

Manuel Jos Gmez

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

78
papers

3,403
citations

32
h-index

57
g-index

86
ext. papers

3,933
ext. citations

5.8
avg, IF

4.68
L-index

#	Paper	IF	Citations
78	Trained immunity induction by the inactivated mucosal vaccine MV130 protects against experimental viral respiratory infections.. <i>Cell Reports</i> , 2022 , 38, 110184	10.6	3
77	DNGR-1 limits Flt3L-mediated antitumor immunity by restraining tumor-infiltrating type I conventional dendritic cells 2021 , 9,		5
76	MiRNA post-transcriptional modification dynamics in T cell activation. <i>iScience</i> , 2021 , 24, 102530	6.1	1
75	Activation of amino acid metabolic program in cardiac HIF1-alpha-deficient mice. <i>iScience</i> , 2021 , 24, 102124	6.1	2
74	JNK-mediated disruption of bile acid homeostasis promotes intrahepatic cholangiocarcinoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 16492-16499 ^{11.5}	11.5	22
73	Expression of miR-135b in Psoriatic Skin and Its Association with Disease Improvement. <i>Cells</i> , 2020 , 9,	7.9	4
72	Rescue of Advanced Pompe Disease in Mice with Hepatic Expression of Secretable Acid Glucosidase. <i>Molecular Therapy</i> , 2020 , 28, 2056-2072	11.7	8
71	Photocatalytically Active Graphitic Carbon Nitride as an Effective and Safe 2D Material for In Vitro and In Vivo Photodynamic Therapy. <i>Small</i> , 2020 , 16, e1904619	11	35
70	Gene therapy with secreted acid alpha-glucosidase rescues Pompe disease in a novel mouse model with early-onset spinal cord and respiratory defects. <i>EBioMedicine</i> , 2020 , 61, 103052	8.8	3
69	Identification of a peripheral blood gene signature predicting aortic valve calcification. <i>Physiological Genomics</i> , 2020 , 52, 563-574	3.6	2
68	Sox17 Controls Emergence and Remodeling of Nestin-Expressing Coronary Vessels. <i>Circulation Research</i> , 2020 , 127, e252-e270	15.7	8
67	Caveolin1 and YAP drive mechanically induced mesothelial to mesenchymal transition and fibrosis. <i>Cell Death and Disease</i> , 2020 , 11, 647	9.8	22
66	PGC-1 β deficiency causes spontaneous kidney inflammation and increases the severity of nephrotoxic AKI. <i>Journal of Pathology</i> , 2019 , 249, 65-78	9.4	41
65	Coronary arterial development is regulated by a Dll4-Jag1-EphrinB2 signaling cascade. <i>ELife</i> , 2019 , 8,	8.9	14
64	regulates expression at the exit from pluripotency during gastrulation. <i>Biology Open</i> , 2019 , 8,	2.2	6
63	Von Hippel-Lindau Protein Is Required for Optimal Alveolar Macrophage Terminal Differentiation, Self-Renewal, and Function. <i>Cell Reports</i> , 2018 , 24, 1738-1746	10.6	14
62	Prokaryotic diversity and community composition in the Salar de Uyuni, a large scale, chaotrophic salt flat. <i>Environmental Microbiology</i> , 2017 , 19, 3745-3754	5.2	33

