

Julio Vera

List of Publications by Year in descending order

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Version: 2024-02-01

125
papers

3,327
citations

136950

32
h-index

197818

49
g-index

136
all docs

136
docs citations

136
times ranked

4800
citing authors

#	ARTICLE	IF	CITATIONS
1	Locally renewing resident synovial macrophages provide a protective barrier for the joint. <i>Nature</i> , 2019, 572, 670-675.	27.8	345
2	Understanding microRNA-mediated gene regulatory networks through mathematical modelling. <i>Nucleic Acids Research</i> , 2016, 44, 6019-6035.	14.5	135
3	Systems biology-based investigation of cooperating microRNAs as monotherapy or adjuvant therapy in cancer. <i>Nucleic Acids Research</i> , 2019, 47, 7753-7766.	14.5	126
4	Unraveling a tumor type-specific regulatory core underlying E2F1-mediated epithelial-mesenchymal transition to predict receptor protein signatures. <i>Nature Communications</i> , 2017, 8, 198.	12.8	84
5	Computational analysis of target hub gene repression regulated by multiple and cooperative miRNAs. <i>Nucleic Acids Research</i> , 2012, 40, 8818-8834.	14.5	77
6	Artificial intelligence in cancer target identification and drug discovery. <i>Signal Transduction and Targeted Therapy</i> , 2022, 7, 156.	17.1	77
7	Cooperative gene regulation by microRNA pairs and their identification using a computational workflow. <i>Nucleic Acids Research</i> , 2014, 42, 7539-7552.	14.5	72
8	miR-638 promotes melanoma metastasis and protects melanoma cells from apoptosis and autophagy. <i>Oncotarget</i> , 2015, 6, 2966-2980.	1.8	72
9	Multicriteria optimization of biochemical systems by linear programming: Application to production of ethanol by <i>Saccharomyces cerevisiae</i> . <i>Biotechnology and Bioengineering</i> , 2003, 83, 335-343.	3.3	70
10	The AP-1 Transcription Factor c-Jun Promotes Arthritis by Regulating Cyclooxygenase-2 and Arginase-1 Expression in Macrophages. <i>Journal of Immunology</i> , 2017, 198, 3605-3614.	0.8	67
11	IL-33-induced metabolic reprogramming controls the differentiation of alternatively activated macrophages and the resolution of inflammation. <i>Immunity</i> , 2021, 54, 2531-2546.e5.	14.3	67
12	Power-law models of signal transduction pathways. <i>Cellular Signalling</i> , 2007, 19, 1531-1541.	3.6	66
13	Emerging functional markers for cancer stem cell-based therapies: Understanding signaling networks for targeting metastasis. <i>Seminars in Cancer Biology</i> , 2018, 53, 90-109.	9.6	62
14	MiR-205-5p and miR-342-3p cooperate in the repression of the E2F1 transcription factor in the context of anticancer chemotherapy resistance. <i>Theranostics</i> , 2018, 8, 1106-1120.	10.0	59
15	EMT transcription factor ZEB1 alters the epigenetic landscape of colorectal cancer cells. <i>Cell Death and Disease</i> , 2020, 11, 147.	6.3	58
16	The Role of Immune Checkpoint Blockade in Uveal Melanoma. <i>International Journal of Molecular Sciences</i> , 2020, 21, 879.	4.1	57
17	Kinetic Modeling-Based Detection of Genetic Signatures That Provide Chemoresistance via the E2F1-p73/DNp73-miR-205 Network. <i>Cancer Research</i> , 2013, 73, 3511-3524.	0.9	56
18	Exosomal lncRNAs and cancer: connecting the missing links. <i>Bioinformatics</i> , 2019, 35, 352-360.	4.1	51

