Carlos Flores

List of Publications by Year
in descending order

168 papers	10,809 citations	57758 44 h-index	38395 95 g-index
198 all docs	198 docs citations	198 times ranked	17183 citing authors

#	Article	IF	Citations
1	Human genetic and immunological determinants of critical COVID-19 pneumonia. Nature, 2022, 603, 587-598.	27.8	216
2	Curated variation benchmarks for challenging medically relevant autosomal genes. Nature Biotechnology, 2022, 40, 672-680.	17.5	90
3	Admixture Mapping of Sepsis in European Individuals With African Ancestries. Frontiers in Medicine, 2022, 9, 754440.	2.6	0
4	Association of the Delta SARS-CoV-2 variant with 28-day hospital mortality between December 2020 and September 2021. Journal of Infection, 2022, 85, 90-122.	3.3	2
5	PrecisionFDA Truth Challenge V2: Calling variants from short and long reads in difficult-to-map regions. Cell Genomics, 2022, 2, 100129.	6.5	72
6	Integrating Gene Expression with Genome-Wide Association Summary Statistics to Identify Genes Associated with Idiopathic Pulmonary Fibrosis Survival. , 2022, , .		0
7	Transactive Response DNA-Binding Protein (TARDBP/TDP-43) Regulates Cell Permissivity to HIV-1 Infection by Acting on HDAC6. International Journal of Molecular Sciences, 2022, 23, 6180.	4.1	6
8	Novel genes and sex differences in COVID-19 severity. Human Molecular Genetics, 2022, 31, 3789-3806.	2.9	38
9	Genome-wide association study across five cohorts identifies five novel loci associated with idiopathic pulmonary fibrosis. Thorax, 2022, 77, 829-833.	5.6	47
10	Respiratory viral infections in otherwise healthy humans with inherited IRF7 deficiency. Journal of Experimental Medicine, 2022, 219, .	8.5	21
11	Recessive inborn errors of type I IFN immunity in children with COVID-19 pneumonia. Journal of Experimental Medicine, 2022, 219, .	8.5	59
12	NanoCLUST: a species-level analysis of 16S rRNA nanopore sequencing data. Bioinformatics, 2021, 37, 1600-1601.	4.1	62
13	Proportion of Idiopathic Pulmonary Fibrosis Risk Explained by Known Common Genetic Loci in European Populations. American Journal of Respiratory and Critical Care Medicine, 2021, 203, 775-778.	5.6	17
14	Increasing SARS-CoV-2 RT-qPCR testing capacity by sample pooling. International Journal of Infectious Diseases, 2021, 103, 19-22.	3.3	31
15	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.	5.7	11
16	Nanopore sequencing and its application to the study of microbial communities. Computational and Structural Biotechnology Journal, 2021, 19, 1497-1511.	4.1	106
17	Monitoring the rise of the SARS-CoV-2 lineage B.1.1.7 in Tenerife (Spain) since mid-December 2020. Journal of Infection, 2021, 82, e1-e3.	3.3	6
18	Genetic Ancestry Inference and Its Application for the Genetic Mapping of Human Diseases. International Journal of Molecular Sciences, 2021, 22, 6962.	4.1	8

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19	Identification of ROBO2 as a Potential Locus Associated with Inhaled Corticosteroid Response in Childhood Asthma. Journal of Personalized Medicine, 2021, 11, 733.	2.5	6
20	Longitudinal study of a SARS-CoV-2 infection in an immunocompromised patient with X-linked agammaglobulinemia. Journal of Infection, 2021, 83, 607-635.	3.3	11
21	Admixture mapping analysis reveals differential genetic ancestry associated with Chagas disease susceptibility in the Colombian population. Human Molecular Genetics, 2021, 30, 2503-2512.	2.9	5
22	Lung Transplant Improves Survival and Quality of Life Regardless of Telomere Dysfunction. Frontiers in Medicine, 2021, 8, 695919.	2.6	13
23	Decoding the pharmacogenetics of nonsteroidal antiâ€inflammatory drug hypersensitivity. British Journal of Dermatology, 2021, 185, 697-698.	1.5	0
24	X-linked recessive TLR7 deficiency in ~1% of men under 60 years old with life-threatening COVID-19. Science Immunology, 2021, 6, .	11.9	267
