Eduardo Tejera

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3054721/publications.pdf

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471061 580395 1,021 69 17 citations h-index papers

g-index 76 76 76 1489 docs citations times ranked citing authors all docs

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#	Article	IF	CITATIONS
1	Computational modeling predicts potential effects of the herbal infusion "horchata―against COVID-19. Food Chemistry, 2022, 366, 130589.	4.2	18
2	Comparative organizational network analysis considering formal power-based networks and organizational hierarchies. Heliyon, 2022, 8, e08661.	1.4	1
3	Metabolomic profile and computational analysis for the identification of the potential anti-inflammatory mechanisms of action of the traditional medicinal plants Ocimum basilicum and Ocimum tenuiflorum. Food and Chemical Toxicology, 2022, 164, 113039.	1.8	10
4	Clustering Analysis of the Multi-Microbial Consortium by Lactobacillus Species Against Vaginal Dysbiosis Among Ecuadorian Women. Frontiers in Cellular and Infection Microbiology, 2022, 12, .	1.8	21
5	The search for molecular mimicry in proteins carried by extracellular vesicles secreted by cells infected with <i>Plasmodium falciparum</i> . Communicative and Integrative Biology, 2021, 14, 212-220.	0.6	4
6	A population-based study of preeclampsia and eclampsia in Ecuador: ethnic, geographical and altitudes differences. BMC Pregnancy and Childbirth, 2021, 21, 116.	0.9	6
7	A Multi-Objective Approach for Drug Repurposing in Preeclampsia. Molecules, 2021, 26, 777.	1.7	4
8	In silico Analyses of Immune System Protein Interactome Network, Single-Cell RNA Sequencing of Human Tissues, and Artificial Neural Networks Reveal Potential Therapeutic Targets for Drug Repurposing Against COVID-19. Frontiers in Pharmacology, 2021, 12, 598925.	1.6	16
9	Pre-existing T-cell immunity to SARS-CoV-2 in unexposed healthy controls in Ecuador, as detected with a COVID-19 Interferon-Gamma Release Assay. International Journal of Infectious Diseases, 2021, 105, 21-25.	1.5	43
10	Determining the microbial and chemical contamination in Ecuador's main rivers. Scientific Reports, 2021, 11, 17640.	1.6	12
11	ShadowCaster: Compositional Methods under the Shadow of Phylogenetic Models to Detect Horizontal Gene Transfers in Prokaryotes. Genes, 2020, 11, 756.	1.0	11
12	Drugs Repurposing Using QSAR, Docking and Molecular Dynamics for Possible Inhibitors of the SARS-CoV-2 Mpro Protease. Molecules, 2020, 25, 5172.	1.7	42
13	A Multi-Objective Approach for Anti-Osteosarcoma Cancer Agents Discovery through Drug Repurposing. Pharmaceuticals, 2020, 13, 409.	1.7	6
14	Determination of the Microbial and Chemical Loads in Rivers from the Quito Capital Province of Ecuador (Pichincha)â€"A Preliminary Analysis of Microbial and Chemical Quality of the Main Rivers. International Journal of Environmental Research and Public Health, 2020, 17, 5048.	1.2	16
15	OncoOmics approaches to reveal essential genes in breast cancer: a panoramic view from pathogenesis to precision medicine. Scientific Reports, 2020, 10, 5285.	1.6	36
16	Protective effect of the medicinal herb infusion "horchata" against oxidative damage in cigarette smokers: An ex vivo study. Food and Chemical Toxicology, 2020, 143, 111538.	1.8	6
17	Gene Prioritization through Consensus Strategy, Enrichment Methodologies Analysis, and Networking for Osteosarcoma Pathogenesis. International Journal of Molecular Sciences, 2020, 21, 1053.	1.8	13
18	Prediction of breast cancer proteins involved in immunotherapy, metastasis, and RNA-binding using molecular descriptors and artificial neural networks. Scientific Reports, 2020, 10, 8515.	1.6	29