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19	Transcription factor Fra-1 targets arginase-1 to enhance macrophage-mediated inflammation in arthritis. <i>Journal of Clinical Investigation</i> , 2019, 129, 2669-2684.	8.2	51
20	MicroRNA-Regulated Networks: The Perfect Storm for Classical Molecular Biology, the Ideal Scenario for Systems Biology. <i>Advances in Experimental Medicine and Biology</i> , 2013, 774, 55-76.	1.6	50
21	Whither systems medicine?. <i>Experimental and Molecular Medicine</i> , 2018, 50, e453-e453.	7.7	49
22	Î2-microglobulin triggers NLRP3 inflammasome activation in tumor-associated macrophages to promote multiple myeloma progression. <i>Immunity</i> , 2021, 54, 1772-1787.e9.	14.3	49
23	The systems biology of mitochondrial fission and fusion and implications for disease and aging. <i>Biogerontology</i> , 2014, 15, 1-12.	3.9	46
24	Systems biology of JAK-STAT signalling in human malignancies. <i>Progress in Biophysics and Molecular Biology</i> , 2011, 106, 426-434.	2.9	44
25	Serum levels of miR-320 family members are associated with clinical parameters and diagnosis in prostate cancer patients. <i>Oncotarget</i> , 2018, 9, 10402-10416.	1.8	44
26	14-3-3Ïf gene silencing during melanoma progression and its role in cell cycle control and cellular senescence. <i>Molecular Cancer</i> , 2009, 8, 53.	19.2	42
27	Optimization of biochemical systems through mathematical programming: Methods and applications. <i>Computers and Operations Research</i> , 2010, 37, 1427-1438.	4.0	41
28	Transcription factor Sox10 regulates oligodendroglial Sox9 levels via microRNAs. <i>Glia</i> , 2017, 65, 1089-1102.	4.9	41
29	A systems biology approach to analyse amplification in the JAK2-STAT5 signalling pathway. <i>BMC Systems Biology</i> , 2008, 2, 38.	3.0	37
30	A gene regulatory architecture that controls region-independent dynamics of oligodendrocyte differentiation. <i>Glia</i> , 2019, 67, 825-843.	4.9	36
31	Dynamic energy budget approaches for modelling organismal ageing. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2010, 365, 3443-3454.	4.0	33
32	Chk1 and Wee1 control genotoxic-stress induced G2â€M arrest in melanoma cells. <i>Cellular Signalling</i> , 2015, 27, 951-960.	3.6	33
33	Model based optimization of biochemical systems using multiple objectives: a comparison of several solution strategies. <i>Mathematical and Computer Modelling of Dynamical Systems</i> , 2006, 12, 469-487.	2.2	32
34	Detection of potential enzyme targets by metabolic modelling and optimization: Application to a simple enzymopathy. <i>Bioinformatics</i> , 2007, 23, 2281-2289.	4.1	32
35	A Systemsâ€™ Biology Approach to Study MicroRNA-Mediated Gene Regulatory Networks. <i>BioMed Research International</i> , 2013, 2013, 1-15.	1.9	32
36	Chapter 17 A System Biology Approach to Understand Functional Activity of Cell Communication Systems. <i>Methods in Cell Biology</i> , 2008, 90, 399-415.	1.1	30