25	Whole-Blood Mitochondrial DNA Copies Are Associated With the Prognosis of Acute Respiratory Distress Syndrome After Sepsis. Frontiers in Immunology, 2021, 12, 737369.	4.8	6
26	Complete mitogenome in a population sample from Cameroon. Forensic Science International: Genetics, 2021, 55, 102597.	3.1	0
27	Genome-wide association study of asthma exacerbations despite inhaled corticosteroid use. European Respiratory Journal, 2021, 57, 2003388.	6.7	17
28	A benchmarking of human mitochondrial DNA haplogroup classifiers from whole-genome and whole-exome sequence data. Scientific Reports, 2021, 11, 20510.	3.3	7
29	First Census of Patients with Hereditary Angioedema in the Canary Islands. Journal of Clinical Medicine, 2021, 10, 4711.	2.4	2
30	S63â€…Genome-wide sex-by-SNP interaction analysis of susceptibility to idiopathic pulmonary fibrosis. , 2021, , .		0
31	Targeted analysis of genomic regions enriched in African ancestry reveals novel classical HLA alleles associated with asthma in Southwestern Europeans. Scientific Reports, 2021, 11, 23686.	3.3	4
32	Genome-Wide Association Study of Susceptibility to Idiopathic Pulmonary Fibrosis. American Journal of Respiratory and Critical Care Medicine, 2020, 201, 564-574.	5.6	208
33	Evaluation of Whole-Exome Enrichment Solutions: Lessons from the High-End of the Short-Read Sequencing Scale. Journal of Clinical Medicine, 2020, 9, 3656.	2.4	11
34	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.	8.2	11
35	Sensitivity of different RT-qPCR solutions for SARS-CoV-2 detection. International Journal of Infectious Diseases, 2020, 99, 190-192.	3.3	56
36	Inborn errors of type I IFN immunity in patients with life-threatening COVID-19. Science, 2020, 370, .	12.6	1,749

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37	Autoantibodies against type I IFNs in patients with life-threatening COVID-19. Science, 2020, 370, .	12.6	1,983
38	Early Lung Bacterial Dysbiosis Predicts Patient Mortality by Non-Pulmonary Sepsis. , 2020, , .		0
39	Orthogonal Validation of the Lung Dysbiosis in Non-Pulmonary Sepsis Associated with ICU Mortality Using a Portable Third-Generation DNA Sequencing Device. , 2020, , .		0
40	An Admixture Mapping Study Associates the 8q23.1 Locus in Sepsis Susceptibility. , 2020, , .		0
41	Fast SARS-CoV-2 detection by RT-qPCR in preheated nasopharyngeal swab samples. International Journal of Infectious Diseases, 2020, 97, 66-68.	3.3	73
42	Admixture mapping of asthma in southwestern Europeans with North African ancestry influences. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2020, 318, L965-L975.	2.9	8
43	Sepsis-associated acute respiratory distress syndrome in individuals of European ancestry: a genome-wide association study. Lancet Respiratory Medicine,the, 2020, 8, 258-266.	10.7	38
44	Pharmacogenomic associations of adverse drug reactions in asthma: systematic review and research prioritisation. Pharmacogenomics Journal, 2020, 20, 621-628.	2.0	10
45	Increase in post-transplant survival and quality of life in pulmonary fibrosis with and without telomere dysfunction. , 2020, , .		0
46	Interactive Web-Based Resource for Annotation of Genetic Variants Causing Hereditary Angioedema (HADA): Database Development, Implementation, and Validation. Journal of Medical Internet Research, 2020, 22, e19040.	4.3	4
47	Polymorphisms in CEP68 gene associated with risk of immediate selective reactions to non-steroidal anti-inflammatory drugs. Pharmacogenomics Journal, 2019, 19, 191-199.	2.0	12
48	Genomics and the Acute Respiratory Distress Syndrome: Current and Future Directions. International Journal of Molecular Sciences, 2019, 20, 4004.	4.1	26
49	Role of genomics in asthma exacerbations. Current Opinion in Pulmonary Medicine, 2019, 25, 101-112.	2.6	17
