Esteban Burchard

List of Publications by Year in descending order

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4	41344	2	9157
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ESTERAN RUDCHARD

#	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	Meta-analysis of genome-wide association studies of asthma in ethnically diverse North American populations. Nature Genetics, 2011, 43, 887-892.	21.4	736
3	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
4	Categorization of humans in biomedical research: genes, race and disease. Genome Biology, 2002, 3, comment2007.1.	9.6	605
5	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
6	Genomics for the world. Nature, 2011, 475, 163-165.	27.8	523
7	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. Nature Genetics, 2018, 50, 42-53.	21.4	426
8	Diversity in Clinical and Biomedical Research: A Promise Yet to Be Fulfilled. PLoS Medicine, 2015, 12, e1001918.	8.4	424
9	The genetics of Mexico recapitulates Native American substructure and affects biomedical traits. Science, 2014, 344, 1280-1285.	12.6	420
10	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	27.8	376
11	Race and Genetic Ancestry in Medicine — A Time for Reckoning with Racism. New England Journal of Medicine, 2021, 384, 474-480.	27.0	371
12	Assembly of a pan-genome from deep sequencing of 910 humans of African descent. Nature Genetics, 2019, 51, 30-35.	21.4	276
13	Early-Life Air Pollution and Asthma Risk in Minority Children. The GALA II and SAGE II Studies. American Journal of Respiratory and Critical Care Medicine, 2013, 188, 309-318.	5.6	229
14	The landscape of genomic imprinting across diverse adult human tissues. Genome Research, 2015, 25, 927-936.	5.5	216
15	Sparse PCA corrects for cell type heterogeneity in epigenome-wide association studies. Nature Methods, 2016, 13, 443-445.	19.0	205
16	Dissecting childhood asthma with nasal transcriptomics distinguishes subphenotypes of disease. Journal of Allergy and Clinical Immunology, 2014, 133, 670-678.e12.	2.9	204
17	Differential methylation between ethnic sub-groups reflects the effect of genetic ancestry and environmental exposures. ELife, 2017, 6, .	6.0	153
18	Epigenome-wide meta-analysis of DNA methylation and childhood asthma. Journal of Allergy and Clinical Immunology, 2019, 143, 2062-2074.	2.9	147

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19	Association Between Titin Loss-of-Function Variants and Early-Onset Atrial Fibrillation. JAMA - Journal of the American Medical Association, 2018, 320, 2354.	7.4	144
20	A continuum of admixture in the Western Hemisphere revealed by the African Diaspora genome. Nature Communications, 2016, 7, 12522.	12.8	136
21	Genome-wide association analysis identifies six new loci associated with forced vital capacity. Nature Genetics, 2014, 46, 669-677.	21.4	131
22	Type 2 and interferon inflammation regulate SARS-CoV-2 entry factor expression in the airway epithelium. Nature Communications, 2020, 11, 5139.	12.8	131
23	Childhood Obesity and Asthma Control in the GALA II and SAGE II Studies. American Journal of Respiratory and Critical Care Medicine, 2013, 187, 697-702.	5.6	129
24	Comparing Genetic Ancestry and Self-Described Race in African Americans Born in the United States and in Africa. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 1329-1338.	2.5	122
25	Genome-wide methylation data mirror ancestry information. Epigenetics and Chromatin, 2017, 10, 1.	3.9	120
26	Outdoor Air Pollution and New-Onset Airway Disease. An Official American Thoracic Society Workshop Report. Annals of the American Thoracic Society, 2020, 17, 387-398.	3.2	120
27	Genetic ancestry influences asthma susceptibility and lung function among Latinos. Journal of Allergy and Clinical Immunology, 2015, 135, 228-235.	2.9	113
28	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
29	A genome-wide association study of susceptibility to acute lymphoblastic leukemia in adolescents and young adults. Blood, 2015, 125, 680-686.	1.4	110
30	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
31	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
32	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
33	Melanesian Blond Hair Is Caused by an Amino Acid Change in TYRP1. Science, 2012, 336, 554-554.	12.6	104
34	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
35	Obesity and Bronchodilator Response in Black and Hispanic Children and Adolescents With Asthma. Chest, 2015, 147, 1591-1598.	0.8	90
36	Moving toward <i>True</i> Inclusion of Racial/Ethnic Minorities in Federally Funded Studies. A Key Step for Achieving Respiratory Health Equality in the United States. American Journal of Respiratory and Critical Care Medicine, 2015, 191, 514-521.	5.6	89

