

Sergio Encarnación Guevara

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1383950/publications.pdf>

Version: 2024-02-01

42
papers

1,139
citations

394421

19
h-index

395702

33
g-index

43
all docs

43
docs citations

43
times ranked

1777
citing authors

#	ARTICLE	IF	CITATIONS
1	Interspecies competition triggers virulence and mutability in <i>Candida albicans</i> and <i>Pseudomonas aeruginosa</i> mixed biofilms. ISME Journal, 2014, 8, 1974-1988.	9.8	98
2	Proteomic analysis of <i>Tityus discrepans</i> scorpion venom and amino acid sequence of novel toxins. Proteomics, 2006, 6, 3718-3727.	2.2	89
3	Modeling Core Metabolism in Cancer Cells: Surveying the Topology Underlying the Warburg Effect. PLoS ONE, 2010, 5, e12383.	2.5	70
4	Characterization of the NifA-RpoN Regulon in <i>Rhizobium etli</i> in Free Life and in Symbiosis with <i>Phaseolus vulgaris</i> . Applied and Environmental Microbiology, 2010, 76, 4510-4520.	3.1	62
5	AniA Regulates Reserve Polymer Accumulation and Global Protein Expression in <i>Rhizobium etli</i> . Journal of Bacteriology, 2002, 184, 2287-2295.	2.2	59
6	Role of the Extracytoplasmic Function Sigma Factor RpoE4 in Oxidative and Osmotic Stress Responses in <i>Rhizobium etli</i> . Journal of Bacteriology, 2009, 191, 4122-4132.	2.2	52
7	Engineering the nifH Promoter Region and Abolishing Poly- β -Hydroxybutyrate Accumulation in <i>Rhizobium etli</i> Enhance Nitrogen Fixation in Symbiosis with <i>Phaseolus vulgaris</i> . Applied and Environmental Microbiology, 2004, 70, 3272-3281.	3.1	51
8	Comparative Proteomic Analysis of <i>Aedes aegypti</i> Larval Midgut after Intoxication with Cry11Aa Toxin from <i>Bacillus thuringiensis</i> . PLoS ONE, 2012, 7, e37034.	2.5	51
9	Only one catalase, katG, is detectable in <i>Rhizobium etli</i> , and is encoded along with the regulator OxyR on a plasmid replicon. Microbiology (United Kingdom), 2003, 149, 1165-1176.	1.8	50
10	Nitrogen-Fixing Rhizobial Strains Isolated from Common Bean Seeds: Phylogeny, Physiology, and Genome Analysis. Applied and Environmental Microbiology, 2014, 80, 5644-5654.	3.1	48
11	Eco-evolutionary feedbacks drive species interactions. ISME Journal, 2014, 8, 1041-1054.	9.8	47
12	Systems biology of bacterial nitrogen fixation: High-throughput technology and its integrative description with constraint-based modeling. BMC Systems Biology, 2011, 5, 120.	3.0	43
13	Proteome analysis of aerobic and fermentative metabolism in <i>Rhizobium etli</i> CE3. Proteomics, 2003, 3, 1077-1085.	2.2	39
14	Comparative proteomics using 2-D gel electrophoresis and mass spectrometry as tools to dissect stimulons and regulons in bacteria with sequenced or partially sequenced genomes. Biological Procedures Online, 2005, 7, 117-135.	2.9	39
15	Lysine acetylation stoichiometry and proteomics analyses reveal pathways regulated by sirtuin 1 in human cells. Journal of Biological Chemistry, 2017, 292, 18129-18144.	3.4	36
16	Functional Modules, Structural Topology, and Optimal Activity in Metabolic Networks. PLoS Computational Biology, 2012, 8, e1002720.	3.2	34
17	Biotin biosynthesis, transport and utilization in rhizobia. FEMS Microbiology Letters, 2005, 246, 159-165.	1.8	25
18	The naringenin-induced exoproteome of <i>Rhizobium etli</i> CE3. Archives of Microbiology, 2017, 199, 737-755.	2.2	24