50	Bacterial salivary microbiome associates with asthma among african american children and young adults. Pediatric Pulmonology, 2019, 54, 1948-1956.	2.0	26
51	Bradykinin-Mediated Angioedema: An Update of the Genetic Causes and the Impact of Genomics. Frontiers in Genetics, 2019, 10, 900.	2.3	34
52	Genomeâ€wide association study of inhaled corticosteroid response in admixed children with asthma. Clinical and Experimental Allergy, 2019, 49, 789-798.	2.9	50
53	Novel idiopathic pulmonary fibrosis susceptibility variants revealed by deepÂsequencing. ERJ Open Research, 2019, 5, 00071-2019.	2.6	24
54	NanoDJ: a Dockerized Jupyter notebook for interactive Oxford Nanopore MinION sequence manipulation and genome assembly. BMC Bioinformatics, 2019, 20, 234.	2.6	2

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55	Whole-Exome Sequencing Identifies Somatic Mutations Associated With Mortality in Metastatic Clear Cell Kidney Carcinoma. Frontiers in Genetics, 2019, 10, 439.	2.3	18
56	Mitogenomes illuminate the origin and migration patterns of the indigenous people of the Canary Islands. PLoS ONE, 2019, 14, e0209125.	2.5	54
57	Genomic Predictors of Asthma Phenotypes and Treatment Response. Frontiers in Pediatrics, 2019, 7, 6.	1.9	61
58	Mitochondrial DNA in Peripheral Blood Is a Prognostic Biomarker in Sepsis-Induced Acute Respiratory Distress Syndrome Patients. , 2019, , .		0
59	Meta-analysis of inhaled corticosteroids response in children with asthma. , 2019, , .		1
60	T1â€…Meta-analysis of idiopathic pulmonary fibrosis genome-wide analyses identifies three novel genetic signals associated with disease susceptibility. , 2019, , .		0
61	Assessing Asthma Medication Responses in U.S. Minority Children by Whole-Genome Sequencing. American Journal of Respiratory and Critical Care Medicine, 2018, 197, 1513-1514.	5.6	1
62	A vascular endothelial growth factor receptor gene variant is associated with susceptibility to acute respiratory distress syndrome. Intensive Care Medicine Experimental, 2018, 6, 16.	1.9	9
63	Genomic analyses of human European diversity at the southwestern edge: isolation, African influence and disease associations in the Canary Islands. Molecular Biology and Evolution, 2018, 35, 3010-3026.	8.9	17
64	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.	4.8	11
65	Genome-wide association and HLA fine-mapping studies identify risk loci and genetic pathways underlying allergic rhinitis. Nature Genetics, 2018, 50, 1072-1080.	21.4	106
66	A pathwayâ€based association study reveals variants from Wnt signalling genes contributing to asthma susceptibility. Clinical and Experimental Allergy, 2017, 47, 618-626.	2.9	29
67	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases. JAMA Oncology, 2017, 3, 636.	7.1	376
68	Identification of a novel locus associated with skin colour in African-admixed populations. Scientific Reports, 2017, 7, 44548.	3.3	31
69	Genetic variants associated with susceptibility to idiopathic pulmonary fibrosis in people of European ancestry: a genome-wide association study. Lancet Respiratory Medicine,the, 2017, 5, 869-880.	10.7	233
70	The road to precision medicine in sepsis: blood transcriptome endotypes. Lancet Respiratory Medicine,the, 2017, 5, 767-768.	10.7	5
71	Rationale and design of the multiethnic Pharmacogenomics in Childhood Asthma consortium. Pharmacogenomics, 2017, 18, 931-943.	1.3	30
72	Biomarkers for the acute respiratory distress syndrome: how to make the diagnosis more precise. Annals of Translational Medicine, 2017, 5, 283-283.	1.7	89

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73	Genome-wide association study of inhaled corticosteroid response in African-admixed children with asthma. , 2017, , .		0
74	Genome-wide association study of asthma exacerbations in European children treated with inhaled corticosteroids. , 2017, , .		0
