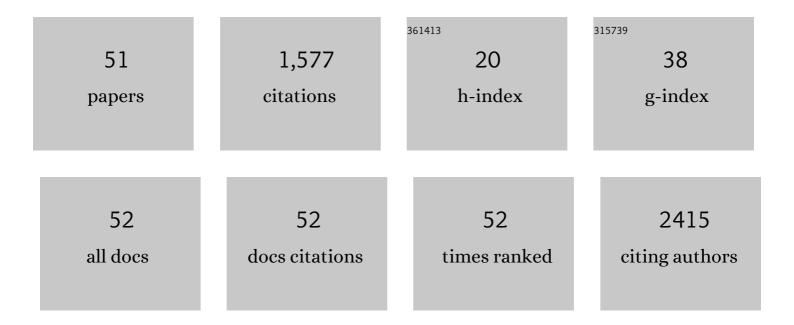
Gabriel Gutiérrez Pozo

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. Current Biology, 2016, 26, 1577-1584.	3.9	175
2	A Phylogenetic Analysis of the Lipocalin Protein Family. Molecular Biology and Evolution, 2000, 17, 114-126.	8.9	136
3	Exon-Intron Structure and Evolution of the Lipocalin Gene Family. Molecular Biology and Evolution, 2003, 20, 775-783.	8.9	90
4	The Histone Acetyltransferase GcnE (GCN5) Plays a Central Role in the Regulation of <i>Aspergillus</i> Asexual Development. Genetics, 2014, 197, 1175-1189.	2.9	79
5	Fungal cryptochrome with DNA repair activity reveals an early stage in cryptochrome evolution. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 15130-15135.	7.1	72
6	A Reanalysis of the Ancient Mitochondrial DNA Sequences Recovered from Neandertal Bones. Molecular Biology and Evolution, 2002, 19, 1359-1366.	8.9	68
7	Defective histone supply causes changes in RNA polymerase II elongation rate and cotranscriptional pre-mRNA splicing. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14840-14845.	7.1	68
8	Molecular evolution of epididymal lipocalin genes localized on mouse chromosome 2. Gene, 2004, 339, 49-59.	2.2	67
9	MicroRNA-Dependent Regulation of Transcription in Non-Small Cell Lung Cancer. PLoS ONE, 2014, 9, e90524.	2.5	65
10	Apolipoprotein D alters the early transcriptional response to oxidative stress in the adult cerebellum. Journal of Neurochemistry, 2011, 117, 949-960.	3.9	49
11	Preference for guanosine at first codon position in highly expressed Escherichia coli genes. A relationship with translational efficiency. Nucleic Acids Research, 1996, 24, 2525-2527.	14.5	47
12	Evolution of the lipocalin family as inferred from a protein sequence phylogeny. BBA - Proteins and Proteomics, 2000, 1482, 35-45.	2.1	43
13	A Relationship between Carotenoid Accumulation and the Distribution of Species of the Fungus Neurospora in Spain. PLoS ONE, 2012, 7, e33658.	2.5	43
14	Downregulation of Lnc-Spry1 mediates TGF-β-induced epithelial–mesenchymal transition by transcriptional and posttranscriptional regulatory mechanisms. Cell Death and Differentiation, 2017, 24, 785-797.	11.2	43
15	On the Origin of the Periodicity of Three in Protein Coding DNA Sequences. Journal of Theoretical Biology, 1994, 167, 413-414.	1.7	40
16	Relationship between G+C content, ORF-length and mRNA concentration inSaccharomyces cerevisiae. Yeast, 2003, 20, 703-711.	1.7	40
17	Comparative gene expression profile of mouse carotid body and adrenal medulla under physiological hypoxia. Journal of Physiology, 2005, 566, 491-503.	2.9	37
18	Patterns of Group I Intron Presence in Nuclear SSU rDNA of the Lichen Family Parmeliaceae. Journal of Molecular Evolution, 2007, 64, 181-195.	1.8	33

