

# Emanuel Gonçalves

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/12044041/publications.pdf>

Version: 2024-02-01

27  
papers

4,612  
citations

304743

22  
h-index

501196

28  
g-index

41  
all docs

41  
docs citations

41  
times ranked

8455  
citing authors

#	ARTICLE	IF	CITATIONS
1	A Landscape of Pharmacogenomic Interactions in Cancer. <i>Cell</i> , 2016, 166, 740-754.	28.9	1,518
2	Prioritization of cancer therapeutic targets using CRISPR-Cas9 screens. <i>Nature</i> , 2019, 568, 511-516.	27.8	886
3	Fumarate is an epigenetic modifier that elicits epithelial-to-mesenchymal transition. <i>Nature</i> , 2016, 537, 544-547.	27.8	443
4	CellNOptR: a flexible toolkit to train protein signaling networks to data using multiple logic formalisms. <i>BMC Systems Biology</i> , 2012, 6, 133.	3.0	198
5	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , 2020, 16, e9110.	7.2	178
6	Agreement between two large pan-cancer CRISPR-Cas9 gene dependency data sets. <i>Nature Communications</i> , 2019, 10, 5817.	12.8	160
7	SBML qualitative models: a model representation format and infrastructure to foster interactions between qualitative modelling formalisms and tools. <i>BMC Systems Biology</i> , 2013, 7, 135.	3.0	145
8	Integrated cross-study datasets of genetic dependencies in cancer. <i>Nature Communications</i> , 2021, 12, 1661.	12.8	135
9	Widespread Post-transcriptional Attenuation of Genomic Copy-Number Variation in Cancer. <i>Cell Systems</i> , 2017, 5, 386-398.e4.	6.2	102
10	Genomic Determinants of Protein Abundance Variation in Colorectal Cancer Cells. <i>Cell Reports</i> , 2017, 20, 2201-2214.	6.4	95
11	Functional linkage of gene fusions to cancer cell fitness assessed by pharmacological and CRISPR-Cas9 screening. <i>Nature Communications</i> , 2019, 10, 2198.	12.8	92
12	Bridging the layers: towards integration of signal transduction, regulation and metabolism into mathematical models. <i>Molecular BioSystems</i> , 2013, 9, 1576.	2.9	83
13	Unsupervised correction of gene-independent cell responses to CRISPR-Cas9 targeting. <i>BMC Genomics</i> , 2018, 19, 604.	2.8	75
14	Drug mechanism-of-action discovery through the integration of pharmacological and <scp>CRISPR</scp> screens. <i>Molecular Systems Biology</i> , 2020, 16, e9405.	7.2	63
15	Combinatorial CRISPR screen identifies fitness effects of gene paralogues. <i>Nature Communications</i> , 2021, 12, 1302.	12.8	59
16	Project Score database: a resource for investigating cancer cell dependencies and prioritizing therapeutic targets. <i>Nucleic Acids Research</i> , 2021, 49, D1365-D1372.	14.5	54
17	Pan-cancer proteomic map of 949 human cell lines. <i>Cancer Cell</i> , 2022, 40, 835-849.e8.	16.8	52
18	Systematic Analysis of Transcriptional and Post-transcriptional Regulation of Metabolism in Yeast. <i>PLoS Computational Biology</i> , 2017, 13, e1005297.	3.2	51

#	ARTICLE	IF	CITATIONS
19	Minimal genome-wide human CRISPR-Cas9 library. <i>Genome Biology</i> , 2021, 22, 40.	8.8	40
20	Structural rearrangements generate cell-specific, gene-independent CRISPR-Cas9 loss of fitness effects. <i>Genome Biology</i> , 2019, 20, 27.	8.8	35
21	Genome-wide CRISPR screens of oral squamous cell carcinoma reveal fitness genes in the Hippo pathway. <i>ELife</i> , 2020, 9, .	6.0	31
22	Post-translational regulation of metabolism in fumarate hydratase deficient cancer cells. <i>Metabolic Engineering</i> , 2018, 45, 149-157.	7.0	27
23	Multi-omics Characterization of Interaction-mediated Control of Human Protein Abundance levels. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S114-S125.	3.8	16
24	A suspension technique for efficient large-scale cancer organoid culturing and perturbation screens. <i>Scientific Reports</i> , 2022, 12, 5571.	3.3	11
25	Genome and metabolome: chance and necessity. <i>Genome Biology</i> , 2021, 22, 276.	8.8	4
26	Cyrface: An interface from Cytoscape to R that provides a user interface to R packages. <i>F1000Research</i> , 2013, 2, 192.	1.6	3
27	Cyrface: An interface from Cytoscape to R that provides a user interface to R packages. <i>F1000Research</i> , 2013, 2, 192.	1.6	2