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37	Baccoside A suppresses epileptic-like seizure/convulsion in <i>Caenorhabditis elegans</i> . <i>Seizure: the Journal of the British Epilepsy Association</i> , 2010, 19, 439-442.	2.0	28
38	The IKZF1-IRF4/IRF5 Axis Controls Polarization of Myeloma-Associated Macrophages. <i>Cancer Immunology Research</i> , 2021, 9, 265-278.	3.4	26
39	Dynamic properties of a delayed protein cross talk model. <i>BioSystems</i> , 2008, 91, 51-68.	2.0	25
40	Modeling miRNA Regulation in Cancer Signaling Systems: miR-34a Regulation of the p53/Sirt1 Signaling Module. <i>Methods in Molecular Biology</i> , 2012, 880, 87-108.	0.9	25
41	Investigating dynamics of inhibitory and feedback loops in ERK signalling using power-law models. <i>Molecular BioSystems</i> , 2010, 6, 2174.	2.9	24
42	Multiplicity of Mathematical Modeling Strategies to Search for Molecular and Cellular Insights into Bacteria Lung Infection. <i>Frontiers in Physiology</i> , 2017, 8, 645.	2.8	24
43	Identification of immunogenic consensus T-cell epitopes in globally distributed influenza-A H1N1 neuraminidase. <i>Infection, Genetics and Evolution</i> , 2011, 11, 308-319.	2.3	23
44	Personalized cancer immunotherapy using Systems Medicine approaches. <i>Briefings in Bioinformatics</i> , 2016, 17, 453-467.	6.5	23
45	Innate extracellular vesicles from melanoma patients suppress β -catenin in tumor cells by miRNA-34a. <i>Life Science Alliance</i> , 2019, 2, e201800205.	2.8	22
46	Multi-objective steady state optimization of biochemical reaction networks using a constrained genetic algorithm. <i>Computers and Chemical Engineering</i> , 2008, 32, 1707-1713.	3.8	21
47	Hybrid modeling of the crosstalk between signaling and transcriptional networks using ordinary differential equations and multi-valued logic. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 289-298.	2.3	21
48	MicroRNAs Constitute a Negative Feedback Loop in <i>Streptococcus pneumoniae</i> -Induced Macrophage Activation. <i>Journal of Infectious Diseases</i> , 2016, 214, 288-299.	4.0	21
49	An Interactive Macrophage Signal Transduction Map Facilitates Comparative Analyses of High-Throughput Data. <i>Journal of Immunology</i> , 2017, 198, 2191-2201.	0.8	21
50	THP-1-derived macrophages render lung epithelial cells hypo-responsive to <i>Legionella pneumophila</i> - a systems biology study. <i>Scientific Reports</i> , 2017, 7, 11988.	3.3	21
51	Biochemical Pathway Modeling Tools for Drug Target Detection in Cancer and Other Complex Diseases. <i>Methods in Enzymology</i> , 2011, 487, 319-369.	1.0	20
52	Third-Kind Encounters in Biomedicine: Immunology Meets Mathematics and Informatics to Become Quantitative and Predictive. <i>Methods in Molecular Biology</i> , 2016, 1386, 135-179.	0.9	20
53	Asthma phenotyping, therapy, and prevention: what can we learn from systems biology?. <i>Pediatric Research</i> , 2013, 73, 543-552.	2.3	19
54	Model-based genotype-phenotype mapping used to investigate gene signatures of immune sensitivity and resistance in melanoma micrometastasis. <i>Scientific Reports</i> , 2016, 6, 24967.	3.3	19

