

Osbaldo Resendis

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

1,952
citations

394421

19
h-index

302126

39
g-index

57
all docs

57
docs citations

57
times ranked

2832
citing authors

#	ARTICLE	IF	CITATIONS
1	Physiological Network Is Disrupted in Severe COVID-19. <i>Frontiers in Physiology</i> , 2022, 13, 848172.	2.8	7
2	Quantitative proteomic analysis of extracellular vesicle subgroups isolated by an optimized method combining polymerase-based precipitation and size exclusion chromatography. <i>Journal of Extracellular Vesicles</i> , 2021, 10, e12087.	12.2	55
3	Sex Differences in the Physiological Network of Healthy Young Subjects. <i>Frontiers in Physiology</i> , 2021, 12, 678507.	2.8	9
4	Transcriptional and Microenvironmental Landscape of Macrophage Transition in Cancer: A Boolean Analysis. <i>Frontiers in Immunology</i> , 2021, 12, 642842.	4.8	20
5	On Deep Landscape Exploration of COVID-19 Patients Cells and Severity Markers. <i>Frontiers in Immunology</i> , 2021, 12, 705646.	4.8	9
6	Stochastic Analysis of the RT-PCR Process in Single-Cell RNA-Seq. <i>Mathematics</i> , 2021, 9, 2515.	2.2	1
7	MicroRNAs Regulate Metabolic Phenotypes During Multicellular Tumor Spheroids Progression. <i>Frontiers in Oncology</i> , 2020, 10, 582396.	2.8	3
8	Analysis of Epithelial-Mesenchymal Transition Metabolism Identifies Possible Cancer Biomarkers Useful in Diverse Genetic Backgrounds. <i>Frontiers in Oncology</i> , 2020, 10, 1309.	2.8	8
9	Unveiling functional heterogeneity in breast cancer multicellular tumor spheroids through single-cell RNA-seq. <i>Scientific Reports</i> , 2020, 10, 12728.	3.3	30
10	Uncovering the Dynamic Mechanisms of the <i>Pseudomonas Aeruginosa</i> Quorum Sensing and Virulence Networks Using Boolean Modelling. <i>IEEE Transactions on Nanobioscience</i> , 2020, 19, 394-402.	3.3	6
11	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020, 38, 272-276.	17.5	314
12	MICOM: Metagenome-Scale Modeling To Infer Metabolic Interactions in the Gut Microbiota. <i>MSystems</i> , 2020, 5, .	3.8	126
13	Progressive Shifts in the Gut Microbiome Reflect Prediabetes and Diabetes Development in a Treatment-Naive Mexican Cohort. <i>Frontiers in Endocrinology</i> , 2020, 11, 602326.	3.5	13
14	Genes Involved in the Transcriptional Regulation of Pluripotency Are Expressed in Malignant Tumors of the Uterine Cervix and Can Induce Tumorigenic Capacity in a Nontumorigenic Cell Line. <i>Stem Cells International</i> , 2019, 2019, 1-14.	2.5	6
15	Synthesis of multi-omic data and community metabolic models reveals insights into the role of hydrogen sulfide in colon cancer. <i>Methods</i> , 2018, 149, 59-68.	3.8	63
16	Distinct microbes, metabolites, and ecologies define the microbiome in deficient and proficient mismatch repair colorectal cancers. <i>Genome Medicine</i> , 2018, 10, 78.	8.2	107
17	<i>Entamoeba histolytica</i> Up-Regulates MicroRNA-643 to Promote Apoptosis by Targeting XIAP in Human Epithelial Colon Cells. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 437.	3.9	20
18	System Biology, Metabolomics, and Breast Cancer: Where We Are and What Are the Possible Consequences on the Clinical Setting. , 2018, , 169-188.		0