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19	MAP17 (PDZKIP1) Expression Determines Sensitivity to the Proteasomal Inhibitor Bortezomib by Preventing Cytoprotective Autophagy and NFήB Activation in Breast Cancer. Molecular Cancer Therapeutics, 2015, 14, 1454-1465.	4.1	26
20	Compositional heterogeneity of the Escherichia coli genome: A role for VSP repair?. Journal of Molecular Evolution, 1994, 39, 340-346.	1.8	23
21	Expression and potential role of apolipoprotein D on the death–survival balance of human colorectal cancer cells under oxidative stress conditions. International Journal of Colorectal Disease, 2013, 28, 751-766.	2.2	23
22	A New Species of the Î ³ -Proteobacterium Francisella, F. adeliensis Sp. Nov., Endocytobiont in an Antarctic Marine Ciliate and Potential Evolutionary Forerunner of Pathogenic Species. Microbial Ecology, 2019, 77, 587-596.	2.8	22
23	Contribution of DNA adenine methylation to gene expression heterogeneity in <i>Salmonella enterica</i> . Nucleic Acids Research, 2020, 48, 11857-11867.	14.5	21
24	The DASH-type Cryptochrome from the Fungus Mucor circinelloides Is a Canonical CPD-Photolyase. Current Biology, 2020, 30, 4483-4490.e4.	3.9	19
25	Transcriptional regulation of fermentative and respiratory metabolism in Saccharomyces cerevisiae industrial bakers' strains. FEMS Yeast Research, 2012, 12, 625-636.	2.3	18
26	Genome sequencing of evolved aspergilli populations reveals robust genomes, transversions in A. flavus, and sexual aberrancy in non-homologous end-joining mutants. BMC Biology, 2019, 17, 88.	3.8	18
27	Subtracting the sequence bias from partially digested MNase-seq data reveals a general contribution of TFIIS to nucleosome positioning. Epigenetics and Chromatin, 2017, 10, 58.	3.9	17
28	Formation of phenotypic lineages in Salmonella enterica by a pleiotropic fimbrial switch. PLoS Genetics, 2018, 14, e1007677.	3.5	17
29	Ubiquitin and Ubiquitin-Like Proteins and Domains in Ribosome Production and Function: Chance or Necessity?. International Journal of Molecular Sciences, 2021, 22, 4359.	4.1	17
30	Global impact of Salmonella type III secretion effector SteA on host cells. Biochemical and Biophysical Research Communications, 2014, 449, 419-424.	2.1	15
31	Identification of Pelomyxa palustris Endosymbionts. Protist, 2017, 168, 408-424.	1.5	15
32	Draft Genome Sequence of Methanobacterium formicicum DSM 3637, an Archaebacterium Isolated from the Methane Producer Amoeba Pelomyxa palustris. Journal of Bacteriology, 2012, 194, 6967-6968.	2.2	14
33	Short-range compositional correlation in the yeast genome depends on transcriptional orientation. Gene, 2004, 333, 151-155.	2.2	13
34	Xrn1 influence on gene transcription results from the combination of general effects on elongating RNA pol II and gene-specific chromatin configuration. RNA Biology, 2021, 18, 1310-1323.	3.1	12
35	Gene length and codon usage bias in Drosophila melanogaster, Saccharomyces cervisiae and Escherichia coli. Nucleic Acids Research, 1998, 26, 4540-4540.	14.5	11
36	A Comparison of Morphological, Chemical and Molecular Characters in Some Parmelioid Genera. Lichenologist, 1999, 31, 451-460.	0.8	11

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37	Lack of reelin modifies the gene expression in the small intestine of mice. Journal of Physiology and Biochemistry, 2012, 68, 205-218.	3.0	10
38	Light regulates a Phycomyces blakesleeanus gene family similar to the carotenogenic repressor gene of Mucor circinelloides. Fungal Biology, 2020, 124, 338-351.	2.5	10
39	Phylogeny and regulation of four lipocalin genes clustered in the chicken genome: evidence of a functional diversification after gene duplication. Gene, 2004, 331, 95-106.	2.2	9
40	Impact of the White Collar Photoreceptor WcoA on the Fusarium fujikuroi Transcriptome. Frontiers in Microbiology, 2020, 11, 619474.	3.5	9
41	An Evolutionary Perspective of the Lipocalin Protein Family. Frontiers in Physiology, 2021, 12, 718983.	2.8	9
42	A novel lncRNA as a positive regulator of carotenoid biosynthesis in Fusarium. Scientific Reports, 2020, 10, 678.	3.3	8
43	Control of the neuroprotective Lipocalin Apolipoprotein D expression by alternative promoter regions and differentially expressed mRNA 5' UTR variants. PLoS ONE, 2020, 15, e0234857.	2.5	4
44	Compound Heterozygous Mutations in the <i>SLC26A3</i> Gene in 2 Spanish Siblings With Congenital Chloride Diarrhea. Journal of Pediatric Gastroenterology and Nutrition, 2011, 52, 106-110.	1.8	3
45	A possible relationship between vsp mismatch repair and gene expression level. Journal of Molecular Evolution, 1996, 43, 161-163.	1.8	2
46	Characterization of mammalian Lipocalin UTRs in silico: Predictions for their role in post-transcriptional regulation. PLoS ONE, 2019, 14, e0213206.	2.5	2
47	An <i>arsRB</i> resistance operon confers tolerance to arsenite in the environmental isolate <i>Terribacillus</i> sp. AE2B 122. FEMS Microbiology Ecology, 2021, 97, .	2.7	2
48	Compositional Correlation Between Open Reading Frames with Opposite Transcriptional Orientations in Escherichia coli. Journal of Molecular Evolution, 1999, 48, 712-716.	1.8	0
49	The carP IncRNA Is a carS-Related Regulatory Element with Broad Effects on the Fusarium fujikuroi Transcriptome. Non-coding RNA, 2021, 7, 46.	2.6	Ο
50	LETTER TO THE EDITOR - The Mysterious Case of the Reverse Sequences. The Open Genomics Journal, 2011, 4, 16-17.	0.5	0
51	Identification of an acetyl esterase in the supernatant of the environmental strain Bacillus sp. HR21-6. Biochimie, 2022, 198, 48-59.	2.6	0