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19	Teletrabajo en tiempos de COVID-19. Interamerican Journal of Psychology, 2020, 54, e1450.	0.1	16
20	Representing Cellular Lines with SVM and Text Processing. , 2020, , .		0
21	NFBTA: A Potent Cytotoxic Agent against Glioblastoma. Molecules, 2019, 24, 2411.	1.7	19
22	Ensemble-Based Modeling of Chemical Compounds with Antimalarial Activity. Current Topics in Medicinal Chemistry, 2019, 19, 957-969.	1.0	8
23	Cell fishing: A similarity based approach and machine learning strategy for multiple cell lines-compound sensitivity prediction. PLoS ONE, 2019, 14, e0223276.	1.1	6
24	CompScore: Boosting Structure-Based Virtual Screening Performance by Incorporating Docking Scoring Function Components into Consensus Scoring. Journal of Chemical Information and Modeling, 2019, 59, 3655-3666.	2.5	20
25	Multioutput Perturbation-Theory Machine Learning (PTML) Model of ChEMBL Data for Antiretroviral Compounds. Molecular Pharmaceutics, 2019, 16, 4200-4212.	2.3	24
26	Chemical Composition and Antioxidant Activity of the Main Fruits Consumed in the Western Coastal Region of Ecuador as a Source of Health-Promoting Compounds. Antioxidants, 2019, 8, 387.	2.2	30
27	Chemical Composition and Antioxidant Activity of the Main Fruits, Tubers and Legumes Traditionally Consumed in the Andean Regions of Ecuador as a Source of Health-Promoting Compounds. Plant Foods for Human Nutrition, 2019, 74, 350-357.	1.4	16
28	Anti-inflammatory effect of the medicinal herbal mixture infusion, Horchata, from southern Ecuador against LPS-induced cytotoxic damage in RAW 264.7 macrophages. Food and Chemical Toxicology, 2019, 131, 110594.	1.8	20
29	A putative antimicrobial peptide from Hymenoptera in the megaplasmid pSCL4 of <i>Streptomyces clavuligerus</i> ATCC 27064 reveals a singular case of horizontal gene transfer with potential applications. Ecology and Evolution, 2019, 9, 2602-2614.	0.8	1
30	Analysis of organizational power networks through a holistic approach using consensus strategies. Heliyon, 2019, 5, e01172.	1.4	8
31	Physicochemical parameters, chemical composition, antioxidant capacity, microbial contamination and antimicrobial activity of <i>Eucalyptus</i> honey from the Andean region of Ecuador. Journal of Apicultural Research, 2018, 57, 382-394.	0.7	36
32	Breast Cancer Risk Associated with Genotype Polymorphisms of the Aurora Kinase a Gene (AURKA): a Case-Control Study in a High Altitude Ecuadorian Mestizo Population. Pathology and Oncology Research, 2018, 24, 457-465.	0.9	11
33	Gene prioritization, communality analysis, networking and metabolic integrated pathway to better understand breast cancer pathogenesis. Scientific Reports, 2018, 8, 16679.	1.6	29
34	The dilemma of bacterial expansins evolution. The unusual case of Streptomyces acidiscabies and Kutzneria sp. 744. Communicative and Integrative Biology, 2018, 11, e1539612.	0.6	2
35	Influence of Botanical Origin and Chemical Composition on the Protective Effect against Oxidative Damage and the Capacity to Reduce In Vitro Bacterial Biofilms of Monofloral Honeys from the Andean Region of Ecuador. International Journal of Molecular Sciences, 2018, 19, 45.	1.8	34
36	A desirability-based multi objective approach for the virtual screening discovery of broad-spectrum anti-gastric cancer agents. PLoS ONE, 2018, 13, e0192176.	1.1	15

