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	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	O
2	Race- and Ethnicity-Based Spirometry Reference Equations. Chest, 2022, 162, 184-195.	0.8	6
3	Epigenome-wide association study of lung function in Latino children and youth with asthma. Clinical Epigenetics, 2022, 14, 9.	4.1	12
4	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	6.5	29
5	Nasal airway transcriptome-wide association study of asthma reveals genetically driven mucus pathobiology. Nature Communications, 2022, 13, 1632.	12.8	24
6	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
7	A genome-wide association study of severe asthma exacerbations in Latino children and adolescents. European Respiratory Journal, 2021, 57, 2002693.	6.7	15
8	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
9	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
10	A genome-wide association study of asthma hospitalizations in adults. Journal of Allergy and Clinical Immunology, 2021, 147, 933-940.	2.9	23
11	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
12	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
13	Robust, flexible, and scalable tests for Hardy–Weinberg equilibrium across diverse ancestries. Genetics, 2021, 218, .	2.9	6
14	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
15	<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
16	Paths and timings of the peopling of Polynesia inferred from genomic networks. Nature, 2021, 597, 522-526.	27.8	31
17	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
18	Genome-wide association study of asthma exacerbations despite inhaled corticosteroid use. European Respiratory Journal, 2021, 57, 2003388.	6.7	17

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19	Lymph node–resident dendritic cells drive T _H 2 cell development involving MARCH1. Science Immunology, 2021, 6, eabh0707.	11.9	10
20	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
21	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
22	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
23	Type 2 and interferon inflammation regulate SARS-CoV-2 entry factor expression in the airway epithelium. Nature Communications, 2020, 11, 5139.	12.8	131
24	Single-Cell and Population Transcriptomics Reveal Pan-epithelial Remodeling in Type 2-High Asthma. Cell Reports, 2020, 32, 107872.	6.4	78
25	On the cross-population generalizability of gene expression prediction models. PLoS Genetics, 2020, 16, e1008927.	3.5	41
26	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
27	Differential asthma odds following respiratory infection in children from three minority populations. PLoS ONE, 2020, 15, e0231782.	2.5	8
28	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
29	Native American gene flow into Polynesia predating Easter Island settlement. Nature, 2020, 583, 572-577.	27.8	64
30	Expression of SMARCD1 interacts with age in association with asthma control on inhaled corticosteroid therapy. Respiratory Research, 2020, 21, 31.	3.6	6
31	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
32	On the cross-population generalizability of gene expression prediction models., 2020, 16, e1008927.		0
33	On the cross-population generalizability of gene expression prediction models., 2020, 16, e1008927.		0
34	On the cross-population generalizability of gene expression prediction models., 2020, 16, e1008927.		0
35	On the cross-population generalizability of gene expression prediction models., 2020, 16, e1008927.		0
36	On the cross-population generalizability of gene expression prediction models., 2020, 16, e1008927.		0

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37	On the cross-population generalizability of gene expression prediction models., 2020, 16, e1008927.		O
38	Title is missing!. , 2020, 15, e0231782.		0
39	Title is missing!. , 2020, 15, e0231782.		0
40	Title is missing!. , 2020, 15, e0231782.		0
41	Title is missing!. , 2020, 15, e0231782.		0
42	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
43	In utero tobacco smoke exposure, DNA methylation, and asthma in Latino children. Environmental Epidemiology, 2019, 3, e048.	3.0	24
44	Bacterial salivary microbiome associates with asthma among african american children and young adults. Pediatric Pulmonology, 2019, 54, 1948-1956.	2.0	26
45	Ancestry-Dependent Enrichment of Deleterious Homozygotes in Runs of Homozygosity. American Journal of Human Genetics, 2019, 105, 747-762.	6.2	36
46	Whole Genome Sequencing Identifies CRISPLD2 as a Lung Function Gene in Children With Asthma. Chest, 2019, 156, 1068-1079.	0.8	5
47	Genomeâ€wide association study of inhaled corticosteroid response in admixed children with asthma. Clinical and Experimental Allergy, 2019, 49, 789-798.	2.9	50
48	Epigenome-wide meta-analysis of DNA methylation and childhood asthma. Journal of Allergy and Clinical Immunology, 2019, 143, 2062-2074.	2.9	147
49	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
50	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
51	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
52	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
53	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
54	Assembly of a pan-genome from deep sequencing of 910 humans of African descent. Nature Genetics, 2019, 51, 30-35.	21.4	276

