

# Osbaldo Resendis

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/105603/publications.pdf>

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	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020, 38, 272-276.	17.5	314
2	Robustness and evolvability in genetic regulatory networks. <i>Journal of Theoretical Biology</i> , 2007, 245, 433-448.	1.7	242
3	Regulation by transcription factors in bacteria: beyond description. <i>FEMS Microbiology Reviews</i> , 2009, 33, 133-151.	8.6	185
4	MICOM: Metagenome-Scale Modeling To Infer Metabolic Interactions in the Gut Microbiota. <i>MSystems</i> , 2020, 5, .	3.8	126
5	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
6	Modular analysis of the transcriptional regulatory network of <i>E. coli</i> . <i>Trends in Genetics</i> , 2005, 21, 16-20.	6.7	99
7	Metabolic Reconstruction and Modeling of Nitrogen Fixation in <i>Rhizobium etli</i> . <i>PLoS Computational Biology</i> , 2007, 3, e192.	3.2	85
8	Modeling Core Metabolism in Cancer Cells: Surveying the Topology Underlying the Warburg Effect. <i>PLoS ONE</i> , 2010, 5, e12383.	2.5	70
9	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
10	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
11	Evolution of Centrality Measurements for the Detection of Essential Proteins in Biological Networks. <i>Frontiers in Physiology</i> , 2016, 7, 375.	2.8	56
12	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
13	Proteomic patterns of cervical cancer cell lines, a network perspective. <i>BMC Systems Biology</i> , 2011, 5, 96.	3.0	52
14	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
15	Host-Microbiome Interaction and Cancer: Potential Application in Precision Medicine. <i>Frontiers in Physiology</i> , 2016, 7, 606.	2.8	40
16	Functional Modules, Structural Topology, and Optimal Activity in Metabolic Networks. <i>PLoS Computational Biology</i> , 2012, 8, e1002720.	3.2	34
17	Unveiling functional heterogeneity in breast cancer multicellular tumor spheroids through single-cell RNA-seq. <i>Scientific Reports</i> , 2020, 10, 12728.	3.3	30
18	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

#	ARTICLE	IF	CITATIONS
19	Filling Kinetic Gaps: Dynamic Modeling of Metabolism Where Detailed Kinetic Information Is Lacking. PLoS ONE, 2009, 4, e4967.	2.5	21
20	Entamoeba histolytica Up-Regulates MicroRNA-643 to Promote Apoptosis by Targeting XIAP in Human Epithelial Colon Cells. Frontiers in Cellular and Infection Microbiology, 2018, 8, 437.	3.9	20
21	Transcriptional and Microenvironmental Landscape of Macrophage Transition in Cancer: A Boolean Analysis. Frontiers in Immunology, 2021, 12, 642842.	4.8	20
22	Systems biology of cancer: moving toward the integrative study of the metabolic alterations in cancer cells. Frontiers in Physiology, 2013, 3, 481.	2.8	17
23	Personalized Prediction of Proliferation Rates and Metabolic Liabilities in Cancer Biopsies. Frontiers in Physiology, 2016, 7, 644.	2.8	16
24	The space of enzyme regulation in HeLa cells can be inferred from its intracellular metabolome. Scientific Reports, 2016, 6, 28415.	3.3	15
25	Progressive Shifts in the Gut Microbiome Reflect Prediabetes and Diabetes Development in a Treatment-Naive Mexican Cohort. Frontiers in Endocrinology, 2020, 11, 602326.	3.5	13
26	Natural selection drove metabolic specialization of the chromatophore in Paulinella chromatophora. BMC Evolutionary Biology, 2017, 17, 99.	3.2	11
27	Sex Differences in the Physiological Network of Healthy Young Subjects. Frontiers in Physiology, 2021, 12, 678507.	2.8	9
28	On Deep Landscape Exploration of COVID-19 Patients Cells and Severity Markers. Frontiers in Immunology, 2021, 12, 705646.	4.8	9
29	Analysis of Epithelial-Mesenchymal Transition Metabolism Identifies Possible Cancer Biomarkers Useful in Diverse Genetic Backgrounds. Frontiers in Oncology, 2020, 10, 1309.	2.8	8
30	Physiological Network Is Disrupted in Severe COVID-19. Frontiers in Physiology, 2022, 13, 848172.	2.8	7
31	Criticality, adaptability and early-warning signals in time series in a discrete quasispecies model. Frontiers in Biology, 2013, 8, 247-259.	0.7	6
32	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. Stem Cells International, 2019, 2019, 1-14.	2.5	6
33	Uncovering the Dynamic Mechanisms of the <i>Pseudomonas Aeruginosa</i> Quorum Sensing and Virulence Networks Using Boolean Modelling. IEEE Transactions on Nanobioscience, 2020, 19, 394-402.	3.3	6
34	“Gestaltomics” Systems Biology Schemes for the Study of Neuropsychiatric Diseases. Frontiers in Physiology, 2017, 8, 286.	2.8	4
35	A statistical model of DNA denaturation. Physica A: Statistical Mechanics and Its Applications, 2003, 318, 435-446.	2.6	3
36	MicroRNAs Regulate Metabolic Phenotypes During Multicellular Tumor Spheroids Progression. Frontiers in Oncology, 2020, 10, 582396.	2.8	3

#	ARTICLE	IF	CITATIONS
37	Jacobian Matrix. , 2013, , 1061-1062.		3
38	Editorial: Systems Biology and the Challenge of Deciphering the Metabolic Mechanisms Underlying Cancer. <i>Frontiers in Physiology</i> , 2017, 8, 537.	2.8	2
39	Constraint-based Modeling. , 2013, , 494-498.		2
40	Metabolism Nitrogen Fixation. , 2013, , 1275-1279.		1
41	Stochastic Analysis of the RT-PCR Process in Single-Cell RNA-Seq. <i>Mathematics</i> , 2021, 9, 2515.	2.2	1
42	Hierarchical Structure. , 2013, , 887-888.		1
43	Dynamic Metabolic Networks, <i>k</i> -Cone. , 2013, , 624-629.		1
44	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
45	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
46	A Roadmap Towards a Systems Biology Description of Bacterial Nitrogen Fixation. <i>Soil Biology</i> , 2013, , 27-51.	0.8	0
47	Modules, Identification Methods and Biological Function. , 2013, , 1450-1453.		0
48	System Biology, Metabolomics, and Breast Cancer: Where We Are and What Are the Possible Consequences on the Clinical Setting. , 2018, , 169-188.		0