Manuel José Gómez

List of Publications by Year in descending order

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79 papers

4,298 citations

35 h-index 63 g-index

86 all docs 86 docs citations

86 times ranked 5968 citing authors

#	Article	IF	CITATIONS
1	Trained immunity induction by the inactivated mucosal vaccine MV130 protects against experimental viral respiratory infections. Cell Reports, 2022, 38, 110184.	6.4	34
2	Activation of amino acid metabolic program in cardiac HIF1-alpha-deficient mice. IScience, 2021, 24, 102124.	4.1	10
3	DNGR-1 limits Flt3L-mediated antitumor immunity by restraining tumor-infiltrating type I conventional dendritic cells., 2021, 9, e002054.		22
4	MiRNA post-transcriptional modification dynamics in TÂcell activation. IScience, 2021, 24, 102530.	4.1	10
5	Gene therapy with secreted acid alpha-glucosidase rescues Pompe disease in a novel mouse model with early-onset spinal cord and respiratory defects. EBioMedicine, 2020, 61, 103052.	6.1	14
6	Identification of a peripheral blood gene signature predicting aortic valve calcification. Physiological Genomics, 2020, 52, 563-574.	2.3	11
7	Sox17 Controls Emergence and Remodeling of Nestin-Expressing Coronary Vessels. Circulation Research, 2020, 127, e252-e270.	4.5	19
8	Caveolin1 and YAP drive mechanically induced mesothelial to mesenchymal transition and fibrosis. Cell Death and Disease, 2020, 11, 647.	6.3	39
9	JNK-mediated disruption of bile acid homeostasis promotes intrahepatic cholangiocarcinoma. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 16492-16499.	7.1	43
10	Expression of miR-135b in Psoriatic Skin and Its Association with Disease Improvement. Cells, 2020, 9, 1603.	4.1	10
11	Rescue of Advanced Pompe Disease in Mice with Hepatic Expression of Secretable Acid α-Glucosidase. Molecular Therapy, 2020, 28, 2056-2072.	8.2	16
12	Photocatalytically Active Graphitic Carbon Nitride as an Effective and Safe 2D Material for In Vitro and In Vivo Photodynamic Therapy. Small, 2020, 16, e1904619.	10.0	53
13	Abstract 16335: Metabolic Reprogramming From Glycolysis to Amino Acid Utilization in Cardiac Hif1 Alpha Deficient Mice. Circulation, 2020, 142, .	1.6	0
14	PGCâ€1α deficiency causes spontaneous kidney inflammation and increases the severity of nephrotoxic AKI. Journal of Pathology, 2019, 249, 65-78.	4.5	70
15	Functional, biochemical and transcriptional rescue of advanced Pompe disease in mice with liver expression of secretable GAA. Molecular Genetics and Metabolism, 2019, 126, S35.	1.1	0
16	Nanog regulates Pou3f1 expression at the exit from pluripotency during gastrulation. Biology Open, 2019, 8, .	1.2	11
17	Coronary arterial development is regulated by a Dll4-Jag1-EphrinB2 signaling cascade. ELife, 2019, 8, .	6.0	27
18	Von Hippel-Lindau Protein Is Required for Optimal Alveolar Macrophage Terminal Differentiation, Self-Renewal, and Function. Cell Reports, 2018, 24, 1738-1746.	6.4	26

