

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	Clinical determinants of long-term survival in metastatic uveal melanoma. <i>Cancer Immunology, Immunotherapy</i> , 2022, 71, 1467-1477.	4.2	10
2	A disease network-based deep learning approach for characterizing melanoma. <i>International Journal of Cancer</i> , 2022, 150, 1029-1044.	5.1	16
3	Artificial intelligence in cancer target identification and drug discovery. <i>Signal Transduction and Targeted Therapy</i> , 2022, 7, 156.	17.1	77
4	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
5	The IKZF1-IRF4/IRF5 Axis Controls Polarization of Myeloma-Associated Macrophages. <i>Cancer Immunology Research</i> , 2021, 9, 265-278.	3.4	26
6	β 2-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
7	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
8	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
9	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
10	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
11	Single-Molecule RNA Sequencing Reveals IFN γ -Induced Differential Expression of Immune Escape Genes in Merkel Cell Polyomavirus-Positive MCC Cell Lines. <i>Frontiers in Microbiology</i> , 2021, 12, 785662.	3.5	1
12	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
13	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
14	Evidence for liver and peripheral immune cells secreting tumor-suppressive extracellular vesicles in melanoma patients. <i>EBioMedicine</i> , 2020, 62, 103119.	6.1	8
15	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
16	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
17	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
18	EMT transcription factor ZEB1 alters the epigenetic landscape of colorectal cancer cells. <i>Cell Death and Disease</i> , 2020, 11, 147.	6.3	58

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19	Transcriptional analysis identifies potential biomarkers and molecular regulators in pneumonia and COPD exacerbation. <i>Scientific Reports</i> , 2020, 10, 241.	3.3	17
20	The role of cooperativity in a p53-miR34 dynamical mathematical model. <i>Journal of Theoretical Biology</i> , 2020, 495, 110252.	1.7	2
21	The Role of Immune Checkpoint Blockade in Uveal Melanoma. <i>International Journal of Molecular Sciences</i> , 2020, 21, 879.	4.1	57
22	Envisioning the Application of Systems Biology in Cancer Immunology. , 2020, , 599-624.		0
23	Exosomal lncRNAs and cancer: connecting the missing links. <i>Bioinformatics</i> , 2019, 35, 352-360.	4.1	51
24	Locally renewing resident synovial macrophages provide a protective barrier for the joint. <i>Nature</i> , 2019, 572, 670-675.	27.8	345
25	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
26	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
27	Modelling of Protein Kinase Signaling Pathways in Melanoma and Other Cancers. <i>Cancers</i> , 2019, 11, 465.	3.7	14
28	A gene regulatory architecture that controls region-independent dynamics of oligodendrocyte differentiation. <i>Glia</i> , 2019, 67, 825-843.	4.9	36
29	Computational Approaches in microRNA Biology. , 2019, , 317-330.		1
30	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
31	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
32	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
33	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
34	Whither systems medicine?. <i>Experimental and Molecular Medicine</i> , 2018, 50, e453-e453.	7.7	49
35	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
36	Can Gamification Contribute to Computer Modeling-Driven Biomedical Research?. <i>Frontiers in Physiology</i> , 2018, 9, 908.	2.8	4

