

# Carlos Flores

## List of Publications by Year in descending order

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Version: 2024-02-01

168  
papers

10,809  
citations

57719

44  
h-index

38368

95  
g-index

198  
all docs

198  
docs citations

198  
times ranked

17183  
citing authors

#	ARTICLE	IF	CITATIONS
1	Autoantibodies against type I IFNs in patients with life-threatening COVID-19. <i>Science</i> , 2020, 370, .	6.0	1,983
2	Inborn errors of type I IFN immunity in patients with life-threatening COVID-19. <i>Science</i> , 2020, 370, .	6.0	1,749
3	Genetic variants associated with idiopathic pulmonary fibrosis susceptibility and mortality: a genome-wide association study. <i>Lancet Respiratory Medicine</i> , the, 2013, 1, 309-317.	5.2	486
4	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases. <i>JAMA Oncology</i> , 2017, 3, 636.	3.4	376
5	Major genomic mitochondrial lineages delineate early human expansions. <i>BMC Genetics</i> , 2001, 2, 13.	2.7	311
6	X-linked recessive TLR7 deficiency in ~1% of men under 60 years old with life-threatening COVID-19. <i>Science Immunology</i> , 2021, 6, .	5.6	267
7	Genetic variants associated with susceptibility to idiopathic pulmonary fibrosis in people of European ancestry: a genome-wide association study. <i>Lancet Respiratory Medicine</i> , the, 2017, 5, 869-880.	5.2	233
8	Human genetic and immunological determinants of critical COVID-19 pneumonia. <i>Nature</i> , 2022, 603, 587-598.	13.7	216
9	Genome-Wide Association Study of Susceptibility to Idiopathic Pulmonary Fibrosis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020, 201, 564-574.	2.5	208
10	Gene flow from North Africa contributes to differential human genetic diversity in southern Europe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11791-11796.	3.3	174
11	Variation in the myosin light chain kinase gene is associated with development of acute lung injury after major trauma*. <i>Critical Care Medicine</i> , 2008, 36, 2794-2800.	0.4	120
12	Ancient mtDNA analysis and the origin of the Guanches. <i>European Journal of Human Genetics</i> , 2004, 12, 155-162.	1.4	106
13	Genome-wide association and HLA fine-mapping studies identify risk loci and genetic pathways underlying allergic rhinitis. <i>Nature Genetics</i> , 2018, 50, 1072-1080.	9.4	106
14	Nanopore sequencing and its application to the study of microbial communities. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 1497-1511.	1.9	106
15	Macrophage migration inhibitory factor in acute lung injury: expression, biomarker, and associations. <i>Translational Research</i> , 2007, 150, 18-29.	2.2	91
16	Mitochondrial DNA transit between West Asia and North Africa inferred from U6 phylogeography. <i>BMC Genetics</i> , 2003, 4, 15.	2.7	90
17	Curated variation benchmarks for challenging medically relevant autosomal genes. <i>Nature Biotechnology</i> , 2022, 40, 672-680.	9.4	90
18	Biomarkers for the acute respiratory distress syndrome: how to make the diagnosis more precise. <i>Annals of Translational Medicine</i> , 2017, 5, 283-283.	0.7	89