#	ARTICLE	IF	CITATIONS
19	The extracellular proteome of <i>Rhizobium etli</i> CE3 in exponential and stationary growth phase. <i>Proteome Science</i> , 2010, 8, 51.	1.7	22
20	A <i>Pseudomonas aeruginosa</i> PAO1 acetylcholinesterase is encoded by the PA4921 gene and belongs to the SGNH hydrolase family. <i>Microbiological Research</i> , 2012, 167, 317-325.	5.3	17
21	Transcriptomic analysis of the process of biofilm formation in <i>Rhizobium etli</i> CFN42. <i>Archives of Microbiology</i> , 2016, 198, 847-860.	2.2	17
22	Proteins in the periplasmic space and outer membrane vesicles of <i>Rhizobium etli</i> CE3 grown in minimal medium are largely distinct and change with growth phase. <i>Microbiology (United Kingdom)</i> , 2019, 165, 638-650.	1.8	17
23	Phenotypic differences between BCG vaccines at the proteome level. <i>Tuberculosis</i> , 2009, 89, 126-135.	1.9	16
24	Differential Proteomic Analysis of the Pancreas of Diabetic db/db Mice Reveals the Proteins Involved in the Development of Complications of Diabetes Mellitus. <i>International Journal of Molecular Sciences</i> , 2014, 15, 9579-9593.	4.1	15
25	Transcriptional analysis reveals the metabolic state of <i>Burkholderia zhejiangensis</i> CEIB S4-3 during methyl parathion degradation. <i>PeerJ</i> , 2019, 7, e6822.	2.0	15
26	Effect of <i>aniA</i> (Carbon Flux Regulator) and <i>phaC</i> (Poly- β -Hydroxybutyrate Synthase) Mutations on Pyruvate Metabolism in <i>Rhizobium etli</i> . <i>Journal of Bacteriology</i> , 2002, 184, 2296-2299.	2.2	12
27	Proteomic and morphometric study of the in vitro interaction between <i>Oncidium sphacelatum</i> Lindl. (Orchidaceae) and <i>Thanatephorus</i> sp. RG26 (Ceratobasidiaceae). <i>Mycorrhiza</i> , 2016, 26, 353-365.	2.8	12
28	Qualitative changes in proteins contained in outer membrane vesicles produced by <i>Rhizobium etli</i> grown in the presence of the nod gene inducer naringenin. <i>Archives of Microbiology</i> , 2019, 201, 1173-1194.	2.2	11
29	The CRISPR-Cas System Is Involved in <i>OmpR</i> Genetic Regulation for Outer Membrane Protein Synthesis in <i>Salmonella Typhi</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 657404.	3.5	10
30	<i>argC</i> Orthologs from Rhizobiales Show Diverse Profiles of Transcriptional Efficiency and Functionality in <i>Sinorhizobium meliloti</i> . <i>Journal of Bacteriology</i> , 2011, 193, 460-472.	2.2	9
31	Analysis of differentially upregulated proteins in <i>ptsH</i> and <i>rppH</i> mutants in <i>Escherichia coli</i> during an adaptive laboratory evolution experiment. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 10193-10208.	3.6	9
32	Analysis and Prediction of Pathways in HeLa Cells by Integrating Biological Levels of Organization with Systems-Biology Approaches. <i>PLoS ONE</i> , 2013, 8, e65433.	2.5	8
33	Quantitative Proteomic Analysis of Cervical Cancer Tissues Identifies Proteins Associated With Cancer Progression. <i>Cancer Genomics and Proteomics</i> , 2022, 19, 241-258.	2.0	8
34	Proteomic insights into lysine acetylation and the implications for medical research. <i>Expert Review of Proteomics</i> , 2019, 16, 1-3.	3.0	7
35	Transcriptomic analysis of <i>Burkholderia cenocepacia</i> CEIB S5-2 during methyl parathion degradation. <i>Environmental Science and Pollution Research</i> , 2021, 28, 42414-42431.	5.3	7
36	The dawn and the first twenty-five years of proteomics in Mexico: a personal chronicle. <i>Boletín Médico Del Hospital Infantil De México</i> , 2017, 74, 208-211.	0.3	3

#	ARTICLE	IF	CITATIONS
37	Displacers improve the selectivity of phosphopeptide enrichment by metal oxide affinity chromatography. <i>Boletín Médico Del Hospital Infantil De México</i> , 2017, 74, 200-207.	0.3	3
38	Thiamine limitation determines the transition from aerobic to fermentative-like metabolism in <i>Rhizobium etli</i> CE3. <i>FEMS Microbiology Letters</i> , 2008, 279, 48-55.	1.8	2
39	The human bile salt sodium deoxycholate induces metabolic and cell envelope changes in <i>Salmonella Typhi</i> leading to bile resistance. <i>Journal of Medical Microbiology</i> , 2022, 71, .	1.8	2
40	Data for a comparative proteomic analysis of chloroplast biogenesis (clb) mutants. <i>Data in Brief</i> , 2014, 1, 15-18.	1.0	0
41	Clinical Proteomics in Mexico: where do we stand?. <i>Boletín Médico Del Hospital Infantil De México</i> , 2017, 74, 173-174.	0.3	0
42	GPX3 Level in Serum of Diffuse Large B Cell Lymphoma Patients Is a Predictive Biomarker for Refractoriness Before Treatment. <i>Blood</i> , 2012, 120, 5102-5102.	1.4	0