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37	Delay in antibiotic therapy results in fatal disease outcome in murine pneumococcal pneumonia. <i>Critical Care</i> , 2018, 22, 287.	5.8	15
38	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
39	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
40	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
41	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
42	Editorial: Foundations of Theoretical Approaches in Systems Biology. <i>Frontiers in Genetics</i> , 2018, 9, 290.	2.3	0
43	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
44	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
45	Identification of miRNA-mRNA Modules in Colorectal Cancer Using Rough Hypercuboid Based Supervised Clustering. <i>Scientific Reports</i> , 2017, 7, 42809.	3.3	13
46	Transcription factor Sox10 regulates oligodendroglial Sox9 levels via microRNAs. <i>Glia</i> , 2017, 65, 1089-1102.	4.9	41
47	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
48	01.12â€¦Fra-1 transcription factor expression in macrophages foster inflammation during rheumatoid arthritis development. , 2017, , .		0
49	THP-1-derived macrophages render lung epithelial cells hypo-responsive to <i>Legionella pneumophila</i> â€œ a systems biology study. <i>Scientific Reports</i> , 2017, 7, 11988.	3.3	21
50	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
51	02.24â€¦The ap-1 transcription factor c-jun promotes arthritis by regulating cyclooxygenase-2 expression in macrophages. , 2017, , .		0
52	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
53	A new semisynthetic cardenolide analog 3 ¹² -[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
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	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
56	Understanding microRNA-mediated gene regulatory networks through mathematical modelling. <i>Nucleic Acids Research</i> , 2016, 44, 6019-6035.	14.5	135
57	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
58	The RNA world in the 21st century—a systems approach to finding non-coding keys to clinical questions. <i>Briefings in Bioinformatics</i> , 2016, 17, 380-392.	6.5	19
59	Personalized cancer immunotherapy using Systems Medicine approaches. <i>Briefings in Bioinformatics</i> , 2016, 17, 453-467.	6.5	23
60	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
61	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
62	microRNAs constitute a negative feedback loop in <i>streptococcus pneumoniae</i> induced macrophage activation. , 2016, , .		0
63	Genome-wide chromatin profiling of <i>legionella pneumophila</i> -infected human macrophages reveals activation of the pro-bacterial host factor TNFAIP2. , 2016, , .		0
64	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
65	Rough hypercuboid based supervised clustering of miRNAs. <i>Molecular BioSystems</i> , 2015, 11, 2068-2081.	2.9	5
66	Envisioning the Application of Systems Biology in Cancer Immunology. , 2015, , 429-449.		3
67	Chk1 and Wee1 control genotoxic-stress induced G2/M arrest in melanoma cells. <i>Cellular Signalling</i> , 2015, 27, 951-960.	3.6	33
68	miR-638 promotes melanoma metastasis and protects melanoma cells from apoptosis and autophagy. <i>Oncotarget</i> , 2015, 6, 2966-2980.	1.8	72
69	Supervised Cluster Analysis of miRNA Expression Data Using Rough Hypercuboid Partition Matrix. <i>Lecture Notes in Computer Science</i> , 2015, , 482-494.	1.3	0
70	Dissecting Long-Term Glucose Metabolism Identifies New Susceptibility Period for Metabolic Dysfunction in Aged Mice. <i>PLoS ONE</i> , 2015, 10, e0140858.	2.5	2
71	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
72	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

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73	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
74	The systems biology of mitochondrial fission and fusion and implications for disease and aging. <i>Biogerontology</i> , 2014, 15, 1-12.	3.9	46
75	Systems Biology Approaches in Aging Research. <i>Interdisciplinary Topics in Gerontology</i> , 2014, 40, 155-176.	3.6	7
76	Tumors as chaotic attractors. <i>Molecular BioSystems</i> , 2014, 10, 172-179.	2.9	17
77	Asthma phenotyping, therapy, and prevention: what can we learn from systems biology?. <i>Pediatric Research</i> , 2013, 73, 543-552.	2.3	19
78	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
79	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
80	A Systems Biology Approach to Study MicroRNA-Mediated Gene Regulatory Networks. <i>BioMed Research International</i> , 2013, 2013, 1-15.	1.9	32
81	In Silico Approaches and the Role of Ontologies in Aging Research. <i>Rejuvenation Research</i> , 2013, 16, 540-546.	1.8	2
82	Computational microRNA Biology. , 2013, , 473-480.		1
83	Nonlinear Dynamics, miRNA Circuits. , 2013, , 1541-1545.		0
84	MicroRNA-embedding Regulation Networks, Logical Modeling. , 2013, , 1350-1354.		0
85	Biochemical Systems Optimization Through Mathematical Programming. , 2013, , 92-101.		0
86	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
87	Dynamics of a miRNA Model with Two Delays. <i>Biotechnology and Biotechnological Equipment</i> , 2012, 26, 3315-3320.	1.3	10
88	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
89	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
90	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