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19	Bench-to-bedside review: understanding genetic predisposition to sepsis. <i>Critical Care</i> , 2004, 8, 180.	2.5	82
20	Mitochondrial DNA affinities at the Atlantic fringe of Europe. <i>American Journal of Physical Anthropology</i> , 2003, 120, 391-404.	2.1	76
21	Reduced genetic structure of the Iberian peninsula revealed by Y-chromosome analysis: implications for population demography. <i>European Journal of Human Genetics</i> , 2004, 12, 855-863.	1.4	76
22	Tachykinins and tachykinin receptors in human uterus. <i>British Journal of Pharmacology</i> , 2003, 139, 523-532.	2.7	73
23	The place of the Basques in the European Y-chromosome diversity landscape. <i>European Journal of Human Genetics</i> , 2005, 13, 1293-1302.	1.4	73
24	Fast SARS-CoV-2 detection by RT-qPCR in preheated nasopharyngeal swab samples. <i>International Journal of Infectious Diseases</i> , 2020, 97, 66-68.	1.5	73
25	PrecisionFDA Truth Challenge V2: Calling variants from short and long reads in difficult-to-map regions. <i>Cell Genomics</i> , 2022, 2, 100129.	3.0	72
26	A Predominant European Ancestry of Paternal Lineages from Canary Islanders. <i>Annals of Human Genetics</i> , 2003, 67, 138-152.	0.3	68
27	Injurious mechanical ventilation affects neuronal activation in ventilated rats. <i>Critical Care</i> , 2011, 15, R124.	2.5	67
28	The epithelial sodium channel $\beta$ -subunit: new notes for an old song. <i>American Journal of Physiology - Renal Physiology</i> , 2012, 303, F328-F338.	1.3	67
29	Positive end-expiratory pressure modulates local and systemic inflammatory responses in a sepsis-induced lung injury model. <i>Intensive Care Medicine</i> , 2003, 29, 1345-1353.	3.9	66
30	NanoCLUST: a species-level analysis of 16S rRNA nanopore sequencing data. <i>Bioinformatics</i> , 2021, 37, 1600-1601.	1.8	62
31	Activation of the Wnt/ $\beta$ -Catenin Signaling Pathway by Mechanical Ventilation Is Associated with Ventilator-Induced Pulmonary Fibrosis in Healthy Lungs. <i>PLoS ONE</i> , 2011, 6, e23914.	1.1	62
32	Genomic Predictors of Asthma Phenotypes and Treatment Response. <i>Frontiers in Pediatrics</i> , 2019, 7, 6.	0.9	61
33	A variant of the myosin light chain kinase gene is associated with severe asthma in African Americans. <i>Genetic Epidemiology</i> , 2007, 31, 296-305.	0.6	60
34	Type 2 Deiodinase and Host Responses of Sepsis and Acute Lung Injury. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2011, 45, 1203-1211.	1.4	60
35	African Ancestry Is Associated with Asthma Risk in African Americans. <i>PLoS ONE</i> , 2012, 7, e26807.	1.1	60
36	Inhibition of Nitrobenzylthioinosine-Sensitive Adenosine Transport by Elevated d -Glucose Involves Activation of P 2Y2 Purinoceptors in Human Umbilical Vein Endothelial Cells. <i>Circulation Research</i> , 2002, 90, 570-577.	2.0	59

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37	Recessive inborn errors of type I IFN immunity in children with COVID-19 pneumonia. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	59
38	Sensitivity of different RT-qPCR solutions for SARS-CoV-2 detection. <i>International Journal of Infectious Diseases</i> , 2020, 99, 190-192.	1.5	56
39	IL6 gene-wide haplotype is associated with susceptibility to acute lung injury. <i>Translational Research</i> , 2008, 152, 11-17.	2.2	55
40	Mitogenomes illuminate the origin and migration patterns of the indigenous people of the Canary Islands. <i>PLoS ONE</i> , 2019, 14, e0209125.	1.1	54
41	Mitochondrial DNA characterisation of European isolates: The Maragatos from Spain. <i>European Journal of Human Genetics</i> , 2001, 9, 708-716.	1.4	52
42	Rapid Stimulation of l -Arginine Transport by d -Glucose Involves p42/44 mapk and Nitric Oxide in Human Umbilical Vein Endothelium. <i>Circulation Research</i> , 2003, 92, 64-72.	2.0	52
43	A Tale of Aborigines, Conquerors and Slaves: Alu Insertion Polymorphisms and the Peopling of Canary Islands. <i>Annals of Human Genetics</i> , 2004, 68, 600-605.	0.3	51
44	Serum Lipopolysaccharide Binding Protein Levels Predict Severity of Lung Injury and Mortality in Patients with Severe Sepsis. <i>PLoS ONE</i> , 2009, 4, e6818.	1.1	51
45	Genome-wide association study of inhaled corticosteroid response in admixed children with asthma. <i>Clinical and Experimental Allergy</i> , 2019, 49, 789-798.	1.4	50
46	Genetic variants of the arachidonic acid pathway in non-steroidal anti-inflammatory drug-induced acute urticaria. <i>Clinical and Experimental Allergy</i> , 2012, 42, 1772-1781.	1.4	49
47	Genome-wide association study across five cohorts identifies five novel loci associated with idiopathic pulmonary fibrosis. <i>Thorax</i> , 2022, 77, 829-833.	2.7	47
48	Angiotensin-converting enzyme insertion/deletion polymorphism is not associated with susceptibility and outcome in sepsis and acute respiratory distress syndrome. <i>Intensive Care Medicine</i> , 2008, 34, 488-495.	3.9	46
49	Cell signalling-mediated insulin increase of mRNA expression for cationic amino acid transporters-1 and -2 and membrane hyperpolarization in human umbilical vein endothelial cells. <i>Pflugers Archiv European Journal of Physiology</i> , 2004, 448, 383-94.	1.3	45
50	Mechanical ventilation modulates Toll-like receptor signaling pathway in a sepsis-induced lung injury model. <i>Intensive Care Medicine</i> , 2010, 36, 1049-1057.	3.9	45
51	WNT/ $\beta$ -catenin signaling is modulated by mechanical ventilation in an experimental model of acute lung injury. <i>Intensive Care Medicine</i> , 2011, 37, 1201-1209.	3.9	45
52	Y Chromosome and Mitochondrial DNA Characterization of Pasiegos, a Human Isolate from Cantabria (Spain). <i>Annals of Human Genetics</i> , 2003, 67, 329-339.	0.3	44
53	Early activation of pro-fibrotic WNT5A in sepsis-induced acute lung injury. <i>Critical Care</i> , 2014, 18, 568.	2.5	44
54	Use of consomic rats for genomic insights into ventilator-associated lung injury. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2007, 293, L292-L302.	1.3	43