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37	CRISPR–Cas9-mediated gene knockout in primary human airway epithelial cells reveals a proinflammatory role for MUC18. Gene Therapy, 2015, 22, 822-829.	4.5	86
38	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. Nature Communications, 2018, 9, 2976.	12.8	85
39	Childhood asthma exacerbations and the Arg16 β2-receptor polymorphism: AÂmeta-analysis stratified by treatment. Journal of Allergy and Clinical Immunology, 2016, 138, 107-113.e5.	2.9	80
40	Single-Cell and Population Transcriptomics Reveal Pan-epithelial Remodeling in Type 2-High Asthma. Cell Reports, 2020, 32, 107872.	6.4	78
41	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
42	Genome-wide interaction studies reveal sex-specific asthma risk alleles. Human Molecular Genetics, 2014, 23, 5251-5259.	2.9	70
43	The TAM family receptor tyrosine kinase TYRO3 is a negative regulator of type 2 immunity. Science, 2016, 352, 99-103.	12.6	67
44	Ethnic-specific associations of rare and low-frequency DNA sequence variants with asthma. Nature Communications, 2015, 6, 5965.	12.8	66
45	Effect of secondhand smoke on asthma control among black and Latino children. Journal of Allergy and Clinical Immunology, 2012, 129, 1478-1483.e7.	2.9	65
46	Native American gene flow into Polynesia predating Easter Island settlement. Nature, 2020, 583, 572-577.	27.8	64
47	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
48	Genetic Ancestry and Risk Factors for Breast Cancer among Latinas in the San Francisco Bay Area. Cancer Epidemiology Biomarkers and Prevention, 2006, 15, 1878-1885.	2.5	61
49	Novel genetic risk factors for asthma in African American children: Precision Medicine and the SAGE II Study. Immunogenetics, 2016, 68, 391-400.	2.4	61
50	Differences in allergic sensitization by self-reported race and genetic ancestry. Journal of Allergy and Clinical Immunology, 2008, 122, 820-827.e9.	2.9	60
51	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
52	Air Pollution and Lung Function in Minority Youth with Asthma in the GALA II (Genes–Environments) Tj ETQq0 0	0 rgBT /0 5.6	overlock 10 54
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

54Case-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

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55	An epigenome-wide association study of total serum IgE in Hispanic children. Journal of Allergy and Clinical Immunology, 2017, 140, 571-577.	2.9	53
56	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
57	A meta-analysis of genome-wide association studies of asthma in PuertoÂRicans. European Respiratory Journal, 2017, 49, 1601505.	6.7	51
58	Dysregulated invertebrate tropomyosin–dectin-1 interaction confers susceptibility to allergic diseases. Science Immunology, 2018, 3, .	11.9	51
59	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
60	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
61	Genomeâ€wide association study of inhaled corticosteroid response in admixed children with asthma. Clinical and Experimental Allergy, 2019, 49, 789-798.	2.9	50
62	Current Status and Future Opportunities in Lung Precision Medicine Research with a Focus on Biomarkers. An American Thoracic Society/National Heart, Lung, and Blood Institute Research Statement. American Journal of Respiratory and Critical Care Medicine, 2018, 198, e116-e136.	5.6	49
63	Novel susceptibility variants at the ERG locus for childhood acute lymphoblastic leukemia in Hispanics. Blood, 2019, 133, 724-729.	1.4	44
64	Making Precision Medicine Socially Precise. Take a Deep Breath. American Journal of Respiratory and Critical Care Medicine, 2016, 193, 348-350.	5.6	43
65	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
66	Population History and Gene Divergence in Native Mexicans Inferred from 76 Human Exomes. Molecular Biology and Evolution, 2020, 37, 994-1006.	8.9	43
67	Population sequencing data reveal a compendium of mutational processes in the human germ line. Science, 2021, 373, 1030-1035.	12.6	43
68	Whole-Genome Sequencing of Individuals from a Founder Population Identifies Candidate Genes for Asthma. PLoS ONE, 2014, 9, e104396.	2.5	42
69	Pulmonary function disparities exist and persist in Hispanic patients with cystic fibrosis: A longitudinal analysis. Pediatric Pulmonology, 2017, 52, 1550-1557.	2.0	42
70	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
71	Medical research: Missing patients. Nature, 2014, 513, 301-302.	27.8	42
72	Genetic and socioeconomic study of mate choice in Latinos reveals novel assortment patterns. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 13621-13626.	7.1	41

