Andres Fernando Gonzalez Barrios

List of Publications by Year
in descending order

71 papers	1,511 citations	516215 16 h-index	329751 37 g-index
73 all docs	73 docs citations	73 times ranked	2377 citing authors

#	Article	IF	Citations
1	Autoinducer 2 Controls Biofilm Formation in Escherichia coli through a Novel Motility Quorum-Sensing Regulator (MqsR, B3022). Journal of Bacteriology, 2006, 188, 305-316.	1.0	478
2	Motility influences biofilm architecture in Escherichia coli. Applied Microbiology and Biotechnology, 2006, 72, 361-367.	1.7	286
3	Hha, YbaJ, and OmpA regulateEscherichia coli K12 biofilm formation and conjugation plasmids abolish motility. Biotechnology and Bioengineering, 2006, 93, 188-200.	1.7	96
4	Phage Î¦Pan70, a Putative Temperate Phage, Controls Pseudomonas aeruginosa in Planktonic, Biofilm and Burn Mouse Model Assays. Viruses, 2015, 7, 4602-4623.	1.5	42
5	Lipid Metabolic Versatility in Malassezia spp. Yeasts Studied through Metabolic Modeling. Frontiers in Microbiology, 2017, 8, 1772.	1.5	31
6	Draft Genome Sequence of the Animal and Human Pathogen <i>Malassezia pachydermatis</i> Strain CBS 1879. Genome Announcements, 2015, 3, .	0.8	30
7	Magnetiteâ€"OmpA Nanobioconjugates as Cell-Penetrating Vehicles with Endosomal Escape Abilities. ACS Biomaterials Science and Engineering, 2020, 6, 415-424.	2.6	28
8	Economic evaluation of the development of a phage therapy product for the control of <i>Salmonella</i> in poultry. Biotechnology Progress, 2019, 35, e2852.	1.3	27
9	Carbon acquisition and accumulation in microalgae Chlamydomonas: Insights from â€œomicsâ€ approaches. Journal of Proteomics, 2013, 94, 207-218.	1.2	24
10	Clostridium butyricum maximizes growth while minimizing enzyme usage and ATP production: metabolic flux distribution of a strain cultured in glycerol. BMC Systems Biology, 2017, 11, 58.	3.0	22
11	Analysis of Malassezia Lipidome Disclosed Differences Among the Species and Reveals Presence of Unusual Yeast Lipids. Frontiers in Cellular and Infection Microbiology, 2020, 10, 338.	1.8	22
12	Characterization of cellulases of fungal endophytes isolated from Espeletia spp.. Journal of Microbiology, 2012, 50, 1009-1013.	1.3	20
13	Impact of the Mode of Extraction on the Lipidomic Profile of Oils Obtained from Selected Amazonian Fruits. Biomolecules, 2019, 9, 329.	1.8	20
14	Development of a <i>Chlamydomonas reinhardtii</i> metabolic network dynamic model to describe distinct phenotypes occurring at different CO₂ levels. PeerJ, 2018, 6, e5528.	0.9	19
15	Modeling of the hypothalamic-pituitary-adrenal axis-mediated interaction between the serotonin regulation pathway and the stress response using a Boolean approximation: a novel study of depression. Theoretical Biology and Medical Modelling, 2013, 10, 59.	2.1	18
16	From industrial byâ€products to valueâ€added compounds: the design of efficient microbial cell factories by coupling systems metabolic engineering and bioprocesses. Biofuels, Bioproducts and Biorefining, 2020, 14, 1228-1238.	1.9	17
17	Analysis of Sensitive CO2 Pathways and Genes Related to Carbon Uptake and Accumulation in Chlamydomonas reinhardtii through Genomic Scale Modeling and Experimental Validation. Frontiers in Plant Science, 2016, 7, 43.	1.7	16
18	A comparison between conventional Pseudomonas aeruginosa rhamnolipids and Escherichia coli transmembrane proteins for oil recovery enhancing. International Biodeterioration and Biodegradation, 2016, 112, 59-65.	1.9	16

