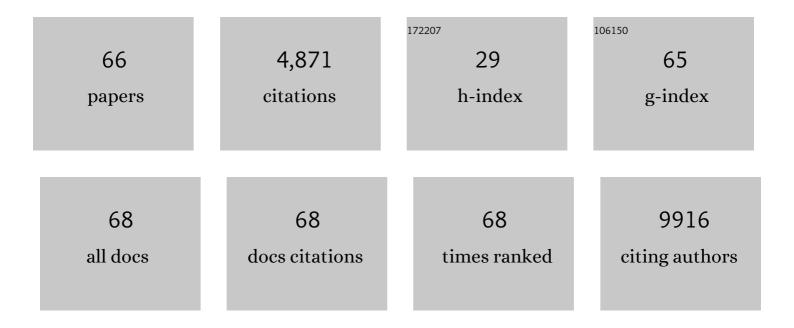
Francesc LÃ³pez-GirÃ;ldez

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1185865/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	De novo mutations in congenital heart disease with neurodevelopmental and other congenital anomalies. Science, 2015, 350, 1262-1266.	6.0	646
2	The Ascomycota Tree of Life: A Phylum-wide Phylogeny Clarifies the Origin and Evolution of Fundamental Reproductive and Ecological Traits. Systematic Biology, 2009, 58, 224-239.	2.7	581
3	The Genetic Basis of Mendelian Phenotypes: Discoveries, Challenges, and Opportunities. American Journal of Human Genetics, 2015, 97, 199-215.	2.6	574
4	Myofibroblast proliferation and heterogeneity are supported by macrophages during skin repair. Science, 2018, 362, .	6.0	318
5	Phylogenetic and phylogenomic overview of the Polyporales. Mycologia, 2013, 105, 1350-1373.	0.8	259
6	PhyDesign: an online application for profiling phylogenetic informativeness. BMC Evolutionary Biology, 2011, 11, 152.	3.2	174
7	Dermal Adipocyte Lipolysis and Myofibroblast Conversion Are Required for Efficient Skin Repair. Cell Stem Cell, 2020, 26, 880-895.e6.	5.2	154
8	In vivo correction of anaemia in Î ² -thalassemic mice by Î ³ PNA-mediated gene editing with nanoparticle delivery. Nature Communications, 2016, 7, 13304.	5.8	143
9	A multigene phylogeny toward a new phylogenetic classification of Leotiomycetes. IMA Fungus, 2019, 10, 1.	1.7	140
10	In utero nanoparticle delivery for site-specific genome editing. Nature Communications, 2018, 9, 2481.	5.8	124
11	De Novo Mutation in Genes Regulating Neural Stem Cell Fate in Human Congenital Hydrocephalus. Neuron, 2018, 99, 302-314.e4.	3.8	112
12	Mutations disrupting neuritogenesis genes confer risk for cerebral palsy. Nature Genetics, 2020, 52, 1046-1056.	9.4	96
13	PD-1H (VISTA)–mediated suppression of autoimmunity in systemic and cutaneous lupus erythematosus. Science Translational Medicine, 2019, 11, .	5.8	90
14	E2F8 as a Novel Therapeutic Target for Lung Cancer. Journal of the National Cancer Institute, 2015, 107,	3.0	80
15	Transcriptome analyses during fruiting body formation in Fusarium graminearum and Fusarium verticillioides reflect species life history and ecology. Fungal Genetics and Biology, 2012, 49, 663-673.	0.9	78
16	Identification of Intrinsic Axon Growth Modulators for Intact CNS Neurons after Injury. Cell Reports, 2017, 18, 2687-2701.	2.9	73
17	Optimal Selection of Gene and Ingroup Taxon Sampling for Resolving Phylogenetic Relationships. Systematic Biology, 2010, 59, 446-457.	2.7	70
18	RBE controls microRNA164 expression to effect floral organogenesis. Development (Cambridge), 2012, 139, 2161-2169.	1.2	69

#	Article	IF	CITATIONS
19	Global Gene Expression and Focused Knockout Analysis Reveals Genes Associated with Fungal Fruiting Body Development in Neurospora crassa. Eukaryotic Cell, 2014, 13, 154-169.	3.4	66
20	The Phylogenetic Informativeness of Nucleotide and Amino Acid Sequences for Reconstructing the Vertebrate Tree. Journal of Molecular Evolution, 2008, 67, 437-447.	0.8	61
21	Mutations in Chromatin Modifier and Ephrin Signaling Genes in Vein of Galen Malformation. Neuron, 2019, 101, 429-443.e4.	3.8	56
22	Molecular chaperone Hsp110 rescues a vesicle transport defect produced by an ALS-associated mutant SOD1 protein in squid axoplasm. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 5428-5433.	3.3	49