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73	On the cross-population generalizability of gene expression prediction models. PLoS Genetics, 2020, 16, e1008927.	3.5	41
74	Gene-based association identifies SPATA13-AS1 as a pharmacogenomic predictor of inhaled short-acting beta-agonist response in multiple population groups. Pharmacogenomics Journal, 2014, 14, 365-371.	2.0	37
75	Ancestry-Dependent Enrichment of Deleterious Homozygotes in Runs of Homozygosity. American Journal of Human Genetics, 2019, 105, 747-762.	6.2	36
76	Genetic Investigation Into the Differential Risk of Atrial Fibrillation Among Black and White Individuals. JAMA Cardiology, 2016, 1, 442.	6.1	35
77	The Hawaii clopidogrel lawsuit: the possible effect on clinical laboratory testing. Personalized Medicine, 2015, 12, 179-181.	1.5	34
78	COMT Val 158 Met polymorphism is associated with nonverbal cognition following mild traumatic brain injury. Neurogenetics, 2016, 17, 31-41.	1.4	33
79	Correcting for cell-type heterogeneity in DNA methylation: a comprehensive evaluation. Nature Methods, 2017, 14, 218-219.	19.0	33
80	Integrative approach identifies corticosteroid response variant in diverse populations with asthma. Journal of Allergy and Clinical Immunology, 2019, 143, 1791-1802.	2.9	33
81	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
82	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
83	Genome-Wide Analysis Reveals Mucociliary Remodeling of the Nasal Airway Epithelium Induced by Urban PM _{2.5} . American Journal of Respiratory Cell and Molecular Biology, 2020, 63, 172-184.	2.9	32
84	Identification of a novel locus associated with skin colour in African-admixed populations. Scientific Reports, 2017, 7, 44548.	3.3	31
85	The Effects of Migration and Assortative Mating on Admixture Linkage Disequilibrium. Genetics, 2017, 205, 375-383.	2.9	31
86	Paths and timings of the peopling of Polynesia inferred from genomic networks. Nature, 2021, 597, 522-526.	27.8	31
87	Rationale and design of the multiethnic Pharmacogenomics in Childhood Asthma consortium. Pharmacogenomics, 2017, 18, 931-943.	1.3	30
88	Secondhand smoke exposure and asthma outcomes among African-American and Latino children with asthma. Thorax, 2018, 73, 1041-1048.	5.6	30
89	Sequencing and imputation in GWAS: Costâ€effective strategies to increase power and genomic coverage across diverse populations. Genetic Epidemiology, 2020, 44, 537-549.	1.3	30
90	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	6.5	29