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19	Prokaryotic diversity and community composition in the Salar de Uyuni, a large scale, chaotropic salt flat. Environmental Microbiology, 2017, 19, 3745-3754.	3.8	42
20	Global assessment of small RNAs reveals a non-coding transcript involved in biofilm formation and attachment in Acinetobacter baumannii ATCC 17978. PLoS ONE, 2017, 12, e0182084.	2.5	19
21	Myocardial VHL-HIF Signaling Controls an Embryonic Metabolic Switch Essential for Cardiac Maturation. Developmental Cell, 2016, 39, 724-739.	7.0	106
22	Sequential Ligand-Dependent Notch Signaling Activation Regulates Valve Primordium Formation and Morphogenesis. Circulation Research, 2016, 118, 1480-1497.	4.5	85
23	Solar Radiation Stress in Natural Acidophilic Biofilms of Euglena mutabilis Revealed by Metatranscriptomics and PAM Fluorometry. Protist, 2016, 167, 67-81.	1,5	8
24	Transposase interaction with the \hat{l}^2 sliding clamp: effects on insertion sequence proliferation and transposition rate. Scientific Reports, 2015, 5, 13329.	3.3	9
25	Pyrosequencing-Based Assessment of the Microbial Community Structure of Pastoruri Glacier Area (Huascarán National Park, Perú), a Natural Extreme Acidic Environment. Microbial Ecology, 2015, 70, 936-947.	2.8	22
26	Whole-genome analysis of Azoarcus sp. strain CIB provides genetic insights to its different lifestyles and predicts novel metabolic features. Systematic and Applied Microbiology, 2015, 38, 462-471.	2.8	73
27	A model for the structure and mechanism of action of pulmonary surfactant protein B. FASEB Journal, 2015, 29, 4236-4247.	0.5	50
28	Transcriptional response to copper excess and identification of genes involved in heavy metal tolerance in the extremophilic microalga Chlamydomonas acidophila. Extremophiles, 2015, 19, 657-672.	2.3	18
29	Telomerase Is Essential for Zebrafish Heart Regeneration. Cell Reports, 2015, 12, 1691-1703.	6.4	67
30	Nickel-Resistance Determinants in Acidiphilium sp. PM Identified by Genome-Wide Functional Screening. PLoS ONE, 2014, 9, e95041.	2.5	11
31	Large-Scale Genomic Analysis Suggests a Neutral Punctuated Dynamics of Transposable Elements in Bacterial Genomes. PLoS Computational Biology, 2014, 10, e1003680.	3.2	32
32	Deep subsurface sulfate reduction and methanogenesis in the Iberian Pyrite Belt revealed through geochemistry and molecular biomarkers. Geobiology, 2014, 12, 34-47.	2.4	33
33	Stage-specific differential gene expression in Leishmania infantum: from the foregut of Phlebotomus perniciosus to the human phagocyte. BMC Genomics, 2014, 15, 849.	2.8	27
34	Chromosomal Replication Dynamics and Interaction with the \hat{l}^2 Sliding Clamp Determine Orientation of Bacterial Transposable Elements. Genome Biology and Evolution, 2014, 6, 727-740.	2.5	18
35	Complete Genome Sequence of the Multiresistant Acinetobacter baumannii Strain AbH12O-A2, Isolated during a Large Outbreak in Spain. Genome Announcements, 2014, 2, .	0.8	19
36	The Dynamic Genomes of Acidophiles. Cellular Origin and Life in Extreme Habitats, 2013, , 81-97.	0.3	1

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37	Metabolic potential of the organicâ€solvent tolerant P seudomonas putida †DOT ―T1E deduced from its annotated genome. Microbial Biotechnology, 2013, 6, 598-611.	4.2	37
38	Whole Transcriptome Analysis of Acinetobacter baumannii Assessed by RNA-Sequencing Reveals Different mRNA Expression Profiles in Biofilm Compared to Planktonic Cells. PLoS ONE, 2013, 8, e72968.	2.5	127
39	Comparative Genomic Analysis Reveals Novel Facts about <i>Leptospirillum</i> spp. Cytochromes. Journal of Molecular Microbiology and Biotechnology, 2012, 22, 94-104.	1.0	12
40	Exploring Bacterial Diversity in Hospital Environments by GS-FLX Titanium Pyrosequencing. PLoS ONE, 2012, 7, e44105.	2.5	52
41	Prokaryotic communities and operating metabolisms in the surface and the permafrost of Deception Island (Antarctica). Environmental Microbiology, 2012, 14, 2495-2510.	3.8	44
42	A Microbial Oasis in the Hypersaline Atacama Subsurface Discovered by a Life Detector Chip: Implications for the Search for Life on Mars. Astrobiology, 2011, 11, 969-996.	3.0	140
43	Partial and complete denitrification in Thermus thermophilus: lessons from genome drafts. Biochemical Society Transactions, 2011, 39, 249-253.	3.4	14
44	The pGRT1 plasmid of <i>Pseudomonas putida</i> DOT‶1E encodes functions relevant for survival under harsh conditions in the environment. Environmental Microbiology, 2011, 13, 2315-2327.	3.8	43
45	Draft Genome Sequence of the Electricigen Acidiphilium sp. Strain PM (DSM 24941). Journal of Bacteriology, 2011, 193, 5585-5586.	2.2	23
46	Complete Genome of the Plant Growth-Promoting Rhizobacterium (i>Pseudomonas putida (i>BIRD-1. Journal of Bacteriology, 2011, 193, 1290-1290.	2,2	52
47	Lateral Transfer of the Denitrification Pathway Genes among <i>Thermus thermophilus</i> Strains. Applied and Environmental Microbiology, 2011, 77, 1352-1358.	3.1	32
48	Temperature increase prevails over acidification in gene expression modulation of amastigote differentiation in Leishmania infantum. BMC Genomics, 2010, 11, 31.	2.8	55
49	Environmental transcriptome analysis reveals physiological differences between biofilm and planktonic modes of life of the iron oxidizing bacteria Leptospirillum spp. in their natural microbial community. BMC Genomics, 2010, 11, 404.	2.8	59
50	Transcriptomics throughout the life cycle of Leishmania infantum: High down-regulation rate in the amastigote stage. International Journal for Parasitology, 2010, 40, 1497-1516.	3.1	77
51	The <i>Mycobacterium tuberculosis</i> Sigma Factor $\ddot{l}f$ ^B Is Required for Full Response to Cell Envelope Stress and Hypoxia In Vitro, but It Is Dispensable for In Vivo Growth. Journal of Bacteriology, 2009, 191, 5628-5633.	2.2	66
52	Genome-wide analysis reveals increased levels of transcripts related with infectivity in peanut lectin non-agglutinated promastigotes of Leishmania infantum. Genomics, 2009, 93, 551-564.	2.9	50
53	The environmental fate of organic pollutants through the global microbial metabolism. Molecular Systems Biology, 2007, 3, 114 .	7.2	43
54	Scoring docking models with evolutionary information. Proteins: Structure, Function and Bioinformatics, 2005, 60, 275-280.	2.6	41

