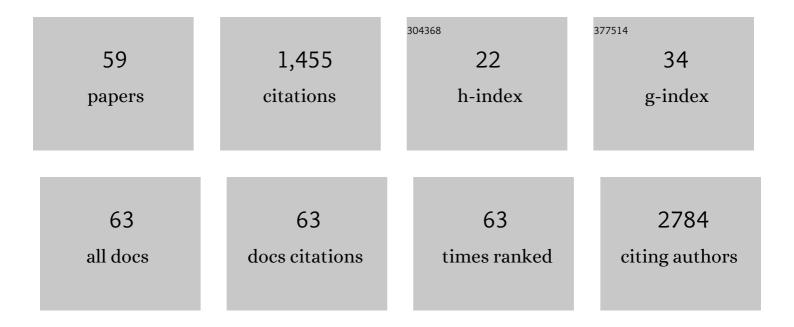
Jacobo J Pardo-Seco

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Nonspecific (Heterologous) Protection of Neonatal BCG Vaccination Against Hospitalization Due to Respiratory Infection and Sepsis. Clinical Infectious Diseases, 2015, 60, 1611-1619.	2.9	173
2	Mapping genome variation of SARS-CoV-2 worldwide highlights the impact of COVID-19 super-spreaders. Genome Research, 2020, 30, 1434-1448.	2.4	91
3	Life-threatening infections in children in Europe (the EUCLIDS Project): a prospective cohort study. The Lancet Child and Adolescent Health, 2018, 2, 404-414.	2.7	69
4	Viral Co-Infections in Pediatric Patients Hospitalized with Lower Tract Acute Respiratory Infections. PLoS ONE, 2015, 10, e0136526.	1.1	67
5	Incidence and risk factor prevalence of community-acquired pneumonia in adults in primary care in Spain (NEUMO-ES-RISK project). BMC Infectious Diseases, 2016, 16, 645.	1.3	64
6	The peopling of South America and the trans-Andean gene flow of the first settlers. Genome Research, 2018, 28, 767-779.	2.4	59
7	Does Viral Co-Infection Influence the Severity of Acute Respiratory Infection in Children?. PLoS ONE, 2016, 11, e0152481.	1.1	46
8	The Genetic Legacy of the Pre-Colonial Period in Contemporary Bolivians. PLoS ONE, 2013, 8, e58980.	1.1	42
9	Development and Validation of a New Clinical Scale for Infants with Acute Respiratory Infection: The ReSVinet Scale. PLoS ONE, 2016, 11, e0157665.	1.1	41
10	Impact of Rotavirus Vaccination on Childhood Hospitalization for Seizures. Pediatric Infectious Disease Journal, 2015, 34, 769-773.	1.1	40
11	Bacteremia in Children Hospitalized with Respiratory Syncytial Virus Infection. PLoS ONE, 2016, 11, e0146599.	1.1	36
12	Phylogeography of SARS-CoV-2 pandemic in Spain: a story of multiple introductions, micro-geographic stratification, founder effects, and super-spreaders. Zoological Research, 2020, 41, 605-620.	0.9	34
13	Natural resistance to Meningococcal Disease related to CFH loci: Meta-analysis of genome-wide association studies. Scientific Reports, 2016, 6, 35842.	1.6	33
14	Rotavirus infection beyond the gut. Infection and Drug Resistance, 2019, Volume 12, 55-64.	1.1	32
15	The complete mitogenome of a 500-year-old Inca child mummy. Scientific Reports, 2015, 5, 16462.	1.6	31
16	Superspreading in the emergence of COVID-19 variants. Trends in Genetics, 2021, 37, 1069-1080.	2.9	31
17	Evaluating the accuracy of AIM panels at quantifying genome ancestry. BMC Genomics, 2014, 15, 543.	1.2	29
18	Whole Exome Sequencing reveals new candidate genes in host genomic susceptibility to Respiratory Syncytial Virus Disease. Scientific Reports, 2017, 7, 15888.	1.6	29

JACOBO J PARDO-SECO

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19	The Burden of Pediatric Invasive Meningococcal Disease in Spain (2008–2013). Pediatric Infectious Disease Journal, 2016, 35, 407-413.	1.1	27
20	A qPCR expression assay of IFI44L gene differentiates viral from bacterial infections in febrile children. Scientific Reports, 2019, 9, 11780.	1.6	27
21	Ancestry analysis reveals a predominant Native American component with moderate European admixture in Bolivians. Forensic Science International: Genetics, 2013, 7, 537-542.	1.6	26
22	Indian Signatures in the Westernmost Edge of the European Romani Diaspora: New Insight from Mitogenomes. PLoS ONE, 2013, 8, e75397.	1.1	24
23	A Genome-Wide Study of Modern-Day Tuscans: Revisiting Herodotus's Theory on the Origin of the Etruscans. PLoS ONE, 2014, 9, e105920.	1.1	23
24	A multi-tissue study of immune gene expression profiling highlights the key role of the nasal epithelium in COVID-19 severity. Environmental Research, 2022, 210, 112890.	3.7	23
25	A 2-transcript host cell signature distinguishes viral from bacterial diarrhea and it is influenced by the severity of symptoms. Scientific Reports, 2018, 8, 8043.	1.6	20
26	Development and Evaluation of the Ancestry Informative Marker Panel of the VISAGE Basic Tool. Genes, 2021, 12, 1284.	1.0	20
27	The geographic mosaic of Ecuadorian Y-chromosome ancestry. Forensic Science International: Genetics, 2018, 33, 59-65.	1.6	19
28	Lifestyle and comorbid conditions as risk factors for community-acquired pneumonia in outpatient adults (NEUMO-ES-RISK project). BMJ Open Respiratory Research, 2019, 6, e000359.	1.2	19
29	Seroprevalence of SARS-CoV-2 Among Pediatric Healthcare Workers in Spain. Frontiers in Pediatrics, 2020, 8, 547.	0.9	19
30	The multiethnic ancestry of Bolivians as revealed by the analysis of Y-chromosome markers. Forensic Science International: Genetics, 2015, 14, 210-218.	1.6	18
31	Phylogeographic and genome-wide investigations of Vietnam ethnic groups reveal signatures of complex historical demographic movements. Scientific Reports, 2017, 7, 12630.	1.6	17
32	Ancestry patterns inferred from massive RNA-seq data. Rna, 2019, 25, 857-868.	1.6	16
33	Mitogenomes from The 1000 Genome Project Reveal New Near Eastern Features in Present-Day Tuscans. PLoS ONE, 2015, 10, e0119242.	1.1	15
34	Clinical respiratory scales: which one should we use?. Expert Review of Respiratory Medicine, 2017, 11, 1-19.	1.0	13
35	Role of Vitamin D in Hospitalized Children With Lower Tract Acute Respiratory Infections. Journal of Pediatric Gastroenterology and Nutrition, 2016, 62, 479-485.	0.9	12
36	Analysis of Y-chromosome STRs in Chile confirms an extensive introgression of European male lineages in urban populations. Forensic Science International: Genetics, 2016, 21, 76-80.	1.6	12