75	Copy number variation in ALOX5 and PTGER1 is associated with NSAIDs-induced urticaria and/or angioedema. Pharmacogenetics and Genomics, 2016, 26, 280-287.	1.5	15
76	Genome-wide association study in Spanish identifies ADAM metallopeptidase with thrombospondin type 1 motif, 9 (ADAMTS9), as a novel asthma susceptibility gene. Journal of Allergy and Clinical Immunology, 2016, 137, 964-966.	2.9	15
77	Genomic Insights Into Sepsis Course Using Whole Exome Sequencing. EBioMedicine, 2016, 12, 18-19.	6.1	1
78	What Ancestry Can Tell Us About the Genetic Origins of Inter-Ethnic Differences in Asthma Expression. Current Allergy and Asthma Reports, 2016, 16, 53.	5.3	21
79	Streptococcal group B integrative and mobilizable element IMESag- rpsI encodes a functional relaxase involved in its transfer. Open Biology, 2016, 6, 160084.	3.6	9
80	Genetic Variants of Thymic Stromal Lymphopoietin in Nonsteroidal Anti-Inflammatory Drug-Induced Urticaria/Angioedema. International Archives of Allergy and Immunology, 2016, 169, 249-255.	2.1	7
81	Defining uncontrolled childhood asthma in the global PiCA consortium. , 2016, , .		0
82	Altered Profile of Circulating Endothelial-Derived Microparticles in Ventilator-Induced Lung Injury*. Critical Care Medicine, 2015, 43, e551-e559.	0.9	25
83	Common variants of NFE2L2 gene predisposes to acute respiratory distress syndrome in patients with severe sepsis. Critical Care, 2015, 19, 256.	5.8	17
84	Fine mapping of the myosin light chain kinase (MYLK) gene replicates the association with asthma in populations of Spanish descent. Journal of Allergy and Clinical Immunology, 2015, 136, 1116-1118.e9.	2.9	8
85	Host genetics shapes adult sepsis survival. Lancet Respiratory Medicine,the, 2015, 3, 7-8.	10.7	4
86	IonGAP: integrative bacterial genome analysis for Ion Torrent sequence data. Bioinformatics, 2015, 31, 2870-2873.	4.1	12
87	Lung Transcriptomics during Protective Ventilatory Support in Sepsis-Induced Acute Lung Injury. PLoS ONE, 2015, 10, e0132296.	2.5	20
88	Variants of CEP68 Gene Are Associated with Acute Urticaria/Angioedema Induced by Multiple Non-Steroidal Anti-Inflammatory Drugs. PLoS ONE, 2014, 9, e90966.	2.5	17
89	GADD45a Promoter Regulation by a Functional Genetic Variant Associated with Acute Lung Injury. PLoS ONE, 2014, 9, e100169.	2.5	13
90	Assessing the quality of studies supporting genetic susceptibility and outcomes of ARDS. Frontiers in Genetics, 2014, 5, 20.	2.3	22

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91	The NAMPT Promoter Is Regulated by Mechanical Stress, Signal Transducer and Activator of Transcription 5, and Acute Respiratory Distress Syndromeâ€“Associated Genetic Variants. American Journal of Respiratory Cell and Molecular Biology, 2014, 51, 660-667.	2.9	40
92	Early activation of pro-fibrotic WNT5A in sepsis-induced acute lung injury. Critical Care, 2014, 18, 568.	5.8	44
93	HLA-DRB1*15:01 allele protects from asthma susceptibility. Journal of Allergy and Clinical Immunology, 2014, 134, 1201-1203.	2.9	9
94	Soluble platelet-endothelial cell adhesion molecule-1, a biomarker of ventilator-induced lung injury. Critical Care, 2014, 18, R41.	5.8	14
95	The Interplay between Natural Selection and Susceptibility to Melanoma on Allele 374F of SLC45A2 Gene in a South European Population. PLoS ONE, 2014, 9, e104367.	2.5	20
96	Simultaneous Purifying Selection on the Ancestral MC1R Allele and Positive Selection on the Melanoma-Risk Allele V60L in South Europeans. Molecular Biology and Evolution, 2013, 30, 2654-2665.	8.9	30
97	Genetic variants associated with idiopathic pulmonary fibrosis susceptibility and mortality: a genome-wide association study. Lancet Respiratory Medicine,the, 2013, 1, 309-317.	10.7	486