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55	Accessible Protein Interaction Data for Network Modeling. Structure of the Information and Available Repositories. Lecture Notes in Computer Science, 2005, , 1-13.	1.3	3
56	The Biodegradation Network, a New Scenario for Computational Systems Biology Research. Lecture Notes in Computer Science, 2005, , 252-256.	1.3	0
57	Hyperglycosylation of glycopeptidolipid of Mycobacterium smegmatis under nutrient starvation: structural studies. Microbiology (United Kingdom), 2005, 151, 2385-2392.	1.8	32
58	Gene order in Prokaryotes: conservation and implications. , 2004, , 209-237.		3
59	Prediction of Functional Sites in Proteins by Evolutionary Methods. Principles and Practice, 2004, , 319-340.	0.3	8
60	Role of the extracytoplasmicâ€function \(\ilde{\textit{f}}\) \(\frac{\textit{f}}{\textit{b}}\) \(\text{sup}\) \(\text{H}\) \(\text{sup}\) \(\text{in}\) \(\text{in}\) \(\text{Mycobacterium}\) \(\text{tuberculosis}\) \(\text{in}\) \(\text{global gene expression}\). \(\text{Molecular Microbiology}\), 2002, 45, 365-374.	2.5	263
61	Characterization of the Secreted MPT53 Antigen of Mycobacterium tuberculosis. Infection and Immunity, 2001, 69, 5936-5939.	2.2	12
62	Identification of Secreted Proteins of Mycobacterium tuberculosis by a Bioinformatic Approach. Infection and Immunity, 2000, 68, 2323-2327.	2.2	104
63	Use of Coagulase Gene (coa) Repeat Region Nucleotide Sequences for Typing of Methicillin-Resistant Staphylococcus aureus Strains. Journal of Clinical Microbiology, 2000, 38, 3453-3456.	3.9	83
64	Evaluation of Protein A Gene Polymorphic Region DNA Sequencing for Typing of <i>Staphylococcus aureus</i> Strains. Journal of Clinical Microbiology, 1999, 37, 3556-3563.	3.9	898
65	Identification and characterization of two divergently transcribed iron regulated genes in Mycobacterium tuberculosis. Tubercle and Lung Disease, 1999, 79, 287-298.	2.1	50
66	, an essential gene at the cluster of codes for a cytoplasmic protein with methyltransferase activity. Biochimie, 1999, 81, 879-888.	2.6	37
67	Transcriptional Control of the Iron-Responsive <i>fxbA</i> Gene by the Mycobacterial Regulator IdeR. Journal of Bacteriology, 1999, 181, 3402-3408.	2.2	92
68	Extra and intracellular expression of Mycobacterium tuberculosis genes. Tubercle and Lung Disease, 1998, 79, 91-97.	2.1	13
69	Regulation of transcription of cell division genes in the Escherichia coli dcw cluster. Cellular and Molecular Life Sciences, 1998, 54, 317-324.	5.4	77
70	sigAis an essential gene inMycobacterium smegmatis. Molecular Microbiology, 1998, 29, 617-628.	2.5	84
71	Identification of a new ${}^{\circ}\!$	2.2	7

Expression of the Bacillus subtilis spolVB gene is under dual ÂF/ÂG control. Microbiology (United) Tj ETQq0 0 0 rgBT_/gverlock 10 Tf 50 control.

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73	Transcription of spoIVB is the only role of sigma G that is essential for pro-sigma K processing during spore formation in Bacillus subtilis. Journal of Bacteriology, 1995, 177, 4825-4827.	2.2	38
74	Variations in the Metabolism of Peptidoglycan Prior to Polymerization. , 1993, , 127-138.		0
75	Membrane intermediates in the peptidoglycan metabolism of Escherichia coli: possible roles of PBP 1b and PBP 3. Journal of Bacteriology, 1992, 174, 3549-3557.	2.2	151
76	Nucleotide sequence of the regulatory region of the genepbpBofEscherichia coli. Nucleic Acids Research, 1990, 18, 2813-2813.	14.5	8
77	A new beta-lactam-binding protein derived from penicillin-binding protein 3 of Escherichia coli. Journal of Bacteriology, 1989, 171, 5194-5198.	2.2	9
78	Evaluation of Glycosylated Hemoglobin in Diabetic Patients. Diabetes, 1981, 30, 613-617.	0.6	277
79	Gene Expression and Regulation. , 0, , 59-92.		3