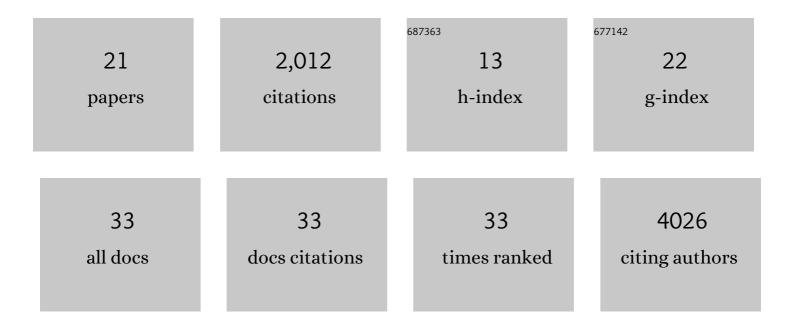
Aurélien Dugourd

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2736701/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	FUNKI: interactive functional footprint-based analysis of omics data. Bioinformatics, 2022, 38, 2075-2076.	4.1	4
2	decoupleR: ensemble of computational methods to infer biological activities from omics data. Bioinformatics Advances, 2022, 2, .	2.4	127
3	Reducing lipid bilayer stress by monounsaturated fatty acids protects renal proximal tubules in diabetes. ELife, 2022, 11, .	6.0	18
4	Comparison of methods and resources for cell-cell communication inference from single-cell RNA-Seq data. Nature Communications, 2022, 13, .	12.8	143
5	PHONEMeS: Efficient Modeling of Signaling Networks Derived from Large-Scale Mass Spectrometry Data. Journal of Proteome Research, 2021, 20, 2138-2144.	3.7	15
6	Macrophage beta2-adrenergic receptor is dispensable for the adipose tissue inflammation and function. Molecular Metabolism, 2021, 48, 101220.	6.5	11
7	SREBP1-induced fatty acid synthesis depletes macrophages antioxidant defences to promote their alternative activation. Nature Metabolism, 2021, 3, 1150-1162.	11.9	29
8	Causal integration of multiâ€omics data with prior knowledge to generate mechanistic hypotheses. Molecular Systems Biology, 2021, 17, e9730.	7.2	78
9	Norepinephrine promotes triglyceride storage in macrophages via beta2â€adrenergic receptor activation. FASEB Journal, 2021, 35, e21266.	0.5	11
10	Systems approach reveals distinct and shared signaling networks of the four PGE ₂ receptors in T cells. Science Signaling, 2021, 14, eabc8579.	3.6	5
11	COVID19 Disease Map, a computational knowledge repository of virus–host interaction mechanisms. Molecular Systems Biology, 2021, 17, e10387.	7.2	53
12	Kinetic modelling of quantitative proteome data predicts metabolic reprogramming of liver cancer. British Journal of Cancer, 2020, 122, 233-244.	6.4	16
13	Converting networks to predictive logic models from perturbation signalling data with CellNOpt. Bioinformatics, 2020, 36, 4523-4524.	4.1	17
14	Increased CXCL4 expression in hematopoietic cells links inflammation and progression of bone marrow fibrosis in MPN. Blood, 2020, 136, 2051-2064.	1.4	56
15	The Global Phosphorylation Landscape of SARS-CoV-2 Infection. Cell, 2020, 182, 685-712.e19.	28.9	825
16	Footprint-based functional analysis of multiomic data. Current Opinion in Systems Biology, 2019, 15, 82-90.	2.6	39
17	Prostaglandin E 2 signaling networks in T cells revealed through a systems approach. FASEB Journal, 2019, 33, lb258.	0.5	0
18	NADH Shuttling Couples Cytosolic Reductive Carboxylation of Glutamine with Glycolysis in Cells with Mitochondrial Dysfunction. Molecular Cell, 2018, 69, 581-593.e7.	9.7	171

#	Article	IF	CITATIONS
19	Gli1 + Mesenchymal Stromal Cells Are a Key Driver of Bone Marrow Fibrosis and an Important Cellular Therapeutic Target. Cell Stem Cell, 2017, 20, 785-800.e8.	11.1	195
20	MaBoSS 2.0: an environment for stochastic Boolean modeling. Bioinformatics, 2017, 33, 2226-2228.	4.1	118
21	A comprehensive approach to the molecular determinants of lifespan using a Boolean model of geroconversion. Aging Cell, 2016, 15, 1018-1026.	6.7	16