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55	Functional promoter variants in sphingosine 1-phosphate receptor 3 associate with susceptibility to sepsis-associated acute respiratory distress syndrome. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2013, 305, L467-L477.	1.3	43
56	An Alternative Method of Acute Lung Injury Classification for Use in Observational Studies. <i>Chest</i> , 2010, 138, 1054-1061.	0.4	42
57	Regulation of adenosine transport by D-glucose in human fetal endothelial cells: involvement of nitric oxide, protein kinase C and mitogen-activated protein kinase. <i>Journal of Physiology</i> , 2000, 529, 777-790.	1.3	41
58	Mechanical ventilation modulates TLR4 and IRAK-3 in a non-infectious, ventilator-induced lung injury model. <i>Respiratory Research</i> , 2010, 11, 27.	1.4	40
59	The <i>NAMPT</i> Promoter Is Regulated by Mechanical Stress, Signal Transducer and Activator of Transcription 5, and Acute Respiratory Distress Syndrome-Associated Genetic Variants. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2014, 51, 660-667.	1.4	40
60	Common Variants of TLR1 Associate with Organ Dysfunction and Sustained Pro-Inflammatory Responses during Sepsis. <i>PLoS ONE</i> , 2010, 5, e13759.	1.1	39
61	A quality assessment of genetic association studies supporting susceptibility and outcome in acute lung injury. <i>Critical Care</i> , 2008, 12, R130.	2.5	38
62	Functional variants of the sphingosine-1-phosphate receptor 1 gene associate with asthma susceptibility. <i>Journal of Allergy and Clinical Immunology</i> , 2010, 126, 241-249.e3.	1.5	38
63	Sepsis-associated acute respiratory distress syndrome in individuals of European ancestry: a genome-wide association study. <i>Lancet Respiratory Medicine</i> , 2020, 8, 258-266.	5.2	38
64	Novel genes and sex differences in COVID-19 severity. <i>Human Molecular Genetics</i> , 2022, 31, 3789-3806.	1.4	38
65	Experimental Ventilator-induced Lung Injury. <i>Anesthesiology</i> , 2009, 110, 1341-1347.	1.3	37
66	Bradykinin-Mediated Angioedema: An Update of the Genetic Causes and the Impact of Genomics. <i>Frontiers in Genetics</i> , 2019, 10, 900.	1.1	34
67	The Alu insertion in the <i>CLCN5</i> gene of a patient with Dent's disease leads to exon 11 skipping. <i>Journal of Human Genetics</i> , 2005, 50, 370-374.	1.1	32
68	Isolates in a corridor of migrations: a high-resolution analysis of Y-chromosome variation in Jordan. <i>Journal of Human Genetics</i> , 2005, 50, 435-441.	1.1	32
69	Mitochondrial DNA diversity in 17th-18th century remains from Tenerife (Canary Islands). <i>American Journal of Physical Anthropology</i> , 2005, 127, 418-426.	2.1	31
70	Identification of a novel locus associated with skin colour in African-admixed populations. <i>Scientific Reports</i> , 2017, 7, 44548.	1.6	31
71	Increasing SARS-CoV-2 RT-qPCR testing capacity by sample pooling. <i>International Journal of Infectious Diseases</i> , 2021, 103, 19-22.	1.5	31
72	About the "Pathological" Role of the mtDNA T3308C Mutation. <i>American Journal of Human Genetics</i> , 1999, 65, 1457-1459.	2.6	30

