD8+ cells in patients with active to quiescent giant cell arteritis. <i>BMC Medical Genomics</i> , 2018, 11, 61.	0.7	15
29	Dysregulation of Stemness Pathways in HPV Mediated Cervical Malignant Transformation Identifies Potential Oncotherapy Targets. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 307.	1.8	15
30	Integrated analysis of mRNA and miRNA expression in response to interleukin-6 in hepatocytes. <i>Genomics</i> , 2015, 106, 107-115.	1.3	13
31	CFTR mRNA expression is regulated by an upstream open reading frame and RNA secondary structure in its 5' untranslated region. <i>Human Molecular Genetics</i> , 2015, 24, 899-912.	1.4	9
32	Chemical Modulators of Fibrinogen Production and Their Impact on Venous Thrombosis. <i>Thrombosis and Haemostasis</i> , 2021, 121, 433-448.	1.8	8
33	A model of impaired Langerhans cell maturation associated with HPV induced epithelial hyperplasia. <i>IScience</i> , 2021, 24, 103326.	1.9	7
34	Altered differentiation of endometrial mesenchymal stromal fibroblasts is associated with endometriosis susceptibility. <i>Communications Biology</i> , 2022, 5, .	2.0	4
35	Integrated analysis of mRNA and miRNA expression in response to interleukin-6 in hepatocytes. <i>Data in Brief</i> , 2015, 4, 226-228.	0.5	3
36	Antigen Nonspecific Induction of Distinct Regulatory T Cell States in Oncogene-Driven Hyperproliferative Skin. <i>ImmunoHorizons</i> , 2021, 5, 102-116.	0.8	3

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37	Acquisition of murine splenic myeloid cells for protein and gene expression profiling by advanced flow cytometry and CITE-seq. STAR Protocols, 2021, 2, 100842.	0.5	2
38	RNA-sequencing analysis of biopsies from chronic liver disease patients identifies gene signatures associated with progressive liver disease. Journal of Hepatology, 2018, 68, S401-S402.	1.8	0
39	Reconstruction of Transcriptional Programs of Monocyte to Macrophage Sequential Cell Fate Transition Using Single Cell RNA Sequencing in Sex Mis-Matched Lung Transplantation. Journal of Heart and Lung Transplantation, 2019, 38, S157.	0.3	0
40	A Model of Impaired Langerhans Cell Maturation Associated With HPV Induced Epithelial Hyperplasia. SSRN Electronic Journal, 0, , .	0.4	0
41	Cardiac Directed Differentiation Using Small Molecule WNT Modulation at Single-Cell Resolution. SSRN Electronic Journal, 0, , .	0.4	0