

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	Blood donor exposome and impact of common drugs on red blood cell metabolism. JCI Insight, 2021, 6, .	5.0	39
2	Creation and analysis of biochemical constraint-based models using the COBRA Toolbox v.3.0. Nature Protocols, 2019, 14, 639-702.	12.0	833
3	Development and evaluation of a transfusion medicine genome wide genotyping array. Transfusion, 2019, 59, 101-111.	1.6	30
4	Systems biology as an emerging paradigm in transfusion medicine. BMC Systems Biology, 2018, 12, 31.	3.0	12
5	Systems biology analysis of drivers underlying hallmarks of cancer cell metabolism. Scientific Reports, 2017, 7, 41241.	3.3	87
6	Elucidating dynamic metabolic physiology through network integration of quantitative time-course metabolomics. Scientific Reports, 2017, 7, 46249.	3.3	121
7	Quantitative time-course metabolomics in human red blood cells reveal the temperature dependence of human metabolic networks. Journal of Biological Chemistry, 2017, 292, 19556-19564.	3.4	45
8	Mannose and fructose metabolism in red blood cells during cold storage in SAGM. Transfusion, 2017, 57, 2665-2676.	1.6	14
9	Citrate metabolism in red blood cells stored in additive solution. Transfusion, 2017, 57, 325-336.	1.6	93
10	Interpreting the deluge of omics data: new approaches offer new possibilities. Blood Transfusion, 2017, 15, 189-190.	0.4	3
11	A Multi-scale Computational Platform to Mechanistically Assess the Effect of Genetic Variation on Drug Responses in Human Erythrocyte Metabolism. PLoS Computational Biology, 2016, 12, e1005039.	3.2	12
12	Identified metabolic signature for assessing red blood cell unit quality is associated with endothelial damage markers and clinical outcomes. Transfusion, 2016, 56, 852-862.	1.6	105
13	A Consensus Genome-scale Reconstruction of Chinese Hamster Ovary Cell Metabolism. Cell Systems, 2016, 3, 434-443.e8.	6.2	205
14	Biomarkers defining the metabolic age of red blood cells during cold storage. Blood, 2016, 128, e43-e50.	1.4	115
15	Metabolic fate of adenine in red blood cells during storage in SAGM solution. Transfusion, 2016, 56, 2538-2547.	1.6	39
16	Multi-omic data integration enables discovery of hidden biological regularities. Nature Communications, 2016, 7, 13091.	12.8	141
17	Do genome-scale models need exact solvers or clearer standards?. Molecular Systems Biology, 2015, 11, 831.	7.2	68
18	Pharmacogenomic and clinical data link non-pharmacokinetic metabolic dysregulation to drug side effect pathogenesis. Nature Communications, 2015, 6, 7101.	12.8	41

#	ARTICLE	IF	CITATIONS
19	Personalized Whole-Cell Kinetic Models of Metabolism for Discovery in Genomics and Pharmacodynamics. <i>Cell Systems</i> , 2015, 1, 283-292.	6.2	92
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	Minimal metabolic pathway structure is consistent with associated biomolecular interactions. <i>Molecular Systems Biology</i> , 2014, 10, 737.	7.2	41
22	Constraint-based models predict metabolic and associated cellular functions. <i>Nature Reviews Genetics</i> , 2014, 15, 107-120.	16.3	714
23	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
24	Modeling <i>Mycobacterium tuberculosis</i> H37Rv In Silico. , 2013, , 1-19.		0
25	Model-driven multi-omic data analysis elucidates metabolic immunomodulators of macrophage activation. <i>Molecular Systems Biology</i> , 2012, 8, 558.	7.2	142
26	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
27	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
28	A Systems Biology Approach to the Evolution of Codon Use Pattern. <i>Nature Precedings</i> , 2011, , .	0.1	2
29	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
30	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
31	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
32	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
33	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