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73	Simultaneous Purifying Selection on the Ancestral MC1R Allele and Positive Selection on the Melanoma-Risk Allele V60L in South Europeans. <i>Molecular Biology and Evolution</i> , 2013, 30, 2654-2665.	3.5	30
74	Rationale and design of the multiethnic Pharmacogenomics in Childhood Asthma consortium. <i>Pharmacogenomics</i> , 2017, 18, 931-943.	0.6	30
75	A pathway-based association study reveals variants from Wnt signalling genes contributing to asthma susceptibility. <i>Clinical and Experimental Allergy</i> , 2017, 47, 618-626.	1.4	29
76	Northwest African distribution of the CD4/Alu microsatellite haplotypes. <i>Annals of Human Genetics</i> , 2000, 64, 321-327.	0.3	28
77	Interleukin-1 Receptor-associated Kinase 3 Gene Associates with Susceptibility to Acute Lung Injury. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2011, 45, 740-745.	1.4	27
78	A CXCL2 tandem repeat promoter polymorphism is associated with susceptibility to severe sepsis in the Spanish population. <i>Genes and Immunity</i> , 2006, 7, 141-149.	2.2	26
79	Genomics and the Acute Respiratory Distress Syndrome: Current and Future Directions. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4004.	1.8	26
80	Bacterial salivary microbiome associates with asthma among african american children and young adults. <i>Pediatric Pulmonology</i> , 2019, 54, 1948-1956.	1.0	26
81	Modulation of adenosine transport by insulin in human umbilical artery smooth muscle cells from normal or gestational diabetic pregnancies. <i>Journal of Physiology</i> , 2001, 534, 243-254.	1.3	25
82	A CXCL2 polymorphism is associated with better outcomes in patients with severe sepsis*. <i>Critical Care Medicine</i> , 2007, 35, 2292-E1.	0.4	25
83	Early physiological and biological features in three animal models of induced acute lung injury. <i>Intensive Care Medicine</i> , 2010, 36, 347-355.	3.9	25
84	Altered Profile of Circulating Endothelial-Derived Microparticles in Ventilator-Induced Lung Injury*. <i>Critical Care Medicine</i> , 2015, 43, e551-e559.	0.4	25
85	North African Influences and Potential Bias in Case-Control Association Studies in the Spanish Population. <i>PLoS ONE</i> , 2011, 6, e18389.	1.1	25
86	The Origin of the Canary Island Aborigines and Their Contribution to the Modern Population: A Molecular Genetics Perspective. <i>Current Anthropology</i> , 2001, 42, 749-755.	0.8	24
87	Mitochondrial DNA variation in Jordanians and their genetic relationship to other Middle East populations. <i>Annals of Human Biology</i> , 2008, 35, 212-231.	0.4	24
88	Novel idiopathic pulmonary fibrosis susceptibility variants revealed by deep sequencing. <i>ERJ Open Research</i> , 2019, 5, 00071-2019.	1.1	24
89	A common haplotype of the LBP gene predisposes to severe sepsis *. <i>Critical Care Medicine</i> , 2009, 37, 2759-2766.	0.4	23
90	IL-1 receptor-associated kinase 3 gene (IRAK3) variants associate with asthma in a replication study in the Spanish population. <i>Journal of Allergy and Clinical Immunology</i> , 2012, 129, 573-575.e10.	1.5	22

