Celeste Eng

List of Publications by Year in descending order

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99 papers 7,405 citations

94433 37 h-index 78 g-index

106 all docs

106
docs citations

106 times ranked 15179 citing authors

#	Article	IF	CITATIONS
1	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
2	DNA Methylation in Newborns and Maternal Smoking in Pregnancy: Genome-wide Consortium Meta-analysis. American Journal of Human Genetics, 2016, 98, 680-696.	6.2	717
3	Multi-ancestry genome-wide association study of 21,000 cases and 95,000 controls identifies new risk loci for atopic dermatitis. Nature Genetics, 2015, 47, 1449-1456.	21.4	529
4	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. Nature Genetics, 2018, 50, 42-53.	21.4	426
5	The genetics of Mexico recapitulates Native American substructure and affects biomedical traits. Science, 2014, 344, 1280-1285.	12.6	420
6	Assembly of a pan-genome from deep sequencing of 910 humans of African descent. Nature Genetics, 2019, 51, 30-35.	21.4	276
7	The landscape of genomic imprinting across diverse adult human tissues. Genome Research, 2015, 25, 927-936.	5.5	216
8	Sparse PCA corrects for cell type heterogeneity in epigenome-wide association studies. Nature Methods, 2016, 13, 443-445.	19.0	205
9	Dissecting childhood asthma with nasal transcriptomics distinguishes subphenotypes of disease. Journal of Allergy and Clinical Immunology, 2014, 133, 670-678.e12.	2.9	204
10	Differential methylation between ethnic sub-groups reflects the effect of genetic ancestry and environmental exposures. ELife, 2017, 6, .	6.0	153
11	Epigenome-wide meta-analysis of DNA methylation and childhood asthma. Journal of Allergy and Clinical Immunology, 2019, 143, 2062-2074.	2.9	147
12	A continuum of admixture in the Western Hemisphere revealed by the African Diaspora genome. Nature Communications, 2016, 7, 12522.	12.8	136
13	Type 2 and interferon inflammation regulate SARS-CoV-2 entry factor expression in the airway epithelium. Nature Communications, 2020, 11, 5139.	12.8	131
14	Genome-wide association study of breast cancer in Latinas identifies novel protective variants on 6q25. Nature Communications, 2014, 5, 5260.	12.8	123
15	Genome-wide methylation data mirror ancestry information. Epigenetics and Chromatin, 2017, $10, 1.$	3.9	120
16	Genetic ancestry influences asthma susceptibility and lung function among Latinos. Journal of Allergy and Clinical Immunology, 2015, 135, 228-235.	2.9	113
17	Socioeconomic Status and Childhood Asthma in Urban Minority Youths. The GALA II and SAGE II Studies. American Journal of Respiratory and Critical Care Medicine, 2013, 188, 1202-1209.	5.6	110
18	Genome-wide association study and admixture mapping identify different asthma-associated loci in Latinos: The Genes-environments & Admixture in Latino Americans study. Journal of Allergy and Clinical Immunology, 2014, 134, 295-305.	2.9	106

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19	A genome-wide association study of bronchodilator response in Latinos implicates rare variants. Journal of Allergy and Clinical Immunology, 2014, 133, 370-378.e15.	2.9	105
20	Whole-Genome Sequencing of Pharmacogenetic Drug Response in Racially Diverse Children with Asthma. American Journal of Respiratory and Critical Care Medicine, 2018, 197, 1552-1564.	5.6	102
21	Obesity and Bronchodilator Response in Black and Hispanic Children and Adolescents With Asthma. Chest, 2015, 147, 1591-1598.	0.8	90
22	Single-Cell and Population Transcriptomics Reveal Pan-epithelial Remodeling in Type 2-High Asthma. Cell Reports, 2020, 32, 107872.	6.4	78
23	Perceived Discrimination Associated With Asthma and Related Outcomes in Minority Youth. Chest, 2017, 151, 804-812.	0.8	73
24	Association study in African-admixed populations across the Americas recapitulates asthma risk loci in non-African populations. Nature Communications, 2019, 10, 880.	12.8	71
25	The TAM family receptor tyrosine kinase TYRO3 is a negative regulator of type 2 immunity. Science, 2016, 352, 99-103.	12.6	67
26	Ethnic-specific associations of rare and low-frequency DNA sequence variants with asthma. Nature Communications, 2015, 6, 5965.	12.8	66
27	Native American gene flow into Polynesia predating Easter Island settlement. Nature, 2020, 583, 572-577.	27.8	64
28	Functional genomics of CDHR3 confirms its role in HRV-C infection and childhood asthma exacerbations. Journal of Allergy and Clinical Immunology, 2019, 144, 962-971.	2.9	63
29	Dual RNA-seq reveals viral infections in asthmatic children without respiratory illness which are associated with changes in the airway transcriptome. Genome Biology, 2017, 18, 12.	8.8	59
30	A genome-wide association and admixture mapping study of bronchodilator drug response in African Americans with asthma. Pharmacogenomics Journal, 2019, 19, 249-259.	2.0	54
31	Case-control admixture mapping in Latino populations enriches for known asthma-associated genes. Journal of Allergy and Clinical Immunology, 2012, 130, 76-82.e12.	2.9	53
32	Genome-wide association study and admixture mapping reveal new loci associated with total IgE levels in Latinos. Journal of Allergy and Clinical Immunology, 2015, 135, 1502-1510.	2.9	52
33	Dysregulated invertebrate tropomyosin–dectin-1 interaction confers susceptibility to allergic diseases. Science Immunology, 2018, 3, .	11.9	51
34	Genome-wide association study of lung function phenotypes in a founder population. Journal of Allergy and Clinical Immunology, 2014, 133, 248-255.e10.	2.9	50
35	Genomic insights into the origin and diversification of late maritime hunter-gatherers from the Chilean Patagonia. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E4006-E4012.	7.1	50
36	Genomeâ€wide association study of inhaled corticosteroid response in admixed children with asthma. Clinical and Experimental Allergy, 2019, 49, 789-798.	2.9	50