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19	Dissecting industrial fermentations of fine flavour cocoa through metagenomic analysis. Scientific Reports, 2021, 11, 8638.	1.6	16
20	Quorum quenching analysis in PseudomonasÂaeruginosa and EscherichiaÂcoli: network topology and inhibition mechanism effect on the optimized inhibitor dose. Bioprocess and Biosystems Engineering, 2009, 32, 545-556.	1.7	14
21	The multiscale approach t o the design of bio-based emulsions. Current Opinion in Chemical Engineering, 2020, 27, 65-71.	3.8	13
22	Unraveling the Genome of a High Yielding Colombian Sugarcane Hybrid. Frontiers in Plant Science, 2021, 12, 694859.	1.7	13
23	Dissecting fine-flavor cocoa bean fermentation through metabolomics analysis to break down the current metabolic paradigm. Scientific Reports, 2021, 11, 21904.	1.6	13
24	Escherichia coli autoinducer-2 uptake network does not display hysteretic behavior but AI-2 synthesis rate controls transient bifurcation. BioSystems, 2010, 99, 17-26.	0.9	12
25	Proteins interaction network and modeling of IGVH mutational status in chronic lymphocytic leukemia. Theoretical Biology and Medical Modelling, 2015, 12, 12.	2.1	11
26	Peptides design based on transmembrane Escherichia coli â€™ s OmpA protein through molecular dynamics simulations in waterâ€"dodecane interfaces. Journal of Molecular Graphics and Modelling, 2016, 68, 216-223.	1.3	11
27	Influence of agricultural activities in the structure and metabolic functionality of paramo soil samples in Colombia studied using a metagenomics analysis in dynamic state. Ecological Modelling, 2017, 351, 63-76.	1.2	11
28	Multiscale design of a dairy beverage model composed of Candida utilis single cell protein supplemented with oleic acid. Journal of Dairy Science, 2019, 102, 9749-9762.	1.4	11
29	Effects of metabolic engineering on downstream processing operational cost and energy consumption: the case of <scp><i>Escherichia coli</i></scp><i>'s</i> glycerol conversion to succinic acid. Journal of Chemical Technology and Biotechnology, 2018, 93, 2011-2020.	1.6	10
30	Evaluation of the phenol degradation capacity of microalgae-bacteria consortia from the bay of Cartagena, Colombia. Tecno LÃ³gicas, 2019, 22, 149-158.	0.1	10
31	Clostridium butyricum population balance model: Predicting dynamic metabolic flux distributions using an objective function related to extracellular glycerol content. PLoS ONE, 2018, 13, e0209447.	1.1	9
32	Rational Design of Photo-Electrochemical Hybrid Devices Based on Graphene and Chlamydomonas reinhardtii Light-Harvesting Proteins. Scientific Reports, 2020, 10, 3376.	1.6	9
33	In vitro and in silico characterization of metagenomic soil-derived cellulases capable of hydrolyzing oil palm empty fruit bunch. Biotechnology Reports (Amsterdam, Netherlands), 2017, 15, 55-62.	2.1	8
34	Molecular dynamics approach to investigate the coupling of the hydrophilicâ€"lipophilic balance with the configuration distribution function in biosurfactant-based emulsions. Journal of Molecular Modeling, 2013, 19, 5539-5543.	0.8	7
35	Metagenome level metabolic network reconstruction analysis reveals the microbiome in the BogotÃ¡ River is functionally close to the microbiome in produced water. Ecological Modelling, 2019, 399, 1-12.	1.2	7
36	New Therapeutic Candidates for the Treatment of Malassezia pachydermatis -Associated Infections. Scientific Reports, 2020, 10, 4860.	1.6	7

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37	A synthetic multi-cellular network of coupled self-sustained oscillators. PLoS ONE, 2017, 12, e0180155.	1.1	7
38	Comparative analysis for three different immobilisation strategies in the hexavalent chromium biosorption process using <i>Bacillus sphaericus</i> S‑layer. Canadian Journal of Chemical Engineering, 2011, 89, 1281-1287.	0.9	6
39	Escherichia coli's OmpA as Biosurfactant for Cosmetic Industry: Stability Analysis and Experimental Validation Based on Molecular Simulations. Advances in Intelligent Systems and Computing, 2014, , 265-271.	0.5	6
40	Compartmentalized metabolic network reconstruction of microbial communities to determine the effect of agricultural intervention on soils. PLoS ONE, 2017, 12, e0181826.	1.1	6
41	Everyday chemical product design as platform for teaching transport phenomena. Education for Chemical Engineers, 2018, 25, 9-15.	2.8	6
42	Transcriptomic analysis of a Clostridium thermocellum strain engineered to utilize xylose: responses to xylose versus cellobiose feeding. Scientific Reports, 2020, 10, 14517.	1.6	6
43	<i>cysA, cysP, and rpoS</i> mutations increase the power density in <i>P. aeruginosa</i> microbial fuel cells: Performing enhancement based on metabolic flux analysis. Advances in Bioscience and Biotechnology (Print), 2013, 04, 103-111.	0.3	6
44	Genome-Scale Metabolic Model of Xanthomonas phaseoli pv. manihotis: An Approach to Elucidate Pathogenicity at the Metabolic Level. Frontiers in Genetics, 2020, 11, 837.	1.1	5
45	Discovery of new potential CDK2/VEGFR2 type II inhibitors by fragmentation and virtual screening of natural products. Journal of Biomolecular Structure and Dynamics, 2020, 39, 1-15.	2.0	5
46	Peptidomic analysis of whey protein hydrolysates and prediction of their antioxidant peptides. Food Science and Human Wellness, 2022, 11, 349-355.	2.2	5
47	A network model for biofilm development in Escherichia coli K-12. Theoretical Biology and Medical Modelling, 2011, 8, 34.	2.1	4
48	DYNAMIC FLUX BALANCE ANALYSIS FOR PREDICTING GENE OVEREXPRESSION EFFECTS IN BATCH CULTURES. Journal of Biological Systems, 2014, 22, 327-338.	0.5	4
49	Pushing the Ligand Efficiency Metrics: Relative Group Contribution (RGC) Model as a Helpful Strategy to Promote a Fragment "Rescue" Effect. Frontiers in Chemistry, 2019, 7, 564.	1.8	4
50	In Silico Analysis for Biomass Synthesis under Different CO2 Levels for Chlamydomonas reinhardtii Utilizing a Flux Balance Analysis Approach. Advances in Intelligent Systems and Computing, 2014, , 279-285.	0.5	3
51	Computational approaches for evaluating the effect of sequence variations and the intrinsically disordered C-terminal region of the Helicobacter pylori CagA protein on the interaction with tyrosine kinase Src. Journal of Molecular Modeling, 2014, 20, 2406.	0.8	3
52	A comparison between functional frequency and metabolic flows framed by biogeochemical cycles in metagenomes: The case of "El Coquito" hot spring located at Colombia's national Nevados park. Ecological Modelling, 2015, 313, 259-265.	1.2	3
53	A generalized model for bacterial disinfection: Stochastic approach. Biochemical Engineering Journal, 2016, 114, 218-225.	1.8	3
54	Intramolecular energies of the cytotoxic protein CagA of Helicobacter pylori as a possible descriptor of strains' pathogenicity level. Computational Biology and Chemistry, 2018, 76, 17-22.	1.1	3