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91	Assessing the quality of studies supporting genetic susceptibility and outcomes of ARDS. <i>Frontiers in Genetics</i> , 2014, 5, 20.	1.1	22
92	A common haplotype of the LBP gene predisposes to severe sepsis*. <i>Critical Care Medicine</i> , 2009, 37, 2759-2766.	0.4	21
93	What Ancestry Can Tell Us About the Genetic Origins of Inter-Ethnic Differences in Asthma Expression. <i>Current Allergy and Asthma Reports</i> , 2016, 16, 53.	2.4	21
94	Respiratory viral infections in otherwise healthy humans with inherited IRF7 deficiency. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	21
95	An intronic MYLK variant associated with inflammatory lung disease regulates promoter activity of the smooth muscle myosin light chain kinase isoform. <i>Journal of Molecular Medicine</i> , 2012, 90, 299-308.	1.7	20
96	The Interplay between Natural Selection and Susceptibility to Melanoma on Allele 374F of SLC45A2 Gene in a South European Population. <i>PLoS ONE</i> , 2014, 9, e104367.	1.1	20
97	Lung Transcriptomics during Protective Ventilatory Support in Sepsis-Induced Acute Lung Injury. <i>PLoS ONE</i> , 2015, 10, e0132296.	1.1	20
98	A common cortactin gene variation confers differential susceptibility to severe asthma. <i>Genetic Epidemiology</i> , 2008, 32, 757-766.	0.6	18
99	Whole-Exome Sequencing Identifies Somatic Mutations Associated With Mortality in Metastatic Clear Cell Kidney Carcinoma. <i>Frontiers in Genetics</i> , 2019, 10, 439.	1.1	18
100	Association of common variants, not rare mutations, in <i>IRF6</i> With nonsyndromic clefts in a honduran population. <i>Laryngoscope</i> , 2011, 121, 1756-1759.	1.1	17
101	Variants of CEP68 Gene Are Associated with Acute Urticaria/Angioedema Induced by Multiple Non-Steroidal Anti-Inflammatory Drugs. <i>PLoS ONE</i> , 2014, 9, e90966.	1.1	17
102	Common variants of NFE2L2 gene predisposes to acute respiratory distress syndrome in patients with severe sepsis. <i>Critical Care</i> , 2015, 19, 256.	2.5	17
103	Genomic analyses of human European diversity at the southwestern edge: isolation, African influence and disease associations in the Canary Islands. <i>Molecular Biology and Evolution</i> , 2018, 35, 3010-3026.	3.5	17
104	Role of genomics in asthma exacerbations. <i>Current Opinion in Pulmonary Medicine</i> , 2019, 25, 101-112.	1.2	17
105	Proportion of Idiopathic Pulmonary Fibrosis Risk Explained by Known Common Genetic Loci in European Populations. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2021, 203, 775-778.	2.5	17
106	Genome-wide association study of asthma exacerbations despite inhaled corticosteroid use. <i>European Respiratory Journal</i> , 2021, 57, 2003388.	3.1	17
107	Copy number variation in ALOX5 and PTGER1 is associated with NSAIDs-induced urticaria and/or angioedema. <i>Pharmacogenetics and Genomics</i> , 2016, 26, 280-287.	0.7	15
108	Genome-wide association study in Spanish identifies ADAM metallopeptidase with thrombospondin type 1 motif, 9 (ADAMTS9), as a novel asthma susceptibility gene. <i>Journal of Allergy and Clinical Immunology</i> , 2016, 137, 964-966.	1.5	15