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37	COMT ValMet polymorphism is associated with post-traumatic stress disorder and functional outcome following mild traumatic brain injury. Journal of Clinical Neuroscience, 2017, 35, 109-116.	1.5	43
38	Whole-Genome Sequencing of Individuals from a Founder Population Identifies Candidate Genes for Asthma. PLoS ONE, 2014, 9, e104396.	2.5	42
39	ROP: dumpster diving in RNA-sequencing to find the source of 1 trillion reads across diverse adult human tissues. Genome Biology, 2018, 19, 36.	8.8	42
40	On the cross-population generalizability of gene expression prediction models. PLoS Genetics, 2020, 16, e1008927.	3.5	41
41	Ancestry-Dependent Enrichment of Deleterious Homozygotes in Runs of Homozygosity. American Journal of Human Genetics, 2019, 105, 747-762.	6.2	36
42	COMT Val 158 Met polymorphism is associated with nonverbal cognition following mild traumatic brain injury. Neurogenetics, 2016, 17, 31-41.	1.4	33
43	Correcting for cell-type heterogeneity in DNA methylation: a comprehensive evaluation. Nature Methods, 2017, 14, 218-219.	19.0	33
44	An admixture mapping meta-analysis implicates genetic variation at 18q21 with asthma susceptibility in Latinos. Journal of Allergy and Clinical Immunology, 2019, 143, 957-969.	2.9	33
45	Meta-analysis of GWA studies provides new insights on the genetic architecture of skin pigmentation in recently admixed populations. BMC Genetics, 2019, 20, 59.	2.7	32
46	Identification of a novel locus associated with skin colour in African-admixed populations. Scientific Reports, 2017, 7, 44548.	3.3	31
47	The Effects of Migration and Assortative Mating on Admixture Linkage Disequilibrium. Genetics, 2017, 205, 375-383.	2.9	31
48	Paths and timings of the peopling of Polynesia inferred from genomic networks. Nature, 2021, 597, 522-526.	27.8	31
49	Secondhand smoke exposure and asthma outcomes among African-American and Latino children with asthma. Thorax, 2018, 73, 1041-1048.	5.6	30
50	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	6.5	29
51	Bacterial salivary microbiome associates with asthma among african american children and young adults. Pediatric Pulmonology, 2019, 54, 1948-1956.	2.0	26
52	Ancestry and genetic associations with bronchopulmonary dysplasia in preterm infants. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2018, 315, L858-L869.	2.9	24
53	In utero tobacco smoke exposure, DNA methylation, and asthma in Latino children. Environmental Epidemiology, 2019, 3, e048.	3.0	24
54	Nasal airway transcriptome-wide association study of asthma reveals genetically driven mucus pathobiology. Nature Communications, 2022, 13, 1632.	12.8	24

