Simon Koplev

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Enrichr: a comprehensive gene set enrichment analysis web server 2016 update. Nucleic Acids Research, 2016, 44, W90-W97.	14.5	7,240
2	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. Nature Genetics, 2018, 50, 524-537.	21.4	1,124
3	The Library of Integrated Network-Based Cellular Signatures NIH Program: System-Level Cataloging of Human Cells Response to Perturbations. Cell Systems, 2018, 6, 13-24.	6.2	327
4	Macrophage Trafficking, Inflammatory Resolution, and Genomics in Atherosclerosis. Journal of the American College of Cardiology, 2018, 72, 2181-2197.	2.8	139
5	Unraveling tumor–immune heterogeneity in advanced ovarian cancer uncovers immunogenic effect of chemotherapy. Nature Genetics, 2020, 52, 582-593.	21.4	136
6	Clonally expanding smooth muscle cells promote atherosclerosis by escaping efferocytosis and activating the complement cascade. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 15818-15826.	7.1	83
7	Sex-Stratified Gene Regulatory Networks Reveal Female Key Driver Genes of Atherosclerosis Involved in Smooth Muscle Cell Phenotype Switching. Circulation, 2021, 143, 713-726.	1.6	61
8	A Strategy for Discovery of Endocrine Interactions with Application to Whole-Body Metabolism. Cell Metabolism, 2018, 27, 1138-1155.e6.	16.2	58
9	A mechanistic framework for cardiometabolic and coronary artery diseases. , 2022, 1, 85-100.		51
10	Contribution of Gene Regulatory Networks to Heritability of CoronaryÂArtery Disease. Journal of the American College of Cardiology, 2019, 73, 2946-2957.	2.8	45
11	<i>JCAD</i> , a Gene at the 10p11 Coronary Artery Disease Locus, Regulates Hippo Signaling in Endothelial Cells. Arteriosclerosis, Thrombosis, and Vascular Biology, 2018, 38, 1711-1722.	2.4	36
12	Histone deacetylase 9 promotes endothelial-mesenchymal transition and an unfavorable atherosclerotic plaque phenotype. Journal of Clinical Investigation, 2021, 131, .	8.2	36
13	An integrative multiomic network model links lipid metabolism to glucose regulation in coronary artery disease. Nature Communications, 2021, 12, 547.	12.8	35
14	Integration of pan-cancer transcriptomics with RPPA proteomics reveals mechanisms of epithelial-mesenchymal transition. PLoS Computational Biology, 2018, 14, e1005911.	3.2	33
15	MicroRNA-210, MicroRNA-331, and MicroRNA-7 Are Differentially Regulated in Treated HIV-1–Infected Individuals and Are Associated With Markers of Systemic Inflammation. Journal of Acquired Immune Deficiency Syndromes (1999), 2017, 74, e104-e113.	2.1	31
16	Functional regulatory mechanism of smooth muscle cell-restricted LMOD1 coronary artery disease locus. PLoS Genetics, 2018, 14, e1007755.	3.5	30
17	CD90 Identifies Adventitial Mesenchymal Progenitor Cells in Adult Human Medium- and Large-Sized Arteries. Stem Cell Reports, 2018, 11, 242-257.	4.8	26
18	Functional and transcriptomic insights into pathogenesis of R9C phospholamban mutation using human induced pluripotent stem cell-derived cardiomyocytes. Journal of Molecular and Cellular Cardiology, 2018, 119, 147-154.	1.9	25

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19	Developing a framework for digital objects in the Big Data to Knowledge (BD2K) commons: Report from the Commons Framework Pilots workshop. Journal of Biomedical Informatics, 2017, 71, 49-57.	4.3	24
20	Transcriptome-wide association study of coronary artery disease identifies novel susceptibility genes. Basic Research in Cardiology, 2022, 117, 6.	5.9	22
21	Dynamic Rearrangement of Cell States Detected by Systematic Screening of Sequential Anticancer Treatments. Cell Reports, 2017, 20, 2784-2791.	6.4	20
22	Dynamic changes in chromatin accessibility are associated with the atherogenic transitioning of vascular smooth muscle cells. Cardiovascular Research, 2022, 118, 2792-2804.	3.8	17
23	Integrative Prioritization of Causal Genes for Coronary Artery Disease. Circulation Genomic and Precision Medicine, 2022, 15, CIRCGEN121003365.	3.6	11
24	Systems Pharmacology Identifies an Arterial Wall Regulatory Gene Network Mediating Coronary Artery Disease Side Effects of Antiretroviral Therapy. Circulation Genomic and Precision Medicine, 2019, 12, e002390.	3.6	9
25	83â€The coronary artery disease associated gene JCAD regulates hippo signalling in endothelial cells. , 2018, , .		0