98	Functional promoter variants in sphingosine 1-phosphate receptor 3 associate with susceptibility to sepsis-associated acute respiratory distress syndrome. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2013, 305, L467-L477.	2.9	43
99	Gene flow from North Africa contributes to differential human genetic diversity in southern Europe. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 11791-11796.	7.1	174
100	Assessing the Validity of Asthma Associations for Eight Candidate Genes and Age at Diagnosis Effects. PLoS ONE, 2013, 8, e73157.	2.5	13
101	The epithelial sodium channel Î´-subunit: new notes for an old song. American Journal of Physiology - Renal Physiology, 2012, 303, F328-F338.	2.7	67
102	No association between genetic ancestry and susceptibility to asthma or atopy in Canary Islanders. Immunogenetics, 2012, 64, 705-711.	2.4	2
103	Genetic variants of the arachidonic acid pathway in nonâ€steroidal antiâ€inflammatory drugâ€induced acute urticaria. Clinical and Experimental Allergy, 2012, 42, 1772-1781.	2.9	49
104	IL-1 receptorâ€“associated kinase 3 gene (IRAK3) variants associate with asthma in a replication study in the Spanish population. Journal of Allergy and Clinical Immunology, 2012, 129, 573-575.e10.	2.9	22
105	African Ancestry Is Associated with Asthma Risk in African Americans. PLoS ONE, 2012, 7, e26807.	2.5	60
106	An intronic MYLK variant associated with inflammatory lung disease regulates promoter activity of the smooth muscle myosin light chain kinase isoform. Journal of Molecular Medicine, 2012, 90, 299-308.	3.9	20
107	Injurious mechanical ventilation affects neuronal activation in ventilated rats. Critical Care, 2011, 15, R124.	5.8	67
108	WNT/Î²-catenin signaling is modulated by mechanical ventilation in an experimental model of acute lung injury. Intensive Care Medicine, 2011, 37, 1201-1209.	8.2	45

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109	Association of common variants, not rare mutations, in IRF6 With nonsyndromic clefts in a honduran population. Laryngoscope, 2011, 121, 1756-1759.	2.0	17
110	Type 2 Deiodinase and Host Responses of Sepsis and Acute Lung Injury. American Journal of Respiratory Cell and Molecular Biology, 2011, 45, 1203-1211.	2.9	60
111	Interleukin-1 Receptorâ€“Associated Kinase 3 Gene Associates with Susceptibility to Acute Lung Injury. American Journal of Respiratory Cell and Molecular Biology, 2011, 45, 740-745.	2.9	27
112	North African Influences and Potential Bias in Case-Control Association Studies in the Spanish Population. PLoS ONE, 2011, 6, e18389.	2.5	25
113	Activation of the Wnt/Î²-Catenin Signaling Pathway by Mechanical Ventilation Is Associated with Ventilator-Induced Pulmonary Fibrosis in Healthy Lungs. PLoS ONE, 2011, 6, e23914.	2.5	62
114	An Alternative Method of Acute Lung Injury Classification for Use in Observational Studies. Chest, 2010, 138, 1054-1061.	0.8	42
115	Early physiological and biological features in three animal models of induced acute lung injury. Intensive Care Medicine, 2010, 36, 347-355.	8.2	25
116	Mechanical ventilation modulates Toll-like receptor signaling pathway in a sepsis-induced lung injury model. Intensive Care Medicine, 2010, 36, 1049-1057.	8.2	45
117	Mechanical ventilation modulates TLR4 and IRAK-3 in a non-infectious, ventilator-induced lung injury model. Respiratory Research, 2010, 11, 27.	3.6	40
118	Functional variants of the sphingosine-1-phosphate receptor 1 gene associate with asthma susceptibility. Journal of Allergy and Clinical Immunology, 2010, 126, 241-249.e3.	2.9	38
119	Common Variants of TLR1 Associate with Organ Dysfunction and Sustained Pro-Inflammatory Responses during Sepsis. PLoS ONE, 2010, 5, e13759.	2.5	39
120	The association between interferon regulatory factor 6 (IRF6) and nonsyndromic cleft lip with or without cleft palate in a Honduran population. Laryngoscope, 2009, 119, 1759-1764.	2.0	10