JACOBO J PARDO-SECO

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37	Impact of rotavirus vaccination on childhood hospitalizations for seizures: Heterologous or unforeseen direct vaccine effects?. Vaccine, 2019, 37, 3362-3368.	1.7	11
38	A Generalized Model to Estimate the Statistical Power in Mitochondrial Disease Studies Involving 2×k Tables. PLoS ONE, 2013, 8, e73567.	1.1	11
39	Charting the Y-chromosome ancestry of present-day Argentinean Mennonites. Journal of Human Genetics, 2016, 61, 507-513.	1.1	10
40	BCG vaccination improves DTaP immune responses in mice and is associated with lower pertussis incidence in ecological epidemiological studies. EBioMedicine, 2021, 65, 103254.	2.7	10
41	Mapping the genomic mosaic of two â€~Afro-Bolivians' from the isolated Yungas valleys. BMC Genomics, 2016, 17, 207.	1.2	9
42	A comprehensive Y-STR portrait of Argentinean populations. Forensic Science International: Genetics, 2016, 20, 1-5.	1.6	9
43	Whole Exome Sequencing Identifies New Host Genomic Susceptibility Factors in Empyema Caused by Streptococcus pneumoniae in Children: A Pilot Study. Genes, 2018, 9, 240.	1.0	9
44	The Genomic Legacy of the Transatlantic Slave Trade in the Yungas Valley of Bolivia. PLoS ONE, 2015, 10, e0134129.	1.1	8
45	Biogeographical origin and timing of the founder ichthyosis TGM1 c.1187G > A mutation in an isolate Ecuadorian population. Scientific Reports, 2019, 9, 7175.	d 1.6	7
46	Pitfalls of barcodes in the study of worldwide SARS-CoV-2 variation and phylodynamics. Zoological Research, 2021, 42, 87-93.	0.9	7
47	Identification of a Minimal 3-Transcript Signature to Differentiate Viral from Bacterial Infection from Best Genome-Wide Host RNA Biomarkers: A Multi-Cohort Analysis. International Journal of Molecular Sciences, 2021, 22, 3148.	1.8	6
48	Rotavirus intestinal infection induces an oral mucosa cytokine response. PLoS ONE, 2018, 13, e0195314.	1.1	5
49	Y-chromosome Peruvian origin of the 500-year-old Inca child mummy sacrificed in Cerro Aconcagua (Argentina). Science Bulletin, 2018, 63, 1457-1459.	4.3	5
50	<p>Further considerations on rotavirus vaccination and seizure-related hospitalization rates</p> . Infection and Drug Resistance, 2019, Volume 12, 989-991.	1.1	5
51	Routine infant vaccination of pneumococcal conjugate vaccines has decreased pneumonia across all age groups in Northern Spain. Human Vaccines and Immunotherapeutics, 2020, 16, 1446-1453.	1.4	5
52	CovidPhy: A tool for phylogeographic analysis of SARS-CoV-2 variation. Environmental Research, 2022, 204, 111909.	3.7	5
53	Genomic continuity of Argentinean Mennonites. Scientific Reports, 2016, 6, 36392.	1.6	4
54	Salivary epidermal growth factor correlates with hospitalization length in rotavirus infection. BMC Infectious Diseases, 2017, 17, 370.	1.3	4

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55	Evaluation of BNT162b2 Vaccine Effectiveness in Galicia, Northwest Spain. International Journal of Environmental Research and Public Health, 2022, 19, 4039.	1.2	4
56	Risk Analysis by Age on the Burden of Meningococcal Disease in Spain. Vaccines, 2022, 10, 592.	2.1	4
57	Phylogenetic and population-based approaches to mitogenome variation do not support association with male infertility. Journal of Human Genetics, 2017, 62, 361-371.	1.1	3
58	Case Report: Two Monochorionic Twins With a Critically Different Course of Progressive Osseous Heteroplasia. Frontiers in Pediatrics, 2021, 9, 662669.	0.9	3
59	Biogeographical informativeness of Y-STR haplotypes. Science Bulletin, 2019, 64, 1381-1384.	4.3	2