23	Differential functional roles of fibroblasts and pericytes in the formation of tissue-engineered microvascular networks in vitro. Npj Regenerative Medicine, 2020, 5, 1.	2.5	48
24	Adult bone marrow progenitors become decidual cells and contribute to embryo implantation and pregnancy. PLoS Biology, 2019, 17, e3000421.	2.6	47
25	Gene Expression Differences among Three Neurospora Species Reveal Genes Required for Sexual Reproduction in Neurospora crassa. PLoS ONE, 2014, 9, e110398.	1.1	39
26	Assessing the Role of Tandem Repeats in Shaping the Genomic Architecture of Great Apes. PLoS ONE, 2011, 6, e27239.	1.1	35
27	RPS4Ygene family evolution in primates. BMC Evolutionary Biology, 2008, 8, 142.	3.2	33
28	<i>DIAPH1</i> Variants in Non–East Asian Patients With Sporadic Moyamoya Disease. JAMA Neurology, 2021, 78, 993.	4.5	33
29	Macrophage IL-1β promotes arteriogenesis by autocrine STAT3- and NF-κB-mediated transcription of pro-angiogenic VEGF-A. Cell Reports, 2022, 38, 110309.	2.9	33
30	Tasting Soil Fungal Diversity with Earth Tongues: Phylogenetic Test of SATé Alignments for Environmental ITS Data. PLoS ONE, 2011, 6, e19039.	1.1	32
31	A Locus Encompassing the Epstein-Barr Virus bglf4 Kinase Regulates Expression of Genes Encoding Viral Structural Proteins. PLoS Pathogens, 2014, 10, e1004307.	2.1	32
32	Exome Sequencing Implicates Impaired GABA Signaling and Neuronal Ion Transport in Trigeminal Neuralgia. IScience, 2020, 23, 101552.	1.9	32
33	Sex-specific gene expression during asexual development of Neurospora crassa. Fungal Genetics and Biology, 2012, 49, 533-543.	0.9	31
34	LOX: inferring Level Of eXpression from diverse methods of census sequencing. Bioinformatics, 2010, 26, 1918-1919.	1.8	30
35	Targeted protein unfolding uncovers a Golgi-specific transcriptional stress response. Molecular Biology of the Cell, 2018, 29, 1284-1298.	0.9	30
36	The Epstein-Barr Virus Immunoevasins BCRF1 and BPLF1 Are Expressed by a Mechanism Independent of the Canonical Late Pre-initiation Complex. PLoS Pathogens, 2016, 12, e1006008.	2.1	29

#	Article	IF	CITATIONS
37	The Ulp2 <scp>SUMO</scp> protease promotes transcription elongation through regulation of histone sumoylation. EMBO Journal, 2019, 38, e102003.	3.5	28
38	Implication of DNA repair genes in Lynch-like syndrome. Familial Cancer, 2019, 18, 331-342.	0.9	25
39	Genetic Defects in DNAH2 Underlie Male Infertility With Multiple Morphological Abnormalities of the Sperm Flagella in Humans and Mice. Frontiers in Cell and Developmental Biology, 2021, 9, 662903.	1.8	22
40	Distinct adaptive mechanisms drive recovery from aneuploidy caused by loss of the Ulp2 SUMO protease. Nature Communications, 2018, 9, 5417.	5.8	21
41	Metabolism and Development during Conidial Germination in Response to a Carbon-Nitrogen-Rich Synthetic or a Natural Source of Nutrition in <i>Neurospora crassa</i> . MBio, 2019, 10, .	1.8	21
42	Badger hair in shaving brushes comes from protected Eurasian badgers. Biological Conservation, 2006, 128, 425-430.	1.9	20
43	Genetic distinction of American and European mink (Mustela vison and M. lutreola) and European polecat (M. putorius) hair samples by detection of a species-specific SINE and a RFLP assay. Journal of Zoology, 2005, 265, 405-410.	0.8	18
44	Measuring Transcription Factor–Binding Site Turnover: A Maximum Likelihood Approach Using Phylogenies. Genome Biology and Evolution, 2009, 1, 85-98.	1.1	17
45	Evaluating Phylogenetic Informativeness as a Predictor of Phylogenetic Signal for Metazoan, Fungal, and Mammalian Phylogenomic Data Sets. BioMed Research International, 2013, 2013, 1-14.	0.9	17