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55	The RNA world in the 21st centuryâ€”a systems approach to finding non-coding keys to clinical questions. <i>Briefings in Bioinformatics</i> , 2016, 17, 380-392.	6.5	19
56	A multi-level model accounting for the effects of JAK2-STAT5 signal modulation in erythropoiesis. <i>Computational Biology and Chemistry</i> , 2009, 33, 312-324.	2.3	18
57	A model-based strategy to investigate the role of microRNA regulation in cancer signalling networks. <i>Theory in Biosciences</i> , 2011, 130, 55-69.	1.4	18
58	A web platform for the network analysis of high-throughput data in melanoma and its use to investigate mechanisms of resistance to anti-PD1 immunotherapy. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2018, 1864, 2315-2328.	3.8	18
59	RNA Sequencing of Collecting Duct Renal Cell Carcinoma Suggests an Interaction between miRNA and Target Genes and a Predominance of Deregulated Solute Carrier Genes. <i>Cancers</i> , 2020, 12, 64.	3.7	18
60	A new semisynthetic cardenolide analog 3Î²-[2-(1-amantadine)- 1-on-ethylamine]-digitoxigenin (AMANTADIG) affects G2/M cell cycle arrest and miRNA expression profiles and enhances proapoptotic survivin-2B expression in renal cell carcinoma cell lines. <i>Oncotarget</i> , 2017, 8, 11676-11691.	1.8	18
61	Dynamical effects of epigenetic silencing of 14-3-3Î¶ expression. <i>Molecular BioSystems</i> , 2009, 6, 264-273.	2.9	17
62	Non-coding RNA detection methods combined to improve usability, reproducibility and precision. <i>BMC Bioinformatics</i> , 2010, 11, 491.	2.6	17
63	Integration of sensitivity and bifurcation analysis to detect critical processes in a model combining signalling and cell population dynamics. <i>International Journal of Systems Science</i> , 2010, 41, 81-105.	5.5	17
64	Analysis of cell adhesion during early stages of colon cancer based on an extended multi-valued logic approach. <i>Molecular BioSystems</i> , 2012, 8, 1230.	2.9	17
65	Computational Systems Biology Methods in Molecular Biology, Chemistry Biology, Molecular Biomedicine, and Biopharmacy. <i>BioMed Research International</i> , 2014, 2014, 1-2.	1.9	17
66	Tumors as chaotic attractors. <i>Molecular BioSystems</i> , 2014, 10, 172-179.	2.9	17
67	Transcriptional analysis identifies potential biomarkers and molecular regulators in pneumonia and COPD exacerbation. <i>Scientific Reports</i> , 2020, 10, 241.	3.3	17
68	Design of Metabolic Engineering Strategies for Maximizing l-(-)-Carnitine Production by <i>Escherichia coli</i> . Integration of the Metabolic and Bioreactor Levels. <i>Biotechnology Progress</i> , 2008, 21, 329-337.	2.6	16
69	A disease networkâ€”based deep learning approach for characterizing melanoma. <i>International Journal of Cancer</i> , 2022, 150, 1029-1044.	5.1	16
70	Delay in antibiotic therapy results in fatal disease outcome in murine pneumococcal pneumonia. <i>Critical Care</i> , 2018, 22, 287.	5.8	15
71	Community effort endorsing multiscale modelling, multiscale data science and multiscale computing for systems medicine. <i>Briefings in Bioinformatics</i> , 2019, 20, 1057-1062.	6.5	15
72	Role of inhibitory proteins as modulators of oscillations in NFÎ±B signalling. <i>IET Systems Biology</i> , 2009, 3, 59-76.	1.5	14

