

# Sergio Encarnación Guevara

## List of Publications by Year in descending order

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42  
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1,139  
citations

394421

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43  
docs citations

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times ranked

1777  
citing authors

#	ARTICLE	IF	CITATIONS
1	The human bile salt sodium deoxycholate induces metabolic and cell envelope changes in Salmonella Typhi leading to bile resistance. Journal of Medical Microbiology, 2022, 71, .	1.8	2
2	Quantitative Proteomic Analysis of Cervical Cancer Tissues Identifies Proteins Associated With Cancer Progression. Cancer Genomics and Proteomics, 2022, 19, 241-258.	2.0	8
3	The CRISPR-Cas System Is Involved in OmpR Genetic Regulation for Outer Membrane Protein Synthesis in Salmonella Typhi. Frontiers in Microbiology, 2021, 12, 657404.	3.5	10
4	Transcriptomic analysis of Burkholderia cenocepacia CEIB S5-2 during methyl parathion degradation. Environmental Science and Pollution Research, 2021, 28, 42414-42431.	5.3	7
5	Qualitative changes in proteins contained in outer membrane vesicles produced by Rhizobium etli grown in the presence of the nod gene inducer naringenin. Archives of Microbiology, 2019, 201, 1173-1194.	2.2	11
6	Proteomic insights into lysine acetylation and the implications for medical research. Expert Review of Proteomics, 2019, 16, 1-3.	3.0	7
7	Proteins in the periplasmic space and outer membrane vesicles of Rhizobium etli CE3 grown in minimal medium are largely distinct and change with growth phase. Microbiology (United Kingdom), 2019, 165, 638-650.	1.8	17
8	Transcriptional analysis reveals the metabolic state of Burkholderia zhejiangensis CEIB S4-3 during methyl parathion degradation. PeerJ, 2019, 7, e6822.	2.0	15
9	Analysis of differentially upregulated proteins in ptsH <sup>cr</sup> and rppH <sup>cr</sup> mutants in Escherichia coli during an adaptive laboratory evolution experiment. Applied Microbiology and Biotechnology, 2018, 102, 10193-10208.	3.6	9
10	The naringenin-induced exoproteome of Rhizobium etli CE3. Archives of Microbiology, 2017, 199, 737-755.	2.2	24
11	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
12	The dawn and the first twenty-five years of proteomics in Mexico: a personal chronicle. Boletín Médico Del Hospital Infantil De México, 2017, 74, 208-211.	0.3	3
13	Displacers improve the selectivity of phosphopeptide enrichment by metal oxide affinity chromatography. Boletín Médico Del Hospital Infantil De México, 2017, 74, 200-207.	0.3	3
14	Clinical Proteomics in Mexico: where do we stand?. Boletín Médico Del Hospital Infantil De México, 2017, 74, 173-174.	0.3	0
15	Transcriptomic analysis of the process of biofilm formation in Rhizobium etli CFN42. Archives of Microbiology, 2016, 198, 847-860.	2.2	17
16	Proteomic and morphometric study of the in vitro interaction between Oncidium sphacelatum Lindl. (Orchidaceae) and Thanatephorus sp. RG26 (Ceratobasidiaceae). Mycorrhiza, 2016, 26, 353-365.	2.8	12
17	Differential Proteomic Analysis of the Pancreas of Diabetic db/db Mice Reveals the Proteins Involved in the Development of Complications of Diabetes Mellitus. International Journal of Molecular Sciences, 2014, 15, 9579-9593.	4.1	15
18	Interspecies competition triggers virulence and mutability in Candida albicans Pseudomonas aeruginosa mixed biofilms. ISME Journal, 2014, 8, 1974-1988.	9.8	98

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19	Eco-evolutionary feedbacks drive species interactions. <i>ISME Journal</i> , 2014, 8, 1041-1054.	9.8	47
20	Data for a comparative proteomic analysis of chloroplast biogenesis (clb) mutants. <i>Data in Brief</i> , 2014, 1, 15-18.	1.0	0
21	Nitrogen-Fixing Rhizobial Strains Isolated from Common Bean Seeds: Phylogeny, Physiology, and Genome Analysis. <i>Applied and Environmental Microbiology</i> , 2014, 80, 5644-5654.	3.1	48
22	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
23	Functional Modules, Structural Topology, and Optimal Activity in Metabolic Networks. <i>PLoS Computational Biology</i> , 2012, 8, e1002720.	3.2	34
24	Comparative Proteomic Analysis of <i>Aedes aegypti</i> Larval Midgut after Intoxication with Cry11Aa Toxin from <i>Bacillus thuringiensis</i> . <i>PLoS ONE</i> , 2012, 7, e37034.	2.5	51
25	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
26	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
27	Systems biology of bacterial nitrogen fixation: High-throughput technology and its integrative description with constraint-based modeling. <i>BMC Systems Biology</i> , 2011, 5, 120.	3.0	43
28	argC 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
29	Characterization of the NifA-RpoN Regulon in <i>Rhizobium etli</i> in Free Life and in Symbiosis with <i>Phaseolus vulgaris</i> . <i>Applied and Environmental Microbiology</i> , 2010, 76, 4510-4520.	3.1	62
30	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
31	Modeling Core Metabolism in Cancer Cells: Surveying the Topology Underlying the Warburg Effect. <i>PLoS ONE</i> , 2010, 5, e12383.	2.5	70
32	Role of the Extracytoplasmic Function Sigma Factor RpoE4 in Oxidative and Osmotic Stress Responses in <i>Rhizobium etli</i> . <i>Journal of Bacteriology</i> , 2009, 191, 4122-4132.	2.2	52
33	Phenotypic differences between BCG vaccines at the proteome level. <i>Tuberculosis</i> , 2009, 89, 126-135.	1.9	16
34	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
35	Proteomic analysis of <i>Tityus discrepans</i> scorpion venom and amino acid sequence of novel toxins. <i>Proteomics</i> , 2006, 6, 3718-3727.	2.2	89
36	Biotin biosynthesis, transport and utilization in rhizobia. <i>FEMS Microbiology Letters</i> , 2005, 246, 159-165.	1.8	25

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37	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. <i>Biological Procedures Online</i> , 2005, 7, 117-135.	2.9	39
38	Engineering the nifH Promoter Region and Abolishing Poly- $\beta$ -Hydroxybutyrate Accumulation in <i>Rhizobium etli</i> Enhance Nitrogen Fixation in Symbiosis with <i>Phaseolus vulgaris</i> . <i>Applied and Environmental Microbiology</i> , 2004, 70, 3272-3281.	3.1	51
39	Proteome analysis of aerobic and fermentative metabolism in <i>Rhizobium etli</i> CE3. <i>Proteomics</i> , 2003, 3, 1077-1085.	2.2	39
40	Only one catalase, katG, is detectable in <i>Rhizobium etli</i> , and is encoded along with the regulator OxyR on a plasmid replicon. <i>Microbiology (United Kingdom)</i> , 2003, 149, 1165-1176.	1.8	50
41	Effect of aniA (Carbon Flux Regulator) and phaC (Poly- $\beta$ -Hydroxybutyrate Synthase) Mutations on Pyruvate Metabolism in <i>Rhizobium etli</i> . <i>Journal of Bacteriology</i> , 2002, 184, 2296-2299.	2.2	12
42	AniA Regulates Reserve Polymer Accumulation and Global Protein Expression in <i>Rhizobium etli</i> . <i>Journal of Bacteriology</i> , 2002, 184, 2287-2295.	2.2	59