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	Creation and analysis of biochemical constraint-based models using the COBRA Toolbox v.3.0. Nature Protocols, 2019, 14, 639-702.	12.0	833
2	Computing the shortest elementary flux modes in genome-scale metabolic networks. Bioinformatics, 2009, 25, 3158-3165.	4.1	184
3	Joint analysis of miRNA and mRNA expression data. Briefings in Bioinformatics, 2013, 14, 263-278.	6.5	104
4	CANCERTOOL: A Visualization and Representation Interface to Exploit Cancer Datasets. Cancer Research, 2018, 78, 6320-6328.	0.9	76
5	A critical examination of stoichiometric and path-finding approaches to metabolic pathways. Briefings in Bioinformatics, 2008, 9, 422-436.	6.5	50
6	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
7	Path finding methods accounting for stoichiometry in metabolic networks. Genome Biology, 2011, 12, R49.	9.6	45
8	Selection of human tissue-specific elementary flux modes using gene expression data. Bioinformatics, 2013, 29, 2009-2016.	4.1	38
9	Recovering metabolic pathways via optimization. Bioinformatics, 2007, 23, 92-98.	4.1	35
10	An in-silico approach to predict and exploit synthetic lethality in cancer metabolism. Nature Communications, 2017, 8, 459.	12.8	35
11	Direct calculation of elementary flux modes satisfying several biological constraints in genome-scale metabolic networks. Bioinformatics, 2014, 30, 2197-2203.	4.1	31
12	Context-specific metabolic network reconstruction of a naphthalene-degrading bacterial community guided by metaproteomic data. Bioinformatics, 2015, 31, 1771-1779.	4.1	31
13	Characterization of complete lncRNAs transcriptome reveals the functional and clinical impact of lncRNAs in multiple myeloma. Leukemia, 2021, 35, 1438-1450.	7.2	28
14	TreeEFM: calculating elementary flux modes using linear optimization in a tree-based algorithm. Bioinformatics, 2015, 31, 897-904.	4.1	26
15	In-Silico Prediction of Key Metabolic Differences between Two Non-Small Cell Lung Cancer Subtypes. PLoS ONE, 2014, 9, e103998.	2.5	25
16	Advances in network-based metabolic pathway analysis and gene expression data integration. Briefings in Bioinformatics, 2015, 16, 265-279.	6.5	25
17	Refining carbon flux paths using atomic trace data. Bioinformatics, 2014, 30, 975-980.	4.1	19
18	An extended reconstruction of human gut microbiota metabolism of dietary compounds. Nature Communications, 2021, 12, 4728.	12.8	19

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19	*gMCS*: fast computation of genetic minimal cut sets in large networks. Bioinformatics, 2019, 35, 535-537.	4.1	18
20	Path finding approaches and metabolic pathways. Discrete Applied Mathematics, 2009, 157, 2244-2256.	0.9	17
21	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
22	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
23	Direct calculation of minimal cut sets involving a specific reaction knock-out. Bioinformatics, 2016, 32, 2001-2007.	4.1	11
24	Adaptation of the Human Gut Microbiota Metabolic Network During the First Year After Birth. Frontiers in Microbiology, 2019, 10, 848.	3.5	11
25	rMTA: robust metabolic transformation analysis. Bioinformatics, 2019, 35, 4350-4355.	4.1	11
26	Gene expression derived from alternative promoters improves prognostic stratification in multiple myeloma. Leukemia, 2021, 35, 3012-3016.	7.2	11
27	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
28	In-silico gene essentiality analysis of polyamine biosynthesis reveals APRT as a potential target in cancer. Scientific Reports, 2017, 7, 14358.	3.3	10
29	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
30	Do elementary flux modes combine linearly at the â€œatomicâ€•level? Integrating tracer-based metabolomics data and elementary flux modes. BioSystems, 2011, 105, 140-146.	2.0	6
31	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
32	Integrating gene and protein expression data with genome-scale metabolic networks to infer functional pathways. BMC Systems Biology, 2013, 7, 134.	3.0	5
33	On the inconsistent treatment of gene-protein-reaction rules in context-specific metabolic models. Bioinformatics, 2020, 36, 1986-1988.	4.1	5
34	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
35	The bone marrow niche regulates redox and energy balance in MLL::AF9 leukemia stem cells. Leukemia, 2022, 36, 1969-1979.	7.2	5
36	COBRA methods and metabolic drug targets in cancer. Molecular and Cellular Oncology, 2018, 5, e1389672.	0.7	3

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37	TranscriptAchilles: a genome-wide platform to predict isoform biomarkers of gene essentiality in cancer. GigaScience, 2019, 8, .	6.4	3
38	BOSO: A novel feature selection algorithm for linear regression with high-dimensional data. PLoS Computational Biology, 2022, 18, e1010180.	3.2	3
39	Computational approach for collection and prediction of molecular initiating events in developmental toxicity. Reproductive Toxicology, 2020, 94, 55-64.	2.9	2
40	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
41	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
42	Exploring the connectivity structure in metabolic networks: Going beyond graphs via discrete optimization. , 2011, , .		0
43	In silico platform based on bioinformatic and chemoinformatic data to complement zebrafish embryo teratogenicity test. Toxicology Letters, 2017, 280, S121.	0.8	0
44	Lncrnas As New Partners of Novel Chimeric Transcripts in Multiple Myeloma. Blood, 2019, 134, 4356-4356.	1.4	0
45	Computational Systems Biology Models for the Identification of Metabolic Vulnerabilities in Multiple Myeloma. Blood, 2019, 134, 3084-3084.	1.4	0