# Konstantinos Theofilatos

List of Publications by Year
in descending order

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|---|---|---|---|
| 26<br>papers | 734<br>citations | 686830<br>13<br>h-index | 580395<br>25<br>g-index |
| 27<br>all docs | 27<br>docs citations | 27<br>times ranked | 1227<br>citing authors |

| # | Article | IF | Citations |
|---|---------|----|-----------|
| 1 | Association of cardiometabolic microRNAs with COVID-19 severity and mortality. Cardiovascular Research, 2022, 118, 461-474. | 1.8 | 51 |
| 2 | Neutrophil-Derived Protein S100A8/A9 Alters the Platelet Proteome in Acute Myocardial Infarction and Is Associated With Changes in Platelet Reactivity. Arteriosclerosis, Thrombosis, and Vascular Biology, 2022, 42, 49-62. | 1.1 | 31 |
| 3 | Gene editing reverses arrhythmia susceptibility in humanized PLN-R14del mice: modelling a European cardiomyopathy with global impact. Cardiovascular Research, 2022, 118, 3140-3150. | 1.8 | 23 |
| 4 | A survey on computational taste predictors. European Food Research and Technology, 2022, 248, 2215-2235. | 1.6 | 9 |
| 5 | Systems biology in cardiovascular disease: a multiomics approach. Nature Reviews Cardiology, 2021, 18, 313-330. | 6.1 | 134 |
| 6 | Impairment of the ER/mitochondria compartment in human cardiomyocytes with PLN p.Arg14del mutation. EMBO Molecular Medicine, 2021, 13, e13074. | 3.3 | 34 |
| 7 | Pharmacoepigenomics circuits induced by a novel retinoid-polyamine conjugate in human immortalized keratinocytes. Pharmacogenomics Journal, 2021, 21, 638-648. | 0.9 | 3 |
| 8 | SARS-CoV-2 RNAemia and proteomic trajectories inform prognostication in COVID-19 patients admitted to intensive care. Nature Communications, 2021, 12, 3406. | 5.8 | 122 |
| 9 | Protein Aggregation Is an Early Manifestation of Phospholamban p.(Arg14del)â€"Related Cardiomyopathy: Development of PLN-R14delâ€"Related Cardiomyopathy. Circulation: Heart Failure, 2021, 14, e008532. | 1.6 | 17 |
| 10 | On the human taste perception: Molecular-level understanding empowered by computational methods. Trends in Food Science and Technology, 2021, 116, 445-459. | 7.8 | 17 |
| 11 | PCSK9 Activity Is Potentiated Through HDL Binding. Circulation Research, 2021, 129, 1039-1053. | 2.0 | 13 |
| 12 | Extracellular Matrix in Heart Failure: Role of ADAMTS5 in Proteoglycan Remodeling. Circulation, 2021, 144, 2021-2034. | 1.6 | 31 |
| 13 | Paracrine signalling by cardiac calcitonin controls atrial fibrogenesis and arrhythmia. Nature, 2020, 587, 460-465. | 13.7 | 55 |
| 14 | &lt;p&gt;Reducing Opioid Prescriptions by Identifying Responders on Topical Analgesic Treatment Using an Individualized Medicine and Predictive Analytics Approach&lt;/p&gt;. Journal of Pain Research, 2020, Volume 13, 1255-1266. | 0.8 | 8 |
| 15 | Metabolic recovery after weight loss surgery is reflected in serum microRNAs. BMJ Open Diabetes Research and Care, 2020, 8, e001441. | 1.2 | 15 |
| 16 | Identification of Important Biological Pathways for Ischemic Stroke Prediction through a Mathematical Programming Optimisation Model-DIGS. , 2020, , . | | 1 |
| 17 | Discovery of stroke-related blood biomarkers from gene expression network models. BMC Medical Genomics, 2019, 12, 118. | 0.7 | 14 |
| 18 | Comparative Analysis of Circulating Noncoding RNAs Versus Protein Biomarkers in the Detection of Myocardial Injury. Circulation Research, 2019, 125, 328-340. | 2.0 | 86 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 19 | A Bioinformatic Approach for the Identification of Molecular Determinants of Resistance/Sensitivity to Cancer Thermotherapy. Oxidative Medicine and Cellular Longevity, 2019, 2019, 1-13. | 1.9 | 7 |
| 20 | An Adaptive Pipeline To Maximize Isobaric Tagging Data in Large-Scale MS-Based Proteomics. Journal of Proteome Research, 2018, 17, 2165-2173. | 1.8 | 11 |
| 21 | Non-coding RNA Sequences Identification and Classification Using a Multi-class and Multi-label Ensemble Technique. IFIP Advances in Information and Communication Technology, 2018, , 179-188. | 0.5 | 1 |
| 22 | InSyBio ncRNASeq: A web tool for analyzing non-coding RNAs. EMBnet Journal, 2017, 23, 882. | 0.2 | 2 |
| 23 | Predicting overlapping protein complexes from weighted protein interaction graphs by gradually expanding dense neighborhoods. Artificial Intelligence in Medicine, 2016, 71, 62-69. | 3.8 | 8 |
| 24 | InSyBio BioNets: an efficient tool for network-based biomarker discovery. EMBnet Journal, 2016, 22, 871. | 0.2 | 4 |
| 25 | Predicting protein complexes from weighted protein–protein interaction graphs with a novel unsupervised methodology: Evolutionary enhanced Markov clustering. Artificial Intelligence in Medicine, 2015, 63, 181-189. | 3.8 | 26 |
| 26 | Predicting human miRNA target genes using a novel computational intelligent framework. Information Sciences, 2015, 294, 576-585. | 4.0 | 6 |