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109	Genetic Affinities Among Human Populations Inhabiting the Sub-Saharan Area, Northwest Africa, and the Iberian Peninsula. , 2000, , 33-50.		14
110	The peopling of the Canary Islands: a CD4/Alu microsatellite haplotype perspective. Human Immunology, 2001, 62, 949-953.	1.2	14
111	Genomics of Acute Lung Injury. Seminars in Respiratory and Critical Care Medicine, 2006, 27, 389-395.	0.8	14
112	Soluble platelet-endothelial cell adhesion molecule-1, a biomarker of ventilator-induced lung injury. Critical Care, 2014, 18, R41.	2.5	14
113	Assessing the Validity of Asthma Associations for Eight Candidate Genes and Age at Diagnosis Effects. PLoS ONE, 2013, 8, e73157.	1.1	13
114	GADD45a Promoter Regulation by a Functional Genetic Variant Associated with Acute Lung Injury. PLoS ONE, 2014, 9, e100169.	1.1	13
115	Lung Transplant Improves Survival and Quality of Life Regardless of Telomere Dysfunction. Frontiers in Medicine, 2021, 8, 695919.	1.2	13
116	A missense mutation in the chloride/proton ClC-5 antiporter gene results in increased expression of an alternative mRNA form that lacks exons 10 and 11. Identification of seven new CLCN5 mutations in patients with Dent's disease. Journal of Human Genetics, 2007, 52, 255-261.	1.1	12
117	IonGAP: integrative bacterial genome analysis for Ion Torrent sequence data. Bioinformatics, 2015, 31, 2870-2873.	1.8	12
118	Polymorphisms in CEP68 gene associated with risk of immediate selective reactions to non-steroidal anti-inflammatory drugs. Pharmacogenomics Journal, 2019, 19, 191-199.	0.9	12
119	AmpliSeq Screening of Genes Encoding the C-Type Lectin Receptors and Their Signaling Components Reveals a Common Variant in MASP1 Associated with Pulmonary Tuberculosis in an Indian Population. Frontiers in Immunology, 2018, 9, 242.	2.2	11
120	Evaluation of Whole-Exome Enrichment Solutions: Lessons from the High-End of the Short-Read Sequencing Scale. Journal of Clinical Medicine, 2020, 9, 3656.	1.0	11
121	Could lung bacterial dysbiosis predict ICU mortality in patients with extra-pulmonary sepsis? A proof-of-concept study. Intensive Care Medicine, 2020, 46, 2118-2120.	3.9	11
122	Combined analysis of transcriptomic and genetic data for the identification of loci involved in glucocorticosteroid response in asthma. Allergy: European Journal of Allergy and Clinical Immunology, 2021, 76, 1238-1243.	2.7	11
123	Longitudinal study of a SARS-CoV-2 infection in an immunocompromised patient with X-linked agammaglobulinemia. Journal of Infection, 2021, 83, 607-635.	1.7	11
124	The association between interferon regulatory factor 6 ( <i>IRF6</i> ) and nonsyndromic cleft lip with or without cleft palate in a Honduran population. Laryngoscope, 2009, 119, 1759-1764.	1.1	10
125	Pharmacogenomic associations of adverse drug reactions in asthma: systematic review and research prioritisation. Pharmacogenomics Journal, 2020, 20, 621-628.	0.9	10
126	HLA-DRB1*15:01 allele protects from asthma susceptibility. Journal of Allergy and Clinical Immunology, 2014, 134, 1201-1203.	1.5	9