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55	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
56	Dysregulated invertebrate tropomyosin–dectin-1 interaction confers susceptibility to allergic diseases. Science Immunology, 2018, 3, .	11.9	51
57	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
58	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
59	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. Nature Genetics, 2018, 50, 42-53.	21.4	426
60	An ancestryâ€based approach for detecting interactions. Genetic Epidemiology, 2018, 42, 49-63.	1.3	17
61	Genetic Determinants of Telomere Length in African American Youth. Scientific Reports, 2018, 8, 13265.	3.3	20
62	Optimized distributed systems achieve significant performance improvement on sorted merging of massive VCF files. GigaScience, 2018, 7, .	6.4	4
63	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
64	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
65	Secondhand smoke exposure and asthma outcomes among African-American and Latino children with asthma. Thorax, 2018, 73, 1041-1048.	5.6	30
66	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
67	Perceived Discrimination Associated With Asthma and Related Outcomes in Minority Youth. Chest, 2017, 151, 804-812.	0.8	73
68	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
69	Correcting for cell-type heterogeneity in DNA methylation: a comprehensive evaluation. Nature Methods, 2017, 14, 218-219.	19.0	33
70	Identification of a novel locus associated with skin colour in African-admixed populations. Scientific Reports, 2017, 7, 44548.	3.3	31
71	Breastfeeding associated with higher lung function in African American youths with asthma. Journal of Asthma, 2017, 54, 856-865.	1.7	7
72	The Effects of Migration and Assortative Mating on Admixture Linkage Disequilibrium. Genetics, 2017, 205, 375-383.	2.9	31

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73	Genome-wide methylation data mirror ancestry information. Epigenetics and Chromatin, 2017, 10, 1.	3.9	120
74	Self-reported racial/ethnic discrimination and bronchodilator response in African American youth with asthma. PLoS ONE, 2017, 12, e0179091.	2.5	19
75	Differential methylation between ethnic sub-groups reflects the effect of genetic ancestry and environmental exposures. ELife, 2017, 6, .	6.0	153
76	The TAM family receptor tyrosine kinase TYRO3 is a negative regulator of type 2 immunity. Science, 2016, 352, 99-103.	12.6	67
77	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
78	A continuum of admixture in the Western Hemisphere revealed by the African Diaspora genome. Nature Communications, 2016, 7, 12522.	12.8	136
79	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
80	COMT Val 158 Met polymorphism is associated with nonverbal cognition following mild traumatic brain injury. Neurogenetics, 2016, 17, 31-41.	1.4	33
81	Sparse PCA corrects for cell type heterogeneity in epigenome-wide association studies. Nature Methods, 2016, 13, 443-445.	19.0	205
82	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
83	Obesity and Bronchodilator Response in Black and Hispanic Children and Adolescents With Asthma. Chest, 2015, 147, 1591-1598.	0.8	90
84	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
85	Adapt-Mix: learning local genetic correlation structure improves summary statistics-based analyses. Bioinformatics, 2015, 31, i181-i189.	4.1	12
86	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
87	Genetic ancestry influences asthma susceptibility and lung function among Latinos. Journal of Allergy and Clinical Immunology, 2015, 135, 228-235.	2.9	113
88	The landscape of genomic imprinting across diverse adult human tissues. Genome Research, 2015, 25, 927-936.	5.5	216
89	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
90	Ethnic-specific associations of rare and low-frequency DNA sequence variants with asthma. Nature Communications, 2015, 6, 5965.	12.8	66

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91	Whole-Genome Sequencing of Individuals from a Founder Population Identifies Candidate Genes for Asthma. PLoS ONE, 2014, 9, e104396.	2.5	42
92	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
93	Dissecting childhood asthma with nasal transcriptomics distinguishes subphenotypes of disease. Journal of Allergy and Clinical Immunology, 2014, 133, 670-678.e12.	2.9	204
94	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
95	Genome-wide association study of breast cancer in Latinas identifies novel protective variants on 6q25. Nature Communications, 2014, 5, 5260.	12.8	123
96	Genome-wide association study and admixture mapping identify different asthma-associated loci in Latinos: The Genes-environments & amp; Admixture in Latino Americans study. Journal of Allergy and Clinical Immunology, 2014, 134, 295-305.	2.9	106
97	The genetics of Mexico recapitulates Native American substructure and affects biomedical traits. Science, 2014, 344, 1280-1285.	12.6	420
98	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
99	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