

Simon Koplev

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6504487/publications.pdf>

Version: 2024-02-01

25
papers

9,639
citations

430874

18
h-index

580821

25
g-index

30
all docs

30
docs citations

30
times ranked

23389
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Dynamic changes in chromatin accessibility are associated with the atherogenic transitioning of vascular smooth muscle cells. <i>Cardiovascular Research</i> , 2022, 118, 2792-2804. | 3.8 | 17 |
| 2 | A mechanistic framework for cardiometabolic and coronary artery diseases. , 2022, 1, 85-100. | | 51 |
| 3 | Transcriptome-wide association study of coronary artery disease identifies novel susceptibility genes. <i>Basic Research in Cardiology</i> , 2022, 117, 6. | 5.9 | 22 |
| 4 | Integrative Prioritization of Causal Genes for Coronary Artery Disease. <i>Circulation Genomic and Precision Medicine</i> , 2022, 15, CIRCGEN121003365. | 3.6 | 11 |
| 5 | An integrative multiomic network model links lipid metabolism to glucose regulation in coronary artery disease. <i>Nature Communications</i> , 2021, 12, 547. | 12.8 | 35 |
| 6 | Sex-Stratified Gene Regulatory Networks Reveal Female Key Driver Genes of Atherosclerosis Involved in Smooth Muscle Cell Phenotype Switching. <i>Circulation</i> , 2021, 143, 713-726. | 1.6 | 61 |
| 7 | Histone deacetylase 9 promotes endothelial-mesenchymal transition and an unfavorable atherosclerotic plaque phenotype. <i>Journal of Clinical Investigation</i> , 2021, 131, . | 8.2 | 36 |
| 8 | Unraveling tumorâ€™immune heterogeneity in advanced ovarian cancer uncovers immunogenic effect of chemotherapy. <i>Nature Genetics</i> , 2020, 52, 582-593. | 21.4 | 136 |
| 9 | Clonally expanding smooth muscle cells promote atherosclerosis by escaping efferocytosis and activating the complement cascade. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 15818-15826. | 7.1 | 83 |
| 10 | Contribution of Gene Regulatory Networks to Heritability of Coronary Artery Disease. <i>Journal of the American College of Cardiology</i> , 2019, 73, 2946-2957. | 2.8 | 45 |
| 11 | Systems Pharmacology Identifies an Arterial Wall Regulatory Gene Network Mediating Coronary Artery Disease Side Effects of Antiretroviral Therapy. <i>Circulation Genomic and Precision Medicine</i> , 2019, 12, e002390. | 3.6 | 9 |
| 12 | The Library of Integrated Network-Based Cellular Signatures NIH Program: System-Level Cataloging of Human Cells Response to Perturbations. <i>Cell Systems</i> , 2018, 6, 13-24. | 6.2 | 327 |
| 13 | A Strategy for Discovery of Endocrine Interactions with Application to Whole-Body Metabolism. <i>Cell Metabolism</i> , 2018, 27, 1138-1155.e6. | 16.2 | 58 |
| 14 | 83â€™...The coronary artery disease associated gene JCAD regulates hippo signalling in endothelial cells. , 2018, , . | | 0 |
| 15 | Functional regulatory mechanism of smooth muscle cell-restricted LMOD1 coronary artery disease locus. <i>PLoS Genetics</i> , 2018, 14, e1007755. | 3.5 | 30 |
| 16 | Macrophage Trafficking, Inflammatory Resolution, and Genomics in Atherosclerosis. <i>Journal of the American College of Cardiology</i> , 2018, 72, 2181-2197. | 2.8 | 139 |
| 17 | <i>JCAD</i> , a Gene at the 10p11 Coronary Artery Disease Locus, Regulates Hippo Signaling in Endothelial Cells. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2018, 38, 1711-1722. | 2.4 | 36 |
| 18 | CD90 Identifies Adventitial Mesenchymal Progenitor Cells in Adult Human Medium- and Large-Sized Arteries. <i>Stem Cell Reports</i> , 2018, 11, 242-257. | 4.8 | 26 |

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|----|--|------|-----------|
| 19 | Functional and transcriptomic insights into pathogenesis of R9C phospholamban mutation using human induced pluripotent stem cell-derived cardiomyocytes. <i>Journal of Molecular and Cellular Cardiology</i> , 2018, 119, 147-154. | 1.9 | 25 |
| 20 | Integration of pan-cancer transcriptomics with RPPA proteomics reveals mechanisms of epithelial-mesenchymal transition. <i>PLoS Computational Biology</i> , 2018, 14, e1005911. | 3.2 | 33 |
| 21 | Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. <i>Nature Genetics</i> , 2018, 50, 524-537. | 21.4 | 1,124 |
| 22 | Developing a framework for digital objects in the Big Data to Knowledge (BD2K) commons: Report from the Commons Framework Pilots workshop. <i>Journal of Biomedical Informatics</i> , 2017, 71, 49-57. | 4.3 | 24 |
| 23 | MicroRNA-210, MicroRNA-331, and MicroRNA-7 Are Differentially Regulated in Treated HIV-1â€“Infected Individuals and Are Associated With Markers of Systemic Inflammation. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2017, 74, e104-e113. | 2.1 | 31 |
| 24 | Dynamic Rearrangement of Cell States Detected by Systematic Screening of Sequential Anticancer Treatments. <i>Cell Reports</i> , 2017, 20, 2784-2791. | 6.4 | 20 |
| 25 | Enrichr: a comprehensive gene set enrichment analysis web server 2016 update. <i>Nucleic Acids Research</i> , 2016, 44, W90-W97. | 14.5 | 7,240 |