121	Polymorphisms of Interleukin-6 and Tumor Necrosis Factor Gene Promoters and Cardiorespiratory Function Following Liver Transplantation: A Preliminary Study. Transplantation Proceedings, 2009, 41, 1062-1064.	0.6	2
122	A common haplotype of the LBP gene predisposes to severe sepsis*. Critical Care Medicine, 2009, 37, 2759-2766.	0.9	21
123	A common haplotype of the LBP gene predisposes to severe sepsis *. Critical Care Medicine, 2009, 37, 2759-2766.	0.9	23
124	Experimental Ventilator-induced Lung Injury. Anesthesiology, 2009, 110, 1341-1347.	2.5	37
125	Serum Lipopolysaccharide Binding Protein Levels Predict Severity of Lung Injury and Mortality in Patients with Severe Sepsis. PLoS ONE, 2009, 4, e6818.	2.5	51
126	Angiotensin-converting enzyme insertion/deletion polymorphism is not associated with susceptibility and outcome in sepsis and acute respiratory distress syndrome. Intensive Care Medicine, 2008, 34, 488-495.	8.2	46

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127	ACE insertion/deletion polymorphism in sepsis and acute respiratory distress syndrome. Intensive Care Medicine, 2008, 34, 1732-1732.	8.2	0
128	A common cortactin gene variation confers differential susceptibility to severe asthma. Genetic Epidemiology, 2008, 32, 757-766.	1.3	18
129	Mitochondrial DNA variation in Jordanians and their genetic relationship to other Middle East populations. Annals of Human Biology, 2008, 35, 212-231.	1.0	24
130	IL6 gene-wide haplotype is associated with susceptibility to acute lung injury. Translational Research, 2008, 152, 11-17.	5.0	55
131	The D84E variant of the Î±-MSH receptor 1 gene is associated with cutaneous malignant melanoma early onset. Journal of Dermatological Science, 2008, 52, 186-192.	1.9	4
132	A quality assessment of genetic association studies supporting susceptibility and outcome in acute lung injury. Critical Care, 2008, 12, R130.	5.8	38
133	Variation in the myosin light chain kinase gene is associated with development of acute lung injury after major trauma*. Critical Care Medicine, 2008, 36, 2794-2800.	0.9	120
134	Genetic determinants of survival in sepsis and acute lung injury. Minerva Anestesiologica, 2008, 74, 341-5.	1.0	7
135	Use of consomic rats for genomic insights into ventilator-associated lung injury. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2007, 293, L292-L302.	2.9	43
136	A CXCL2 polymorphism is associated with better outcomes in patients with severe sepsis*. Critical Care Medicine, 2007, 35, 2292-E1.	0.9	25
137	Macrophage migration inhibitory factor in acute lung injury: expression, biomarker, and associations. Translational Research, 2007, 150, 18-29.	5.0	91
138	A variant of the myosin light chain kinase gene is associated with severe asthma in African Americans. Genetic Epidemiology, 2007, 31, 296-305.	1.3	60
139	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 Dentâ€™s disease. Journal of Human Genetics, 2007, 52, 255-261.	2.3	12
140	A CXCL2 tandem repeat promoter polymorphism is associated with susceptibility to severe sepsis in the Spanish population. Genes and Immunity, 2006, 7, 141-149.	4.1	26
141	Genomics of Acute Lung Injury. Seminars in Respiratory and Critical Care Medicine, 2006, 27, 389-395.	2.1	14
142	The place of the Basques in the European Y-chromosome diversity landscape. European Journal of Human Genetics, 2005, 13, 1293-1302.	2.8	73
143	Mitochondrial DNA diversity in 17th-18th century remains from Tenerife (Canary Islands). American Journal of Physical Anthropology, 2005, 127, 418-426.	2.1	31
144	The Alu insertion in the CLCN5 gene of a patient with Dentâ€™s disease leads to exon 11 skipping. Journal of Human Genetics, 2005, 50, 370-374.	2.3	32

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145	Isolates in a corridor of migrations: a high-resolution analysis of Y-chromosome variation in Jordan. Journal of Human Genetics, 2005, 50, 435-441.	2.3	32