61	Global assessment of small RNAs reveals a non-coding transcript involved in biofilm formation and attachment in <i>Acinetobacter baumannii</i> ATCC 17978. <i>PLoS ONE</i> , 2017 , 12, e0182084	3.7	8
60	Myocardial VHL-HIF Signaling Controls an Embryonic Metabolic Switch Essential for Cardiac Maturation. <i>Developmental Cell</i> , 2016 , 39, 724-739	10.2	55
59	Sequential Ligand-Dependent Notch Signaling Activation Regulates Valve Primordium Formation and Morphogenesis. <i>Circulation Research</i> , 2016 , 118, 1480-97	15.7	66
58	Solar Radiation Stress in Natural Acidophilic Biofilms of <i>Euglena mutabilis</i> Revealed by Metatranscriptomics and PAM Fluorometry. <i>Protist</i> , 2016 , 167, 67-81	2.5	7
57	Whole-genome analysis of <i>Azoarcus</i> sp. strain CIB provides genetic insights to its different lifestyles and predicts novel metabolic features. <i>Systematic and Applied Microbiology</i> , 2015 , 38, 462-71	4.2	49
56	A model for the structure and mechanism of action of pulmonary surfactant protein B. <i>FASEB Journal</i> , 2015 , 29, 4236-47	0.9	41
55	Transcriptional response to copper excess and identification of genes involved in heavy metal tolerance in the extremophilic microalga <i>Chlamydomonas acidophila</i> . <i>Extremophiles</i> , 2015 , 19, 657-72	3	16
54	Telomerase Is Essential for Zebrafish Heart Regeneration. <i>Cell Reports</i> , 2015 , 12, 1691-703	10.6	56
53	Transposase interaction with the sliding clamp: effects on insertion sequence proliferation and transposition rate. <i>Scientific Reports</i> , 2015 , 5, 13329	4.9	7
52	Pyrosequencing-Based Assessment of the Microbial Community Structure of Pastoruri Glacier Area (Huascarán National Park, Peru), a Natural Extreme Acidic Environment. <i>Microbial Ecology</i> , 2015 , 70, 936-47	4.4	15
51	Complete Genome Sequence of the Multiresistant <i>Acinetobacter baumannii</i> Strain AbH12O-A2, Isolated during a Large Outbreak in Spain. <i>Genome Announcements</i> , 2014 , 2,		13
50	Nickel-resistance determinants in <i>Acidiphilium</i> sp. PM identified by genome-wide functional screening. <i>PLoS ONE</i> , 2014 , 9, e95041	3.7	10
49	Large-scale genomic analysis suggests a neutral punctuated dynamics of transposable elements in bacterial genomes. <i>PLoS Computational Biology</i> , 2014 , 10, e1003680	5	22
48	Deep subsurface sulfate reduction and methanogenesis in the Iberian Pyrite Belt revealed through geochemistry and molecular biomarkers. <i>Geobiology</i> , 2014 , 12, 34-47	4.3	20
47	Stage-specific differential gene expression in <i>Leishmania infantum</i> : from the foregut of <i>Phlebotomus perniciosus</i> to the human phagocyte. <i>BMC Genomics</i> , 2014 , 15, 849	4.5	21
46	Chromosomal replication dynamics and interaction with the sliding clamp determine orientation of bacterial transposable elements. <i>Genome Biology and Evolution</i> , 2014 , 6, 727-40	3.9	12
45	The Dynamic Genomes of Acidophiles. <i>Cellular Origin and Life in Extreme Habitats</i> , 2013 , 81-97		1
44	Metabolic potential of the organic-solvent tolerant <i>Pseudomonas putida</i> DOT-T1E deduced from its annotated genome. <i>Microbial Biotechnology</i> , 2013 , 6, 598-611	6.3	29

43	Whole transcriptome analysis of <i>Acinetobacter baumannii</i> assessed by RNA-sequencing reveals different mRNA expression profiles in biofilm compared to planktonic cells. <i>PLoS ONE</i> , 2013 , 8, e72968	3.7	96
42	Prokaryotic communities and operating metabolisms in the surface and the permafrost of Deception Island (Antarctica). <i>Environmental Microbiology</i> , 2012 , 14, 2495-510	5.2	32
41	Comparative genomic analysis reveals novel facts about <i>Leptospirillum</i> spp. cytochromes. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2012 , 22, 94-104	0.9	8
40	Exploring bacterial diversity in hospital environments by GS-FLX Titanium pyrosequencing. <i>PLoS ONE</i> , 2012 , 7, e44105	3.7	40
39	Partial and complete denitrification in <i>Thermus thermophilus</i> : lessons from genome drafts. <i>Biochemical Society Transactions</i> , 2011 , 39, 249-53	5.1	12
38	The pGRT1 plasmid of <i>Pseudomonas putida</i> DOT-T1E encodes functions relevant for survival under harsh conditions in the environment. <i>Environmental Microbiology</i> , 2011 , 13, 2315-27	5.2	40
37	A microbial oasis in the hypersaline Atacama subsurface discovered by a life detector chip: implications for the search for life on Mars. <i>Astrobiology</i> , 2011 , 11, 969-96	3.7	90
36	Draft genome sequence of the electricigen <i>Acidiphilium</i> sp. strain PM (DSM 24941). <i>Journal of Bacteriology</i> , 2011 , 193, 5585-6	3.5	19
35	Complete genome of the plant growth-promoting rhizobacterium <i>Pseudomonas putida</i> BIRD-1. <i>Journal of Bacteriology</i> , 2011 , 193, 1290	3.5	45
34	Lateral transfer of the denitrification pathway genes among <i>Thermus thermophilus</i> strains. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 1352-8	4.8	28
33	Temperature increase prevails over acidification in gene expression modulation of amastigote differentiation in <i>Leishmania infantum</i> . <i>BMC Genomics</i> , 2010 , 11, 31	4.5	50
32	Environmental transcriptome analysis reveals physiological differences between biofilm and planktonic modes of life of the iron oxidizing bacteria <i>Leptospirillum</i> spp. in their natural microbial community. <i>BMC Genomics</i> , 2010 , 11, 404	4.5	53
31	Transcriptomics throughout the life cycle of <i>Leishmania infantum</i> : high down-regulation rate in the amastigote stage. <i>International Journal for Parasitology</i> , 2010 , 40, 1497-516	4.3	54
30	The <i>Mycobacterium tuberculosis</i> sigma factor sigmaB is required for full response to cell envelope stress and hypoxia in vitro, but it is dispensable for in vivo growth. <i>Journal of Bacteriology</i> , 2009 , 191, 5628-33	3.5	55
29	Genome-wide analysis reveals increased levels of transcripts related with infectivity in peanut lectin non-agglutinated promastigotes of <i>Leishmania infantum</i> . <i>Genomics</i> , 2009 , 93, 551-64	4.3	40
28	The environmental fate of organic pollutants through the global microbial metabolism. <i>Molecular Systems Biology</i> , 2007 , 3, 114	12.2	38
27	Scoring docking models with evolutionary information. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 60, 275-80	4.2	37
26	Accessible Protein Interaction Data for Network Modeling. Structure of the Information and Available Repositories. <i>Lecture Notes in Computer Science</i> , 2005 , 1-13	0.9	2