46	Alternative genomic diagnoses for individuals with a clinical diagnosis of Dubowitz syndrome. American Journal of Medical Genetics, Part A, 2021, 185, 119-133.	0.7	17
47	Progenitor-derived human endothelial cells evade alloimmunity by CRISPR/Cas9-mediated complete ablation of MHC expression. JCI Insight, 2019, 4, .	2.3	17
48	Analyses of carnivore microsatellites and their intimate association with tRNA-derived SINEs. BMC Genomics, 2006, 7, 269.	1.2	16
49	Interferon-Î ³ converts human microvascular pericytes into negative regulators of alloimmunity through induction of indoleamine 2,3-dioxygenase 1. JCI Insight, 2018, 3, .	2.3	16
50	Phylogenetic inference and comparative evolution of a complex microsatellite and its flanking regions in carnivores. Genetical Research, 2005, 85, 223-233.	0.3	14
51	Multi-targeted priming for genome-wide gene expression assays. BMC Genomics, 2010, 11, 477.	1.2	14
52	Insulin-stimulated endoproteolytic TUG cleavage links energy expenditure with glucose uptake. Nature Metabolism, 2021, 3, 378-393.	5.1	13
53	Tumor necrosis factorâ€induced ArhGEF10 selectively activates RhoB contributing to human microvascular endothelial cell tight junction disruption. FASEB Journal, 2021, 35, e21627.	0.2	10
54	Tumor progression and chromatin landscape of lung cancer are regulated by the lineage factor GATA6. Oncogene, 2020, 39, 3726-3737.	2.6	9

#	Article	IF	CITATIONS
55	CCM3 Loss-Induced Lymphatic Defect Is Mediated by the Augmented VEGFR3-ERK1/2 Signaling. Arteriosclerosis, Thrombosis, and Vascular Biology, 2021, 41, 2943-2960.	1.1	9
56	Congenital Heart Defects Due to <i>TAF1</i> Missense Variants. Circulation Genomic and Precision Medicine, 2020, 13, e002843.	1.6	8
57	High Incidence of Nonslippage Mechanisms Generating Variability and Complexity in Eurasian Badger Microsatellites. Journal of Heredity, 2007, 98, 620-628.	1.0	7
58	Integrative Activity of Mating Loci, Environmentally Responsive Genes, and Secondary Metabolism Pathways during Sexual Development of Chaetomium globosum. MBio, 2019, 10, .	1.8	7
59	Comparative Genomics within and across Bilaterians Illuminates the Evolutionary History of ALK and LTK Proto-Oncogene Origination and Diversification. Genome Biology and Evolution, 2021, 13, .	1.1	6
60	The role of SPAG1 in the assembly of axonemal dyneins in human airway epithelia. Journal of Cell Science, 2022, 135, .	1.2	5
61	Identification and functional characterization of natural human melanocortin 1 receptor mutant alleles in Pakistani population. Pigment Cell and Melanoma Research, 2015, 28, 730-735.	1.5	4
62	Genomic and Immune Profiling of a Patient With Triple-Negative Breast Cancer That Progressed During Neoadjuvant Chemotherapy Plus PD-L1 Blockade. JCO Precision Oncology, 2019, 3, 1-6.	1.5	3
63	ArhGEF12 activates Rap1A and not RhoA in human dermal microvascular endothelial cells to reduce tumor necrosis factorâ€induced leak. FASEB Journal, 2022, 36, e22254.	0.2	3
64	Whole-exome sequencing reveals damaging gene variants associated with hypoalphalipoproteinemia. Journal of Lipid Research, 2022, 63, 100209.	2.0	2
65	Secondary Metabolism Gene Clusters Exhibit Increasingly Dynamic and Differential Expression during Asexual Growth, Conidiation, and Sexual Development in Neurospora crassa. MSystems, 2022, 7, .	1.7	2
66	Whole-Exome Sequencing of Germline Variants in Non-BRCA Families with Hereditary Breast Cancer. Biomedicines, 2022, 10, 1004.	1.4	1