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55	A genome-wide association study of asthma hospitalizations in adults. Journal of Allergy and Clinical Immunology, 2021, 147, 933-940.	2.9	23
56	Genetic Determinants of Telomere Length in African American Youth. Scientific Reports, 2018, 8, 13265.	3.3	20
57	Self-reported racial/ethnic discrimination and bronchodilator response in African American youth with asthma. PLoS ONE, 2017, 12, e0179091.	2.5	19
58	Development of a small panel of SNPs to infer ancestry in Chileans that distinguishes Aymara and Mapuche components. Biological Research, 2020, 53, 15.	3.4	18
59	An ancestryâ€based approach for detecting interactions. Genetic Epidemiology, 2018, 42, 49-63.	1.3	17
60	Racial/Ethnicâ€Specific Differences in the Effects of Inhaled Corticosteroid Use on Bronchodilator Response in Patients With Asthma. Clinical Pharmacology and Therapeutics, 2019, 106, 1133-1140.	4.7	17
61	Genomeâ€wide association study reveals a novel locus for asthma with severe exacerbations in diverse populations. Pediatric Allergy and Immunology, 2021, 32, 106-115.	2.6	17
62	Genome-wide association study of asthma exacerbations despite inhaled corticosteroid use. European Respiratory Journal, 2021, 57, 2003388.	6.7	17
63	Early-life ozone exposure associated with asthma without sensitization in Latino children. Journal of Allergy and Clinical Immunology, 2016, 138, 1703-1706.e1.	2.9	16
64	A genome-wide association study of severe asthma exacerbations in Latino children and adolescents. European Respiratory Journal, 2021, 57, 2002693.	6.7	15
65	Acculturation is associated with asthma burden and pulmonary function in Latino youth: The GALA II study. Journal of Allergy and Clinical Immunology, 2019, 143, 1914-1922.	2.9	14
66	Adapt-Mix: learning local genetic correlation structure improves summary statistics-based analyses. Bioinformatics, 2015, 31, i181-i189.	4.1	12
67	Epigenome-wide association study of lung function in Latino children and youth with asthma. Clinical Epigenetics, 2022, 14, 9.	4.1	12
68	Lung Function in African American Children with Asthma Is Associated with Novel Regulatory Variants of the KIT Ligand <i>KITLG/SCF </i> and Gene-By-Air-Pollution Interaction. Genetics, 2020, 215, 869-886.	2.9	11
69	Whole-Genome Sequencing Identifies Novel Functional Loci Associated with Lung Function in Puerto Rican Youth. American Journal of Respiratory and Critical Care Medicine, 2020, 202, 962-972.	5.6	11
70	NLRP1 variant M1184V decreases inflammasome activation in the context of DPP9 inhibition and asthma severity. Journal of Allergy and Clinical Immunology, 2021, 147, 2134-2145.e20.	2.9	11
71	A genome-wide study of DNA methylation in white blood cells and asthma in Latino children and youth. Epigenetics, 2021, 16, 577-585.	2.7	10
72	Lymph node–resident dendritic cells drive T _H 2 cell development involving MARCH1. Science Immunology, 2021, 6, eabh0707.	11.9	10

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73	Pharmacogenetic studies of long-acting beta agonist and inhaled corticosteroid responsiveness in randomised controlled trials of individuals of African descent with asthma. The Lancet Child and Adolescent Health, 2021, 5, 862-872.	5.6	10
74	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
75	Differential asthma odds following respiratory infection in children from three minority populations. PLoS ONE, 2020, 15, e0231782.	2.5	8
76	Breastfeeding associated with higher lung function in African American youths with asthma. Journal of Asthma, 2017, 54, 856-865.	1.7	7
77	Role of Sex on the Genetic Susceptibility to Childhood Asthma in Latinos and African Americans. Journal of Personalized Medicine, 2021, 11, 1140.	2.5	7
78	Expression of SMARCD1 interacts with age in association with asthma control on inhaled corticosteroid therapy. Respiratory Research, 2020, 21, 31.	3.6	6
79	Robust, flexible, and scalable tests for Hardy–Weinberg equilibrium across diverse ancestries. Genetics, 2021, 218, .	2.9	6
80	<i>ADRB2</i> haplotypes and asthma exacerbations in children and young adults: An individual participant data metaâ€analysis. Clinical and Experimental Allergy, 2021, 51, 1157-1171.	2.9	6
81	Race- and Ethnicity-Based Spirometry Reference Equations. Chest, 2022, 162, 184-195.	0.8	6
82	Whole Genome Sequencing Identifies CRISPLD2 as a Lung Function Gene in Children With Asthma. Chest, 2019, 156, 1068-1079.	0.8	5
83	Identification of CFTR variants in Latino patients with cystic fibrosis from the Dominican Republic and Puerto Rico. Pediatric Pulmonology, 2020, 55, 533-540.	2.0	5
84	Association of a PAI-1 Gene Polymorphism and Early Life Infections with Asthma Risk, Exacerbations, and Reduced Lung Function. PLoS ONE, 2016, 11, e0157848.	2.5	5
85	Optimized distributed systems achieve significant performance improvement on sorted merging of massive VCF files. GigaScience, 2018, 7, .	6.4	4
86	Integrative genomic analysis in African American children with asthma finds three novel loci associated with lung function. Genetic Epidemiology, 2021, 45, 190-208.	1.3	4
87	A deoxyribonuclease 1–like 3 genetic variant associates with asthma exacerbations. Journal of Allergy and Clinical Immunology, 2021, 147, 1095-1097.e10.	2.9	3
88	Native American Ancestry and Air Pollution Interact to Impact Bronchodilator Response in Puerto Rican Children with Asthma. Ethnicity and Disease, 2021, 31, 77-88.	2.3	2
89	Disentangling the impact of alcohol use and hepatitis C on insulin action in Latino individuals. Alcoholism: Clinical and Experimental Research, 2022, 46, 87-99.	2.4	0
90	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		O

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91	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		O
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