25	The Biodegradation Network, a New Scenario for Computational Systems Biology Research. <i>Lecture Notes in Computer Science</i> , 2005 , 252-256	0.9	
24	Hyperglycosylation of glycopeptidolipid of <i>Mycobacterium smegmatis</i> under nutrient starvation: structural studies. <i>Microbiology (United Kingdom)</i> , 2005 , 151, 2385-2392	2.9	28
23	Gene order in Prokaryotes: conservation and implications 2004 , 209-237		2
22	Prediction of Functional Sites in Proteins by Evolutionary Methods. <i>Principles and Practice</i> , 2004 , 319-340		7
21	Role of the extracytoplasmic-function sigma factor sigma(H) in <i>Mycobacterium tuberculosis</i> global gene expression. <i>Molecular Microbiology</i> , 2002 , 45, 365-74	4.1	227
20	Characterization of the secreted MPT53 antigen of <i>Mycobacterium tuberculosis</i> . <i>Infection and Immunity</i> , 2001 , 69, 5936-9	3.7	10
19	Identification of secreted proteins of <i>Mycobacterium tuberculosis</i> by a bioinformatic approach. <i>Infection and Immunity</i> , 2000 , 68, 2323-7	3.7	91
18	Use of coagulase gene (coa) repeat region nucleotide sequences for typing of methicillin-resistant <i>Staphylococcus aureus</i> strains. <i>Journal of Clinical Microbiology</i> , 2000 , 38, 3453-6	9.7	69
17	Evaluation of protein A gene polymorphic region DNA sequencing for typing of <i>Staphylococcus aureus</i> strains. <i>Journal of Clinical Microbiology</i> , 1999 , 37, 3556-63	9.7	799
16	Identification and characterization of two divergently transcribed iron regulated genes in <i>Mycobacterium tuberculosis</i> . <i>Tubercle and Lung Disease</i> , 1999 , 79, 287-98		46
15	mraW, an essential gene at the dcw cluster of <i>Escherichia coli</i> codes for a cytoplasmic protein with methyltransferase activity. <i>Biochimie</i> , 1999 , 81, 879-88	4.6	30
14	Transcriptional control of the iron-responsive fxbA gene by the mycobacterial regulator IdeR. <i>Journal of Bacteriology</i> , 1999 , 181, 3402-8	3.5	78
13	Extra and intracellular expression of <i>Mycobacterium tuberculosis</i> genes. <i>Tubercle and Lung Disease</i> , 1998 , 79, 91-7		12
12	Regulation of transcription of cell division genes in the <i>Escherichia coli</i> dcw cluster. <i>Cellular and Molecular Life Sciences</i> , 1998 , 54, 317-24	10.3	58
11	sigA is an essential gene in <i>Mycobacterium smegmatis</i> . <i>Molecular Microbiology</i> , 1998 , 29, 617-28	4.1	70
10	Identification of a new sigmaB-controlled gene, csbX, in <i>Bacillus subtilis</i> . <i>Gene</i> , 1997 , 188, 29-33	3.8	7
9	Expression of the <i>Bacillus subtilis</i> spoIVB gene is under dual sigma F/sigma G control. <i>Microbiology (United Kingdom)</i> , 1996 , 142 (Pt 12), 3453-7	2.9	21
8	Transcription of spoIVB is the only role of sigma G that is essential for pro-sigma K processing during spore formation in <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 1995 , 177, 4825-7	3.5	36

7	Variations in the Metabolism of Peptidoglycan Prior to Polymerization 1993 , 127-138		
6	Involvement of the NH ₂ - and COOH-Terminal ends of PBP3 of Escherichia coli on β -Lactam Binding, Membrane Localization, and Function of the Protein 1993 , 309-318		1
5	Membrane intermediates in the peptidoglycan metabolism of Escherichia coli: possible roles of PBP 1b and PBP 3. <i>Journal of Bacteriology</i> , 1992 , 174, 3549-57	3.5	133
4	Nucleotide sequence of the regulatory region of the gene pbpB of Escherichia coli. <i>Nucleic Acids Research</i> , 1990 , 18, 2813	20.1	7
3	A new beta-lactam-binding protein derived from penicillin-binding protein 3 of Escherichia coli. <i>Journal of Bacteriology</i> , 1989 , 171, 5194-8	3.5	9
2	Evaluation of glycosylated hemoglobin diabetic patients. <i>Diabetes</i> , 1981 , 30, 613-7	0.9	249
1	Gene Expression and Regulation 59-92		3