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91	Systems biology of JAK-STAT signalling in human malignancies. Progress in Biophysics and Molecular Biology, 2011, 106, 426-434.	2.9	44
92	Model-based investigation of the transcriptional activity of p53 and its feedback loop regulation via 14-3-3 β . IET Systems Biology, 2011, 5, 293-307.	1.5	8
93	A model-based strategy to investigate the role of microRNA regulation in cancer signalling networks. Theory in Biosciences, 2011, 130, 55-69.	1.4	18
94	Identification of immunogenic consensus T-cell epitopes in globally distributed influenza-A H1N1 neuraminidase. Infection, Genetics and Evolution, 2011, 11, 308-319.	2.3	23
95	Computational analysis and modeling the effectiveness of Zanamivir TM targeting neuraminidase protein in pandemic H1N1 strains. Infection, Genetics and Evolution, 2011, 11, 1072-1082.	2.3	4
96	Mathematical Tools in Cancer Signalling Systems Biology. , 2011, , 185-212.		5
97	Non-coding RNA detection methods combined to improve usability, reproducibility and precision. BMC Bioinformatics, 2010, 11, 491.	2.6	17
98	Optimization of biochemical systems through mathematical programming: Methods and applications. Computers and Operations Research, 2010, 37, 1427-1438.	4.0	41
99	Dynamic energy budget approaches for modelling organismal ageing. Philosophical Transactions of the Royal Society B: Biological Sciences, 2010, 365, 3443-3454.	4.0	33
100	Baccoside A suppresses epileptic-like seizure/convulsion in Caenorhabditis elegans. Seizure: the Journal of the British Epilepsy Association, 2010, 19, 439-442.	2.0	28
101	Investigating dynamics of inhibitory and feedback loops in ERK signalling using power-law models. Molecular BioSystems, 2010, 6, 2174.	2.9	24
102	Integration of sensitivity and bifurcation analysis to detect critical processes in a model combining signalling and cell population dynamics. International Journal of Systems Science, 2010, 41, 81-105.	5.5	17
103	Role of inhibitory proteins as modulators of oscillations in NF κ B signalling. IET Systems Biology, 2009, 3, 59-76.	1.5	14
104	A multi-level model accounting for the effects of JAK2-STAT5 signal modulation in erythropoiesis. Computational Biology and Chemistry, 2009, 33, 312-324.	2.3	18
105	Exploration of homodimer receptor: homodimer protein interactions. International Journal of Bioinformatics Research and Applications, 2009, 5, 447.	0.2	2
106	14-3-3 β gene silencing during melanoma progression and its role in cell cycle control and cellular senescence. Molecular Cancer, 2009, 8, 53.	19.2	42
107	Dynamical effects of epigenetic silencing of 14-3-3 β expression. Molecular BioSystems, 2009, 6, 264-273.	2.9	17
108	Growth and ligninolytic system production dynamics of the Phanerochaete chrysosporium fungus. Journal of Biotechnology, 2008, 137, 50-58.	3.8	6

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109	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
110	Dynamic properties of a delayed protein cross talk model. <i>BioSystems</i> , 2008, 91, 51-68.	2.0	25
111	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
112	A systems biology approach to analyse amplification in the JAK2-STAT5 signalling pathway. <i>BMC Systems Biology</i> , 2008, 2, 38.	3.0	37
113	Dynamics of receptor and protein transducer homodimerisation. <i>BMC Systems Biology</i> , 2008, 2, 92.	3.0	9
114	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
115	SBML export interface for the systems biology toolbox for MATLAB. <i>Bioinformatics</i> , 2007, 23, 1297-1298.	4.1	8
116	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
117	PLMaddon: a power-law module for the Matlab™ SBToolbox. <i>Bioinformatics</i> , 2007, 23, 2638-2640.	4.1	6
118	Power-law models of signal transduction pathways. <i>Cellular Signalling</i> , 2007, 19, 1531-1541.	3.6	66
119	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
120	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
121	Analysis and Optimisation of Bioprocesses with METMAP. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2004, 37, 553-558.	0.4	1
122	MetMAP: an integrated Matlab package for analysis and optimization of metabolic systems. <i>In Silico Biology</i> , 2004, 4, 97-108.	0.9	5
123	Integrated nonlinear optimization of bioprocesses via linear programming. <i>AIChE Journal</i> , 2003, 49, 3173-3187.	3.6	11
124	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
125	Î² <sub>g</sub>>2</sub>>-Microglobulin - A Trigger for NLRP3 Inflammasome Activation in Tumor-Associated Macrophages Promoting Multiple Myeloma Progression. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0