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73	Modelling of Protein Kinase Signaling Pathways in Melanoma and Other Cancers. <i>Cancers</i> , 2019, 11, 465.	3.7	14
74	Genome-wide Chromatin Profiling of <i>Legionella pneumophila</i> "Infected Human Macrophages Reveals Activation of the Probacterial Host Factor TNFAIP2. <i>Journal of Infectious Diseases</i> , 2016, 214, 454-463.	4.0	13
75	Identification of miRNA-mRNA Modules in Colorectal Cancer Using Rough Hypercuboid Based Supervised Clustering. <i>Scientific Reports</i> , 2017, 7, 42809.	3.3	13
76	Transcriptional Profiling of Ligand Expression in Cell Specific Populations of the Adult Mouse Forebrain That Regulates Neurogenesis. <i>Frontiers in Neuroscience</i> , 2018, 12, 220.	2.8	13
77	Integrated nonlinear optimization of bioprocesses via linear programming. <i>AIChE Journal</i> , 2003, 49, 3173-3187.	3.6	11
78	Dynamics of a miRNA Model with Two Delays. <i>Biotechnology and Biotechnological Equipment</i> , 2012, 26, 3315-3320.	1.3	10
79	Bacterial Adherence and Dwelling Probability: Two Drivers of Early Alveolar Infection by <i>Streptococcus pneumoniae</i> Identified in Multi-Level Mathematical Modeling. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 159.	3.9	10
80	Mycobacterial Cord Factor Reprograms the Macrophage Response to IFN- γ towards Enhanced Inflammation yet Impaired Antigen Presentation and Expression of GBP1. <i>Journal of Immunology</i> , 2020, 205, 1580-1592.	0.8	10
81	Clinical determinants of long-term survival in metastatic uveal melanoma. <i>Cancer Immunology, Immunotherapy</i> , 2022, 71, 1467-1477.	4.2	10
82	Dynamics of receptor and protein transducer homodimerisation. <i>BMC Systems Biology</i> , 2008, 2, 92.	3.0	9
83	Electroporated Antigen-Encoding mRNA Is Not a Danger Signal to Human Mature Monocyte-Derived Dendritic Cells. <i>Journal of Immunology Research</i> , 2015, 2015, 1-9.	2.2	9
84	SBML export interface for the systems biology toolbox for MATLAB. <i>Bioinformatics</i> , 2007, 23, 1297-1298.	4.1	8
85	Model-based investigation of the transcriptional activity of p53 and its feedback loop regulation via 14-3-3 ζ . <i>IET Systems Biology</i> , 2011, 5, 293-307.	1.5	8
86	Evidence for liver and peripheral immune cells secreting tumor-suppressive extracellular vesicles in melanoma patients. <i>EBioMedicine</i> , 2020, 62, 103119.	6.1	8
87	Network- and systems-based re-engineering of dendritic cells with non-coding RNAs for cancer immunotherapy. <i>Theranostics</i> , 2021, 11, 1412-1428.	10.0	8
88	Systems Biology Approaches in Aging Research. <i>Interdisciplinary Topics in Gerontology</i> , 2014, 40, 155-176.	3.6	7
89	Mathematical Modelling in Biomedicine: A Primer for the Curious and the Skeptic. <i>International Journal of Molecular Sciences</i> , 2021, 22, 547.	4.1	7
90	PLMaddon: a power-law module for the Matlab TM SBTtoolbox. <i>Bioinformatics</i> , 2007, 23, 2638-2640.	4.1	6

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91	Growth and ligninolytic system production dynamics of the <i>Phanerochaete chrysosporium</i> fungus. <i>Journal of Biotechnology</i> , 2008, 137, 50-58.	3.8	6
92	An integrative network-driven pipeline for systematic identification of lncRNA-associated regulatory network motifs in metastatic melanoma. <i>BMC Bioinformatics</i> , 2020, 21, 329.	2.6	6
93	Plasma-derived extracellular vesicles discriminate type-1 allergy subjects from non-allergic controls. <i>World Allergy Organization Journal</i> , 2021, 14, 100583.	3.5	6
94	Rough hypercuboid based supervised clustering of miRNAs. <i>Molecular BioSystems</i> , 2015, 11, 2068-2081.	2.9	5
95	Mathematical Tools in Cancer Signalling Systems Biology. , 2011, , 185-212.		5
96	MetMAP: an integrated Matlab package for analysis and optimization of metabolic systems. <i>In Silico Biology</i> , 2004, 4, 97-108.	0.9	5
97	Computational analysis and modeling the effectiveness of Zanamivir™ targeting neuraminidase protein in pandemic H1N1 strains. <i>Infection, Genetics and Evolution</i> , 2011, 11, 1072-1082.	2.3	4
98	Can Gamification Contribute to Computer Modeling-Driven Biomedical Research?. <i>Frontiers in Physiology</i> , 2018, 9, 908.	2.8	4
99	Heterogeneous fate choice of genetically modulated adult neural stem cells in gray and white matter of the central nervous system. <i>Glia</i> , 2020, 68, 393-406.	4.9	4
100	The Role of Age, Neutrophil Infiltration and Antibiotics Timing in the Severity of <i>Streptococcus pneumoniae</i> Pneumonia. Insights from a Multi-Level Mathematical Model Approach. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8428.	4.1	4
101	Systems Medicine for Lung Diseases: Phenotypes and Precision Medicine in Cancer, Infection, and Allergy. <i>Methods in Molecular Biology</i> , 2016, 1386, 119-133.	0.9	4
102	Envisioning the Application of Systems Biology in Cancer Immunology. , 2015, , 429-449.		3
103	Model-Based Phenotypic Signatures Governing the Dynamics of the Stem and Semi-differentiated Cell Populations in Dysplastic Colonic Crypts. <i>Bulletin of Mathematical Biology</i> , 2018, 80, 360-384.	1.9	3
104	Curatopes Melanoma: A Database of Predicted T-cell Epitopes from Overly Expressed Proteins in Metastatic Cutaneous Melanoma. <i>Cancer Research</i> , 2019, 79, 5452-5456.	0.9	3
105	Multi-Level Computational Modeling of Anti-Cancer Dendritic Cell Vaccination Utilized to Select Molecular Targets for Therapy Optimization. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 746359.	3.7	3
106	Exploration of homodimer receptor: homodimer protein interactions. <i>International Journal of Bioinformatics Research and Applications</i> , 2009, 5, 447.	0.2	2
107	In Silico Approaches and the Role of Ontologies in Aging Research. <i>Rejuvenation Research</i> , 2013, 16, 540-546.	1.8	2
108	The role of cooperativity in a p53-miR34 dynamical mathematical model. <i>Journal of Theoretical Biology</i> , 2020, 495, 110252.	1.7	2

