Francisco J Planes

List of Publications by Year
in descending order

45 papers	1,829 citations	516710 16 h-index	302126 39 g-index
49 all docs	49 docs citations	49 times ranked	2856 citing authors

#	Article	IF	Citations
1	Landscape and clinical significance of long noncoding <scp>RNAs</scp> involved in multiple myeloma expressed fusion transcripts. American Journal of Hematology, 2022, 97, .	4.1	1
2	A network-based approach to integrate nutrient microenvironment in the prediction of synthetic lethality in cancer metabolism. PLoS Computational Biology, 2022, 18, e1009395.	3.2	5
3	The bone marrow niche regulates redox and energy balance in MLL::AF9 leukemia stem cells. Leukemia, 2022, 36, 1969-1979.	7.2	5
4	BOSO: A novel feature selection algorithm for linear regression with high-dimensional data. PLoS Computational Biology, 2022, 18, e1010180.	3.2	3
5	Prediction of degradation pathways of phenolic compounds in the human gut microbiota through enzyme promiscuity methods. Npj Systems Biology and Applications, 2022, 8, .	3.0	8
6	Characterization of complete lncRNAs transcriptome reveals the functional and clinical impact of lncRNAs in multiple myeloma. Leukemia, 2021, 35, 1438-1450.	7.2	28
7	Gene expression derived from alternative promoters improves prognostic stratification in multiple myeloma. Leukemia, 2021, 35, 3012-3016.	7.2	11
8	An extended reconstruction of human gut microbiota metabolism of dietary compounds. Nature Communications, 2021, 12, 4728.	12.8	19
9	On the inconsistent treatment of gene-protein-reaction rules in context-specific metabolic models. Bioinformatics, 2020, 36, 1986-1988.	4.1	5
10	DrugSniper, a Tool to Exploit Loss-Of-Function Screens, Identifies CREBBP as a Predictive Biomarker of VOLASERTIB in Small Cell Lung Carcinoma (SCLC). Cancers, 2020, 12, 1824.	3.7	6
11	Computational approach for collection and prediction of molecular initiating events in developmental toxicity. Reproductive Toxicology, 2020, 94, 55-64.	2.9	2
12	<i>gMCS</i>: fast computation of genetic minimal cut sets in large networks. Bioinformatics, 2019, 35, 535-537.	4.1	18
13	Adaptation of the Human Gut Microbiota Metabolic Network During the First Year After Birth. Frontiers in Microbiology, 2019, 10, 848.	3.5	11
14	rMTA: robust metabolic transformation analysis. Bioinformatics, 2019, 35, 4350-4355.	4.1	11
15	TranscriptAchilles: a genome-wide platform to predict isoform biomarkers of gene essentiality in cancer. GigaScience, 2019, 8, .	6.4	3
16	Creation and analysis of biochemical constraint-based models using the COBRA Toolbox v.3.0. Nature Protocols, 2019, 14, 639-702.	12.0	833
17	Characterization of Complete Lncrnas Transcriptome Reveals Expression of Lncrnas As a Prognostic Factor and Linc-Smilo As a Potential Therapeutic Target in Multiple Myeloma. Blood, 2019, 134, 4323-4323.	1.4	1
18	Lncrnas As New Partners of Novel Chimeric Transcripts in Multiple Myeloma. Blood, 2019, 134, 4356-4356.	1.4	0

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19	Computational Systems Biology Models for the Identification of Metabolic Vulnerabilities in Multiple Myeloma. Blood, 2019, 134, 3084-3084.	1.4	0
20	COBRA methods and metabolic drug targets in cancer. Molecular and Cellular Oncology, 2018, 5, e1389672.	0.7	3
21	CANCERTOOL: A Visualization and Representation Interface to Exploit Cancer Datasets. Cancer Research, 2018, 78, 6320-6328.	0.9	76
22	In-silico gene essentiality analysis of polyamine biosynthesis reveals APRT as a potential target in cancer. Scientific Reports, 2017, 7, 14358.	3.3	10
23	An in-silico approach to predict and exploit synthetic lethality in cancer metabolism. Nature Communications, 2017, 8, 459.	12.8	35
24	In silico platform based on bioinformatic and chemoinformatic data to complement zebrafish embryo teratogenicity test. Toxicology Letters, 2017, 280, S121.	0.8	0
25	Direct calculation of minimal cut sets involving a specific reaction knock-out. Bioinformatics, 2016, 32, 2001-2007.	4.1	11
26	Assessment of FBA Based Gene Essentiality Analysis in Cancer with a Fast Context-Specific Network Reconstruction Method. PLoS ONE, 2016, 11, e0154583.	2.5	13
27	Context-specific metabolic network reconstruction of a naphthalene-degrading bacterial community guided by metaproteomic data. Bioinformatics, 2015, 31, 1771-1779.	4.1	31
28	TreeEFM: calculating elementary flux modes using linear optimization in a tree-based algorithm. Bioinformatics, 2015, 31, 897-904.	4.1	26
29	Advances in network-based metabolic pathway analysis and gene expression data integration. Briefings in Bioinformatics, 2015, 16, 265-279.	6.5	25
30	In-Silico Prediction of Key Metabolic Differences between Two Non-Small Cell Lung Cancer Subtypes. PLoS ONE, 2014, 9, e103998.	2.5	25
31	Refining carbon flux paths using atomic trace data. Bioinformatics, 2014, 30, 975-980.	4.1	19
32	Direct calculation of elementary flux modes satisfying several biological constraints in genome-scale metabolic networks. Bioinformatics, 2014, 30, 2197-2203.	4.1	31
33	A network-based approach for predicting key enzymes explaining metabolite abundance alterations in a disease phenotype. BMC Systems Biology, 2013, 7, 62.	3.0	14
34	Integrating gene and protein expression data with genome-scale metabolic networks to infer functional pathways. BMC Systems Biology, 2013, 7, 134.	3.0	5
35	Joint analysis of miRNA and mRNA expression data. Briefings in Bioinformatics, 2013, 14, 263-278.	6.5	104
36	Bioinformatic progress and applications in metaproteogenomics for bridging the gap between genomic sequences and metabolic functions in microbial communities. Proteomics, 2013, 13, 2786-2804.	2.2	46

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37	Selection of human tissue-specific elementary flux modes using gene expression data. Bioinformatics, 2013, 29, 2009-2016.	4.1	38
38	Integrating tracer-based metabolomics data and metabolic fluxes in a linear fashion via Elementary Carbon Modes. Metabolic Engineering, 2012, 14, 344-353.	7.0	10
39	Exploring the connectivity structure in metabolic networks: Going beyond graphs via discrete optimization. , 2011, , .		0
40	Path finding methods accounting for stoichiometry in metabolic networks. Genome Biology, 2011, 12, R49.	9.6	45
41	Do elementary flux modes combine linearly at the "atomic" level? Integrating tracer-based metabolomics data and elementary flux modes. BioSystems, 2011, 105, 140-146.	2.0	6
42	Computing the shortest elementary flux modes in genome-scale metabolic networks. Bioinformatics, 2009, 25, 3158-3165.	4.1	184
43	Path finding approaches and metabolic pathways. Discrete Applied Mathematics, 2009, 157, 2244-2256.	0.9	17
44	A critical examination of stoichiometric and path-finding approaches to metabolic pathways. Briefings in Bioinformatics, 2008, 9, 422-436.	6.5	50
45	Recovering metabolic pathways via optimization. Bioinformatics, 2007, 23, 92-98.	4.1	35