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127	Streptococcal group B integrative and mobilizable element IMESag- rpsI encodes a functional relaxase involved in its transfer. <i>Open Biology</i> , 2016, 6, 160084.	1.5	9
128	A vascular endothelial growth factor receptor gene variant is associated with susceptibility to acute respiratory distress syndrome. <i>Intensive Care Medicine Experimental</i> , 2018, 6, 16.	0.9	9
129	Northwest African distribution of the CD4/Alu microsatellite haplotypes. <i>Annals of Human Genetics</i> , 2000, 64, 321-7.	0.3	9
130	Fine mapping of the myosin light chain kinase (MYLK) gene replicates the association with asthma in populations of Spanish descent. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 136, 1116-1118.e9.	1.5	8
131	Admixture mapping of asthma in southwestern Europeans with North African ancestry influences. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2020, 318, L965-L975.	1.3	8
132	Genetic Ancestry Inference and Its Application for the Genetic Mapping of Human Diseases. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6962.	1.8	8
133	Genetic Variants of Thymic Stromal Lymphopoietin in Nonsteroidal Anti-Inflammatory Drug-Induced Urticaria/Angioedema. <i>International Archives of Allergy and Immunology</i> , 2016, 169, 249-255.	0.9	7
134	A benchmarking of human mitochondrial DNA haplogroup classifiers from whole-genome and whole-exome sequence data. <i>Scientific Reports</i> , 2021, 11, 20510.	1.6	7
135	Genetic determinants of survival in sepsis and acute lung injury. <i>Minerva Anestesiologica</i> , 2008, 74, 341-5.	0.6	7
136	Monitoring the rise of the SARS-CoV-2 lineage B.1.1.7 in Tenerife (Spain) since mid-December 2020. <i>Journal of Infection</i> , 2021, 82, e1-e3.	1.7	6
137	Identification of ROBO2 as a Potential Locus Associated with Inhaled Corticosteroid Response in Childhood Asthma. <i>Journal of Personalized Medicine</i> , 2021, 11, 733.	1.1	6
138	Whole-Blood Mitochondrial DNA Copies Are Associated With the Prognosis of Acute Respiratory Distress Syndrome After Sepsis. <i>Frontiers in Immunology</i> , 2021, 12, 737369.	2.2	6
139	Transactive Response DNA-Binding Protein (TARDBP/TDP-43) Regulates Cell Permissivity to HIV-1 Infection by Acting on HDAC6. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6180.	1.8	6
140	The road to precision medicine in sepsis: blood transcriptome endotypes. <i>Lancet Respiratory Medicine</i> , 2017, 5, 767-768.	5.2	5
141	Admixture mapping analysis reveals differential genetic ancestry associated with Chagas disease susceptibility in the Colombian population. <i>Human Molecular Genetics</i> , 2021, 30, 2503-2512.	1.4	5
142	The D84E variant of the $\beta$ -MSH receptor 1 gene is associated with cutaneous malignant melanoma early onset. <i>Journal of Dermatological Science</i> , 2008, 52, 186-192.	1.0	4
143	Host genetics shapes adult sepsis survival. <i>Lancet Respiratory Medicine</i> , 2015, 3, 7-8.	5.2	4
144	Interactive Web-Based Resource for Annotation of Genetic Variants Causing Hereditary Angioedema (HADA): Database Development, Implementation, and Validation. <i>Journal of Medical Internet Research</i> , 2020, 22, e19040.	2.1	4

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145	Targeted analysis of genomic regions enriched in African ancestry reveals novel classical HLA alleles associated with asthma in Southwestern Europeans. <i>Scientific Reports</i> , 2021, 11, 23686.	1.6	4
146	Polymorphisms of Interleukin-6 and Tumor Necrosis Factor Gene Promoters and Cardiorespiratory Function Following Liver Transplantation: A Preliminary Study. <i>Transplantation Proceedings</i> , 2009, 41, 1062-1064.	0.3	2
147	No association between genetic ancestry and susceptibility to asthma or atopy in Canary Islanders. <i>Immunogenetics</i> , 2012, 64, 705-711.	1.2	2
148	NanoDJ: a Dockerized Jupyter notebook for interactive Oxford Nanopore MinION sequence manipulation and genome assembly. <i>BMC Bioinformatics</i> , 2019, 20, 234.	1.2	2
149	First Census of Patients with Hereditary Angioedema in the Canary Islands. <i>Journal of Clinical Medicine</i> , 2021, 10, 4711.	1.0	2
150	Association of the Delta SARS-CoV-2 variant with 28-day hospital mortality between December 2020 and September 2021. <i>Journal of Infection</i> , 2022, 85, 90-122.	1.7	2
151	Genomic Insights Into Sepsis Course Using Whole Exome Sequencing. <i>EBioMedicine</i> , 2016, 12, 18-19.	2.7	1
152	Assessing Asthma Medication Responses in U.S. Minority Children by Whole-Genome Sequencing. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2018, 197, 1513-1514.	2.5	1
153	Meta-analysis of inhaled corticosteroids response in children with asthma. , 2019, , .		1
154	ACE insertion/deletion polymorphism in sepsis and acute respiratory distress syndrome. <i>Intensive Care Medicine</i> , 2008, 34, 1732-1732.	3.9	0
155	Mitochondrial DNA in Peripheral Blood Is a Prognostic Biomarker in Sepsis-Induced Acute Respiratory Distress Syndrome Patients. , 2019, , .		0
156	Early Lung Bacterial Dysbiosis Predicts Patient Mortality by Non-Pulmonary Sepsis. , 2020, , .		0
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