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55	In silico Design for Systems-Based Metabolic Engineering for the Bioconversion of Valuable Compounds From Industrial By-Products. Frontiers in Genetics, 2021, 12, 633073.	1.1	3
56	Effects of processing conditions on hydrolysates of proteins from whole whey and formation of Maillard reaction products. Journal of Food Processing and Preservation, 2021, 45, e15469.	0.9	3
57	Optimization of the bioconversion of glycerol to ethanol using &lt;i&gt;Escherichia coli&lt;/i&gt; by implementing a bi-level programming framework for proposing gene transcription control strategies based on genetic algorithms. Advances in Bioscience and Biotechnology (Print), 2012, 03, 336-343.	0.3	3
58	Development of a group contribution method for estimating free energy of peptides in a dodecane-water system via molecular dynamic simulations. BMC Bioinformatics, 2016, 17, 522.	1.2	2
59	Insights into the behavior of six rationally designed peptides based on Escherichia coliâ€™s OmpA at the water-dodecane interface. PLoS ONE, 2019, 14, e0223670.	1.1	2
60	Optimization of glycerol consumption in wildâ€type Escherichia coli using central carbon modeling as an alternative approach. Biofuels, Bioproducts and Biorefining, 2021, 15, 825-839.	1.9	2
61	ELUCIDATING THE ROLE OF METABOLITES AS QUORUM SENSING SIGNALS USING PHASE PLANE ANALYSIS: THE CASE OF INDOLE IN ESCHERICHIA COLI. Journal of Biological Systems, 2014, 22, 523-531.	0.5	1
62	Classical MD and metadynamics simulations on back-pocket binders of CDK2 and VEGFR2: a guidepost to design novel small-molecule dual inhibitors. Journal of Biomolecular Structure and Dynamics, 2022, 40, 9030-9041.	2.0	1
63	Non-Extensive Fragmentation of Natural Products and Pharmacophore-Based Virtual Screening as a Practical Approach to Identify Novel Promising Chemical Scaffolds. Frontiers in Chemistry, 2021, 9, 700802.	1.8	1
64	Development of an integrating systems metabolic engineering and bioprocess modeling approach for rational strain improvement. Biochemical Engineering Journal, 2022, 178, 108268.	1.8	1
65	Improved Production of Bacillus thuringiensis by Intermittent Fed-Batch Culture with Total Cell Retention. International Journal of Chemical Reactor Engineering, 2010, 8, .	0.6	0
66	Fagoterapia, alternativa para el control de las infecciones bacterianas. Perspectivas en Colombia. Universitas Scientiarum, 2014, 20, 43.	0.2	0
67	FBA Analysis, Plant-Pathogen Interactions. , 2013, , 733-736.		0
68	Network Modeling of Biochemical Transport Phenomena. , 2013, , 1517-1518.		0
69	Optimization Algorithms for Metabolites Production. , 2013, , 1596-1600.		0
70	Metagenome, Metabolic Reconstruction and Analysis. , 2013, , 1283-1287.		0
71	Analysis of Metabolic Functionality and Thermodynamic Feasibility of a Metagenomic Sample from â€œEl Coquitoâ€•Hot Spring. Advances in Intelligent Systems and Computing, 2014, , 287-293.	0.5	0