

AurÃ©lien Dugourd

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

2,012
citations

687363

13
h-index

677142

22
g-index

33
all docs

33
docs citations

33
times ranked

4026
citing authors

#	ARTICLE	IF	CITATIONS
1	FUNKI: interactive functional footprint-based analysis of omics data. <i>Bioinformatics</i> , 2022, 38, 2075-2076.	4.1	4
2	decoupleR: ensemble of computational methods to infer biological activities from omics data. <i>Bioinformatics Advances</i> , 2022, 2, .	2.4	127
3	Reducing lipid bilayer stress by monounsaturated fatty acids protects renal proximal tubules in diabetes. <i>ELife</i> , 2022, 11, .	6.0	18
4	Comparison of methods and resources for cell-cell communication inference from single-cell RNA-Seq data. <i>Nature Communications</i> , 2022, 13, .	12.8	143
5	PHONEMeS: Efficient Modeling of Signaling Networks Derived from Large-Scale Mass Spectrometry Data. <i>Journal of Proteome Research</i> , 2021, 20, 2138-2144.	3.7	15
6	Macrophage beta2-adrenergic receptor is dispensable for the adipose tissue inflammation and function. <i>Molecular Metabolism</i> , 2021, 48, 101220.	6.5	11
7	SREBP1-induced fatty acid synthesis depletes macrophages antioxidant defences to promote their alternative activation. <i>Nature Metabolism</i> , 2021, 3, 1150-1162.	11.9	29
8	Causal integration of multi-omics data with prior knowledge to generate mechanistic hypotheses. <i>Molecular Systems Biology</i> , 2021, 17, e9730.	7.2	78
9	Norepinephrine promotes triglyceride storage in macrophages via beta2-adrenergic receptor activation. <i>FASEB Journal</i> , 2021, 35, e21266.	0.5	11
10	Systems approach reveals distinct and shared signaling networks of the four PGE ₂ receptors in T cells. <i>Science Signaling</i> , 2021, 14, eabc8579.	3.6	5
11	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. <i>Molecular Systems Biology</i> , 2021, 17, e10387.	7.2	53
12	Kinetic modelling of quantitative proteome data predicts metabolic reprogramming of liver cancer. <i>British Journal of Cancer</i> , 2020, 122, 233-244.	6.4	16
13	Converting networks to predictive logic models from perturbation signalling data with CellNOpt. <i>Bioinformatics</i> , 2020, 36, 4523-4524.	4.1	17
14	Increased CXCL4 expression in hematopoietic cells links inflammation and progression of bone marrow fibrosis in MPN. <i>Blood</i> , 2020, 136, 2051-2064.	1.4	56
15	The Global Phosphorylation Landscape of SARS-CoV-2 Infection. <i>Cell</i> , 2020, 182, 685-712.e19.	28.9	825
16	Footprint-based functional analysis of multiomic data. <i>Current Opinion in Systems Biology</i> , 2019, 15, 82-90.	2.6	39
17	Prostaglandin E ₂ signaling networks in T cells revealed through a systems approach. <i>FASEB Journal</i> , 2019, 33, lb258.	0.5	0
18	NADH Shuttling Couples Cytosolic Reductive Carboxylation of Glutamine with Glycolysis in Cells with Mitochondrial Dysfunction. <i>Molecular Cell</i> , 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. <i>Cell Stem Cell</i> , 2017, 20, 785-800.e8.	11.1	195
20	MaBoSS 2.0: an environment for stochastic Boolean modeling. <i>Bioinformatics</i> , 2017, 33, 2226-2228.	4.1	118
21	A comprehensive approach to the molecular determinants of lifespan using a Boolean model of geroconversion. <i>Aging Cell</i> , 2016, 15, 1018-1026.	6.7	16