146	Ancient mtDNA analysis and the origin of the Guanches. European Journal of Human Genetics, 2004, 12, 155-162.	2.8	106
147	Reduced genetic structure of the Iberian peninsula revealed by Y-chromosome analysis: implications for population demography. European Journal of Human Genetics, 2004, 12, 855-863.	2.8	76
148	Cell signalling-mediating insulin increase of mRNA expression for cationic amino acid transporters-1 and -2 and membrane hyperpolarization in human umbilical vein endothelial cells. Pflugers Archiv European Journal of Physiology, 2004, 448, 383-94.	2.8	45
149	A Tale of Aborigines, Conquerors and Slaves: Alu Insertion Polymorphisms and the Peopling of Canary Islands. Annals of Human Genetics, 2004, 68, 600-605.	0.8	51
150	Bench-to-bedside review: understanding genetic predisposition to sepsis. Critical Care, 2004, 8, 180.	5.8	82
151	Positive end-expiratory pressure modulates local and systemic inflammatory responses in a sepsis-induced lung injury model. Intensive Care Medicine, 2003, 29, 1345-1353.	8.2	66
152	Mitochondrial DNA affinities at the Atlantic fringe of Europe. American Journal of Physical Anthropology, 2003, 120, 391-404.	2.1	76
153	A Predominant European Ancestry of Paternal Lineages from Canary Islanders. Annals of Human Genetics, 2003, 67, 138-152.	0.8	68
154	Y Chromosome and Mitochondrial DNA Characterization of Pasiegos, a Human Isolate from Cantabria (Spain). Annals of Human Genetics, 2003, 67, 329-339.	0.8	44
155	Mitochondrial DNA transit between West Asia and North Africa inferred from U6 phylogeography. BMC Genetics, 2003, 4, 15.	2.7	90
156	Tachykinins and tachykinin receptors in human uterus. British Journal of Pharmacology, 2003, 139, 523-532.	5.4	73
157	Rapid Stimulation of <scp>l</scp> -Arginine Transport by <scp>d</scp> -Glucose Involves p42/44 ^{mapk} and Nitric Oxide in Human Umbilical Vein Endothelium. Circulation Research, 2003, 92, 64-72.	4.5	52
158	Inhibition of Nitrobenzylthioinosine-Sensitive Adenosine Transport by Elevated d -Glucose Involves Activation of P 2Y2 Purinoceptors in Human Umbilical Vein Endothelial Cells. Circulation Research, 2002, 90, 570-577.	4.5	59
159	The peopling of the Canary Islands: a CD4/Alu microsatellite haplotype perspective. Human Immunology, 2001, 62, 949-953.	2.4	14
160	The Origin of the Canary Island Aborigines and Their Contribution to the Modern Population: A Molecular Genetics Perspective. Current Anthropology, 2001, 42, 749-755.	1.6	24
161	Mitochondrial DNA characterisation of European isolates: The Maragatos from Spain. European Journal of Human Genetics, 2001, 9, 708-716.	2.8	52
162	Modulation of adenosine transport by insulin in human umbilical artery smooth muscle cells from normal or gestational diabetic pregnancies. Journal of Physiology, 2001, 534, 243-254.	2.9	25

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163	Major genomic mitochondrial lineages delineate early human expansions. BMC Genetics, 2001, 2, 13.	2.7	311
164	Northwest African distribution of the CD4/Alu microsatellite haplotypes. Annals of Human Genetics, 2000, 64, 321-327.	0.8	28
165	Regulation of adenosine transport by Dâ€glucose in human fetal endothelial cells: involvement of nitric oxide, protein kinase C and mitogenâ€activated protein kinase. Journal of Physiology, 2000, 529, 777-790.	2.9	41
166	Genetic Affinities Among Human Populations Inhabiting the Subsaharan Area, Northwest Africa, and the Iberian Peninsula. , 2000, , 33-50.		14
167	Northwest African distribution of the CD4/Alu microsatellite haplotypes. Annals of Human Genetics, 2000, 64, 321-7.	0.8	9
168	About the â€œPathologicalâ€•Role of the mtDNA T3308C Mutationâ€¦. American Journal of Human Genetics, 1999, 65, 1457-1459.	6.2	30