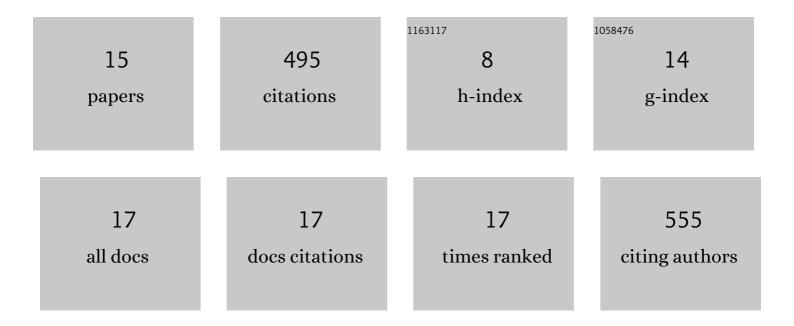
Etienne Boileau

List of Publications by Year in descending order

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FTIENNE ROUEAU

#	Article	IF	CITATIONS
1	A benchmark study of numerical schemes for oneâ€dimensional arterial blood flow modelling. International Journal for Numerical Methods in Biomedical Engineering, 2015, 31, e02732.	2.1	144
2	m ⁶ A-mRNA methylation regulates cardiac gene expression and cellular growth. Life Science Alliance, 2019, 2, e201800233.	2.8	109
3	Monitoring Cell-Type–Specific Gene Expression Using Ribosome Profiling In Vivo During Cardiac Hemodynamic Stress. Circulation Research, 2019, 125, 431-448.	4.5	56
4	Estimating the accuracy of a reducedâ€order model for the calculation of fractional flow reserve (FFR). International Journal for Numerical Methods in Biomedical Engineering, 2018, 34, e2908.	2.1	54
5	A novel method for non-invasively detecting the severity and location of aortic aneurysms. Biomechanics and Modeling in Mechanobiology, 2017, 16, 1225-1242.	2.8	28
6	An advanced computational bioheat transfer model for a human body with an embedded systemic circulation. Biomechanics and Modeling in Mechanobiology, 2016, 15, 1173-1190.	2.8	23
7	Updated and enhanced pig cardiac transcriptome based on long-read RNA sequencing and proteomics. Journal of Molecular and Cellular Cardiology, 2021, 150, 23-31.	1.9	16
8	Muscleâ€specific Cand2 is translationally upregulated by mTORC1 and promotes adverse cardiac remodeling. EMBO Reports, 2021, 22, e52170.	4.5	13
9	One-Dimensional Modelling of the Coronary Circulation. Application to Noninvasive Quantification of Fractional Flow Reserve (FFR). Lecture Notes in Computational Vision and Biomechanics, 2015, , 137-155.	0.5	11
10	Synergy Between Intercellular Communication and Intracellular Ca2+ Handling in Arrhythmogenesis. Annals of Biomedical Engineering, 2015, 43, 1614-1625.	2.5	9
11	Modelling accidental hypothermia effects on a human body under different pathophysiological conditions. Medical and Biological Engineering and Computing, 2017, 55, 2155-2167.	2.8	8
12	Analysis of myocardial cellular gene expression during pressure overload reveals matrix based functional intercellular communication. IScience, 2022, 25, 103965.	4.1	8
13	A Multi-Network Comparative Analysis of Transcriptome and Translatome Identifies Novel Hub Genes in Cardiac Remodeling. Frontiers in Genetics, 2020, 11, 583124.	2.3	4
14	RNA Modification Level Estimation with pulseR. Genes, 2018, 9, 619.	2.4	2
15	Unsupervised Bayesian Prediction of RNA Translation from Ribosome Profiling Data. Methods in Molecular Biology, 2021, 2252, 295-312.	0.9	0