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19	Natural selection drove metabolic specialization of the chromatophore in <i>Paulinella chromatophora</i> . <i>BMC Evolutionary Biology</i> , 2017, 17, 99.	3.2	11
20	“Gestaltomics” Systems Biology Schemes for the Study of Neuropsychiatric Diseases. <i>Frontiers in Physiology</i> , 2017, 8, 286.	2.8	4
21	Editorial: Systems Biology and the Challenge of Deciphering the Metabolic Mechanisms Underlying Cancer. <i>Frontiers in Physiology</i> , 2017, 8, 537.	2.8	2
22	Evolution of Centrality Measurements for the Detection of Essential Proteins in Biological Networks. <i>Frontiers in Physiology</i> , 2016, 7, 375.	2.8	56
23	Host-Microbiome Interaction and Cancer: Potential Application in Precision Medicine. <i>Frontiers in Physiology</i> , 2016, 7, 606.	2.8	40
24	Personalized Prediction of Proliferation Rates and Metabolic Liabilities in Cancer Biopsies. <i>Frontiers in Physiology</i> , 2016, 7, 644.	2.8	16
25	The space of enzyme regulation in HeLa cells can be inferred from its intracellular metabolome. <i>Scientific Reports</i> , 2016, 6, 28415.	3.3	15
26	Modeling metabolism: A window toward a comprehensive interpretation of networks in cancer. <i>Seminars in Cancer Biology</i> , 2015, 30, 79-87.	9.6	26
27	Criticality, adaptability and early-warning signals in time series in a discrete quasispecies model. <i>Frontiers in Biology</i> , 2013, 8, 247-259.	0.7	6
28	Systems biology of cancer: moving toward the integrative study of the metabolic alterations in cancer cells. <i>Frontiers in Physiology</i> , 2013, 3, 481.	2.8	17
29	Constraint-based Modeling. , 2013, , 494-498.		2
30	Metabolism Nitrogen Fixation. , 2013, , 1275-1279.		1
31	Jacobian Matrix. , 2013, , 1061-1062.		3
32	Hierarchical Structure. , 2013, , 887-888.		1
33	A Roadmap Towards a Systems Biology Description of Bacterial Nitrogen Fixation. <i>Soil Biology</i> , 2013, , 27-51.	0.8	0
34	Dynamic Metabolic Networks, k-Cone. , 2013, , 624-629.		1
35	Modules, Identification Methods and Biological Function. , 2013, , 1450-1453.		0
36	Functional Modules, Structural Topology, and Optimal Activity in Metabolic Networks. <i>PLoS Computational Biology</i> , 2012, 8, e1002720.	3.2	34

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37	Systems biology of bacterial nitrogen fixation: High-throughput technology and its integrative description with constraint-based modeling. <i>BMC Systems Biology</i> , 2011, 5, 120.	3.0	43
38	Proteomic patterns of cervical cancer cell lines, a network perspective. <i>BMC Systems Biology</i> , 2011, 5, 96.	3.0	52
39	Modeling Core Metabolism in Cancer Cells: Surveying the Topology Underlying the Warburg Effect. <i>PLoS ONE</i> , 2010, 5, e12383.	2.5	70
40	Filling Kinetic Gaps: Dynamic Modeling of Metabolism Where Detailed Kinetic Information Is Lacking. <i>PLoS ONE</i> , 2009, 4, e4967.	2.5	21
41	Regulation by transcription factors in bacteria: beyond description. <i>FEMS Microbiology Reviews</i> , 2009, 33, 133-151.	8.6	185
42	Metabolic Reconstruction and Modeling of Nitrogen Fixation in <i>Rhizobium etli</i> . <i>PLoS Computational Biology</i> , 2007, 3, e192.	3.2	85
43	Robustness and evolvability in genetic regulatory networks. <i>Journal of Theoretical Biology</i> , 2007, 245, 433-448.	1.7	242
44	Identification of regulatory network topological units coordinating the genome-wide transcriptional response to glucose in <i>Escherichia coli</i> . <i>BMC Microbiology</i> , 2007, 7, 53.	3.3	59
45	Modular analysis of the transcriptional regulatory network of <i>E. coli</i> . <i>Trends in Genetics</i> , 2005, 21, 16-20.	6.7	99
46	The growth of random networks as a diffusion process. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2004, 342, 551-560.	2.6	0
47	A statistical model of DNA denaturation. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2003, 318, 435-446.	2.6	3
48	A Fokker-Planck framework in the PolyC:PolyG denaturation. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2002, 312, 307-314.	2.6	0