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109	Dissecting Long-Term Glucose Metabolism Identifies New Susceptibility Period for Metabolic Dysfunction in Aged Mice. PLoS ONE, 2015, 10, e0140858.	2.5	2
110	Analysis and Optimisation of Bioprocesses with METMAP. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2004, 37, 553-558.	0.4	1
111	Computational Approaches in microRNA Biology. , 2019, , 317-330.		1
112	Computational microRNA Biology. , 2013, , 473-480.		1
113	Single-Molecule RNA Sequencing Reveals IFN β -Induced Differential Expression of Immune Escape Genes in Merkel Cell Polyomavirus β -Positive MCC Cell Lines. Frontiers in Microbiology, 2021, 12, 785662.	3.5	1
114	Optimal Non-Linear Design and Control of Bioprocesses via Linear Programming. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2004, 37, 469-474.	0.4	0
115	01.12 β ...Fra-1 transcription factor expression in macrophages foster inflammation during rheumatoid arthritis development. , 2017, , .		0
116	02.24 β ...The ap-1 transcription factor c-jun promotes arthritis by regulating cyclooxygenase-2 expression in macrophages. , 2017, , .		0
117	Editorial: Foundations of Theoretical Approaches in Systems Biology. Frontiers in Genetics, 2018, 9, 290.	2.3	0
118	β <sub>2</sub>-Microglobulin - A Trigger for NLRP3 Inflammasome Activation in Tumor-Associated Macrophages Promoting Multiple Myeloma Progression. SSRN Electronic Journal, 0, , .	0.4	0
119	Nonlinear Dynamics, miRNA Circuits. , 2013, , 1541-1545.		0
120	MicroRNA-embedding Regulation Networks, Logical Modeling. , 2013, , 1350-1354.		0
121	Biochemical Systems Optimization Through Mathematical Programming. , 2013, , 92-101.		0
122	Supervised Cluster Analysis of miRNA Expression Data Using Rough Hypercuboid Partition Matrix. Lecture Notes in Computer Science, 2015, , 482-494.	1.3	0
123	microRNAs constitute a negative feedback loop in<i>streptococcus pneumoniae</i>induced macrophage activation. , 2016, , .		0
124	Genome-wide chromatin profiling of legionella pneumophila-infected human macrophages reveals activation of the pro-bacterial host factor TNFAIP2. , 2016, , .		0
125	Envisioning the Application of Systems Biology in Cancer Immunology. , 2020, , 599-624.		0