

Aarash Bordbar

List of Publications by Year in descending order

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Version: 2024-02-01

33
papers

5,710
citations

218677

26
h-index

414414

32
g-index

34
all docs

34
docs citations

34
times ranked

6312
citing authors

#	ARTICLE	IF	CITATIONS
1	Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox v2.0. <i>Nature Protocols</i> , 2011, 6, 1290-1307.	12.0	1,408
2	Creation and analysis of biochemical constraint-based models using the COBRA Toolbox v.3.0. <i>Nature Protocols</i> , 2019, 14, 639-702.	12.0	833
3	Constraint-based models predict metabolic and associated cellular functions. <i>Nature Reviews Genetics</i> , 2014, 15, 107-120.	16.3	714
4	Genomic landscapes of Chinese hamster ovary cell lines as revealed by the <i>Cricetulus griseus</i> draft genome. <i>Nature Biotechnology</i> , 2013, 31, 759-765.	17.5	340
5	Insight into human alveolar macrophage and <i>M. tuberculosis</i> interactions via metabolic reconstructions. <i>Molecular Systems Biology</i> , 2010, 6, 422.	7.2	246
6	Large-scale in silico modeling of metabolic interactions between cell types in the human brain. <i>Nature Biotechnology</i> , 2010, 28, 1279-1285.	17.5	246
7	A Consensus Genome-scale Reconstruction of Chinese Hamster Ovary Cell Metabolism. <i>Cell Systems</i> , 2016, 3, 434-443.e8.	6.2	205
8	A multi-tissue type genome-scale metabolic network for analysis of whole-body systems physiology. <i>BMC Systems Biology</i> , 2011, 5, 180.	3.0	166
9	Model-driven multi-omic data analysis elucidates metabolic immunomodulators of macrophage activation. <i>Molecular Systems Biology</i> , 2012, 8, 558.	7.2	142
10	Multi-omic data integration enables discovery of hidden biological regularities. <i>Nature Communications</i> , 2016, 7, 13091.	12.8	141
11	Elucidating dynamic metabolic physiology through network integration of quantitative time-course metabolomics. <i>Scientific Reports</i> , 2017, 7, 46249.	3.3	121
12	Biomarkers defining the metabolic age of red blood cells during cold storage. <i>Blood</i> , 2016, 128, e43-e50.	1.4	115
13	Identified metabolic signature for assessing red blood cell unit quality is associated with endothelial damage markers and clinical outcomes. <i>Transfusion</i> , 2016, 56, 852-862.	1.6	105
14	Multiscale Modeling of Metabolism and Macromolecular Synthesis in <i>E. coli</i> and Its Application to the Evolution of Codon Usage. <i>PLoS ONE</i> , 2012, 7, e45635.	2.5	100
15	Citrate metabolism in red blood cells stored in additive solution. <i>Transfusion</i> , 2017, 57, 325-336.	1.6	93
16	Personalized Whole-Cell Kinetic Models of Metabolism for Discovery in Genomics and Pharmacodynamics. <i>Cell Systems</i> , 2015, 1, 283-292.	6.2	92
17	iAB-RBC-283: A proteomically derived knowledge-base of erythrocyte metabolism that can be used to simulate its physiological and patho-physiological states. <i>BMC Systems Biology</i> , 2011, 5, 110.	3.0	89
18	Systems biology analysis of drivers underlying hallmarks of cancer cell metabolism. <i>Scientific Reports</i> , 2017, 7, 41241.	3.3	87

#	ARTICLE	IF	CITATIONS
19	Do genome-scale models need exact solvers or clearer standards?. <i>Molecular Systems Biology</i> , 2015, 11, 831.	7.2	68
20	A Systems Approach to Predict Oncometabolites via Context-Specific Genome-Scale Metabolic Networks. <i>PLoS Computational Biology</i> , 2014, 10, e1003837.	3.2	63
21	Functional Characterization of Alternate Optimal Solutions of <i>Escherichia coli</i> 's Transcriptional and Translational Machinery. <i>Biophysical Journal</i> , 2010, 98, 2072-2081.	0.5	58
22	Quantitative time-course metabolomics in human red blood cells reveal the temperature dependence of human metabolic networks. <i>Journal of Biological Chemistry</i> , 2017, 292, 19556-19564.	3.4	45
23	Minimal metabolic pathway structure is consistent with associated biomolecular interactions. <i>Molecular Systems Biology</i> , 2014, 10, 737.	7.2	41
24	Pharmacogenomic and clinical data link non-pharmacokinetic metabolic dysregulation to drug side effect pathogenesis. <i>Nature Communications</i> , 2015, 6, 7101.	12.8	41
25	Metabolic fate of adenine in red blood cells during storage in SAGM solution. <i>Transfusion</i> , 2016, 56, 2538-2547.	1.6	39
26	Blood donor exposome and impact of common drugs on red blood cell metabolism. <i>JCI Insight</i> , 2021, 6, .	5.0	39
27	Development and evaluation of a transfusion medicine genome wide genotyping array. <i>Transfusion</i> , 2019, 59, 101-111.	1.6	30
28	Mannose and fructose metabolism in red blood cells during cold storage in SAGM. <i>Transfusion</i> , 2017, 57, 2665-2676.	1.6	14
29	A Multi-scale Computational Platform to Mechanistically Assess the Effect of Genetic Variation on Drug Responses in Human Erythrocyte Metabolism. <i>PLoS Computational Biology</i> , 2016, 12, e1005039.	3.2	12
30	Systems biology as an emerging paradigm in transfusion medicine. <i>BMC Systems Biology</i> , 2018, 12, 31.	3.0	12
31	Interpreting the deluge of omics data: new approaches offer new possibilities. <i>Blood Transfusion</i> , 2017, 15, 189-190.	0.4	3
32	A Systems Biology Approach to the Evolution of Codon Use Pattern. <i>Nature Precedings</i> , 2011, , .	0.1	2
33	Modeling <i>Mycobacterium tuberculosis</i> H37Rv In Silico. , 2013, , 1-19.		0