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37	Systemic QSAR and phenotypic virtual screening: chasing butterflies in drug discovery. Drug Discovery Today, 2017, 22, 994-1007.	3.2	28
38	From flamingo dance to (desirable) drug discovery: a nature-inspired approach. Drug Discovery Today, 2017, 22, 1489-1502.	3.2	28
39	Estudio de relaciones entre cultura, clima y fuerza de clima laboral en Ecuador. Acción Psicológica, 2017, 14, 225-240.	0.1	3
40	Consensus strategy in genes prioritization and combined bioinformatics analysis for preeclampsia pathogenesis. BMC Medical Genomics, 2017, 10, 50.	0.7	18
41	Fusing Docking Scoring Functions Improves the Virtual Screening Performance for Discovering Parkinson's Disease Dual Target Ligands. Current Neuropharmacology, 2017, 15, 1107-1116.	1.4	11
42	Efficient and biologically relevant consensus strategy for Parkinson's disease gene prioritization. BMC Medical Genomics, 2016, 9, 12.	0.7	29
43	Ligand-Based Virtual Screening Using Tailored Ensembles: A Prioritization Tool for Dual A _{2A} Adenosine Receptor Antagonists / Monoamine Oxidase B Inhibitors. Current Pharmaceutical Design, 2016, 22, 3082-3096.	0.9	13
44	Probing the Hypothesis of SAR Continuity Restoration by the Removal of Activity Cliffs Generators in QSAR. Current Pharmaceutical Design, 2016, 22, 5043-5056.	0.9	7
45	Phase transitions in tumor growth: II prostate cancer cell lines. Physica A: Statistical Mechanics and Its Applications, 2015, 426, 88-92.	1.2	12
46	Unravelling the relationship between protein sequence and low-complexity regions entropies: Interactome implications. Journal of Theoretical Biology, 2015, 382, 320-327.	0.8	1
47	Harmonization of QSAR Best Practices and Molecular Docking Provides an Efficient Virtual Screening Tool for Discovering New G-Quadruplex Ligands. Journal of Chemical Information and Modeling, 2015, 55, 2094-2110.	2.5	20
48	First Trimester Aneuploidy Screening Program for Preeclampsia Prediction in a Portuguese Obstetric Population. Obstetrics and Gynecology International, 2014, 2014, 1-7.	0.5	6
49	Protein sequence complexity revisited. Relationship with fractal 3D structure, topological and kinetic parameters. Physica A: Statistical Mechanics and Its Applications, 2014, 410, 287-301.	1.2	1
50	Phase transition in tumor growth: I avascular development. Physica A: Statistical Mechanics and Its Applications, 2013, 392, 6616-6623.	1.2	19
51	Co-expression network analysis and genetic algorithms for gene prioritization in preeclampsia. BMC Medical Genomics, 2013, 6, 51.	0.7	29
52	Relationship between Heart Rate Variability Indexes and Common Biochemical Markers in Normal and Hypertensive Third Trimester Pregnancy. Hypertension in Pregnancy, 2012, 31, 59-69.	0.5	7
53	Desirability-Based Multi-Objective QSAR in Drug Discovery. Mini-Reviews in Medicinal Chemistry, 2012, 12, 920-935.	1.1	13
54	Blood Pressure and Heart Rate Variability Complexity Analysis in Pregnant Women with Hypertension. Hypertension in Pregnancy, 2012, 31, 91-106.	0.5	18

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55	Preeclampsia: a bioinformatics approach through protein-protein interaction networks analysis. BMC Systems Biology, 2012, 6, 97.	3.0	22
56	Artificial neural network for normal, hypertensive, and preeclamptic pregnancy classification using maternal heart rate variability indexes. Journal of Maternal-Fetal and Neonatal Medicine, 2011, 24, 1147-1151.	0.7	31
57	P5. Bioinformatic analysis of protein–protein interaction network in preeclampsia. Pregnancy Hypertension, 2011, 1, 275.	0.6	0
58	Network centrality and multiscale transition asymmetry in the heart rate variability analysis of normal and preeclamptic pregnancies. Communications in Nonlinear Science and Numerical Simulation, 2011, 16, 1589-1596.	1.7	3
59	Unexpected heart rate variability complexity in the aging process of arrhythmic subjects. Communications in Nonlinear Science and Numerical Simulation, 2010, 15, 1858-1863.	1.7	5
60	Lipid Levels Including Oxidized LDL in Women with History of Preeclampsia. Hypertension in Pregnancy, 2010, 29, 93-100.	0.5	14
61	Fractal protein structure revisited: Topological, kinetic and thermodynamic relationships. Physica A: Statistical Mechanics and Its Applications, 2009, 388, 4600-4608.	1.2	16
62	Application of desirability-based multi(bi)-objective optimization in the design of selective arylpiperazine derivates for the 5-HT1A serotonin receptor. European Journal of Medicinal Chemistry, 2009, 44, 5045-5054.	2.6	17
63	Haemostatic factors in women with history of Preeclampsia. Thrombosis Research, 2009, 124, 52-56.	0.8	16
64	Altered alanine aminotransferase and \hat{l}^3 -glutamyl transpeptidase in women with history of preeclampsia: association with waist-to-hip ratio and body mass index. European Journal of Gastroenterology and Hepatology, 2009, 21, 196-200.	0.8	3
65	Adhesion molecules (VCAMâ€1 and ICAMâ€1) and Câ€reactive protein in women with history of preeclampsia. Acta Obstetricia Et Gynecologica Scandinavica, 2008, 87, 969-971.	1.3	16
66	Heart Rate Variability Complexity in the Aging Process. Computational and Mathematical Methods in Medicine, 2007, 8, 287-296.	0.7	7
67	Chemoinformatics Profiling of Ionic Liquids Cytotoxicity—From Machine Learning to Network-Like Similarity Graphs. , 0, , .		0
68	Virtual screening tailored ensembles of QSAR models for the discovery of dual A_{2A} Adenosine Receptor Antagonists / Monoamine Oxidase B Inhibitors .,0,,.		0
69	Improved virtual screening performance through docking scoring fusion in the discovery of dual target ligands for Parkinson’s disease .,0,,.		O