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91	Factors associated with degree of atopy in Latino children in a nationwide pediatric sample: The Genes-environments and Admixture in Latino Asthmatics (GALA II) study. Journal of Allergy and Clinical Immunology, 2013, 132, 896-905.e1.	2.9	27
92	Bacterial salivary microbiome associates with asthma among african american children and young adults. Pediatric Pulmonology, 2019, 54, 1948-1956.	2.0	26
93	Assessing differences in inhaled corticosteroid response by self-reported race-ethnicity and genetic ancestry among asthmatic subjects. Journal of Allergy and Clinical Immunology, 2016, 137, 1364-1369.e2.	2.9	25
94	Predictive Properties of the Asthma Control Test and Its Component Questions for Severe Asthma Exacerbations. Journal of Allergy and Clinical Immunology: in Practice, 2017, 5, 121-127.e2.	3.8	25
95	A genome-wide association study of asthma symptoms in Latin American children. BMC Genetics, 2015, 16, 141.	2.7	24
96	DRD2 C957T polymorphism is associated with improved 6-month verbal learning following traumatic brain injury. Neurogenetics, 2017, 18, 29-38.	1.4	24
97	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
98	Ambient air pollution, asthma drug response, and telomere length in African American youth. Journal of Allergy and Clinical Immunology, 2019, 144, 839-845.e10.	2.9	24
99	In utero tobacco smoke exposure, DNA methylation, and asthma in Latino children. Environmental Epidemiology, 2019, 3, e048.	3.0	24
100	Nasal airway transcriptome-wide association study of asthma reveals genetically driven mucus pathobiology. Nature Communications, 2022, 13, 1632.	12.8	24
101	The genetic diversity of multiple sclerosis risk among Hispanic and African American populations living in the United States. Multiple Sclerosis Journal, 2020, 26, 1329-1339.	3.0	23
102	A genome-wide association study of asthma hospitalizations in adults. Journal of Allergy and Clinical Immunology, 2021, 147, 933-940.	2.9	23
103	17q21 variant increases the risk of exacerbations in asthmatic children despite inhaled corticosteroids use. Allergy: European Journal of Allergy and Clinical Immunology, 2018, 73, 2083-2088.	5.7	22
104	Telomere Length and the Risk of Atrial Fibrillation. Circulation: Arrhythmia and Electrophysiology, 2014, 7, 1026-1032.	4.8	21
105	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
106	Genetic Determinants of Telomere Length in African American Youth. Scientific Reports, 2018, 8, 13265.	3.3	20
107	<i>ST13</i> polymorphisms and their effect on exacerbations in steroidâ€treated asthmatic children and young adults. Clinical and Experimental Allergy, 2015, 45, 1051-1059.	2.9	19
108	Self-reported racial/ethnic discrimination and bronchodilator response in African American youth with asthma. PLoS ONE, 2017, 12, e0179091.	2.5	19

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109	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
110	Inferring parental genomic ancestries using pooled semi-Markov processes. Bioinformatics, 2015, 31, i190-i196.	4.1	17
111	An ancestryâ€based approach for detecting interactions. Genetic Epidemiology, 2018, 42, 49-63.	1.3	17
112	Racial/Ethnicâ€&pecific 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
113	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
114	Genome-wide association study of asthma exacerbations despite inhaled corticosteroid use. European Respiratory Journal, 2021, 57, 2003388.	6.7	17
115	A Genome-Wide Association Study of Post-bronchodilator Lung Function in Children with Asthma. American Journal of Respiratory and Critical Care Medicine, 2015, 192, 634-637.	5.6	16
116	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
117	Racial/ethnic differences in eligibility for asthma biologics among pediatric populations. Journal of Allergy and Clinical Immunology, 2021, 148, 1324-1331.e12.	2.9	16
118	Asthma and its relationship to mitochondrial copy number: Results from the Asthma Translational Genomics Collaborative (ATGC) of the Trans-Omics for Precision Medicine (TOPMed) program. PLoS ONE, 2020, 15, e0242364.	2.5	16
119	A genome-wide association study of severe asthma exacerbations in Latino children and adolescents. European Respiratory Journal, 2021, 57, 2002693.	6.7	15
120	Suggestive association between variants in IL1RAPL and asthma symptoms in Latin American children. European Journal of Human Genetics, 2017, 25, 439-445.	2.8	14
121	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
122	<i>IL1RL1</i> gene variations are associated with asthma exacerbations in children and adolescents using inhaled corticosteroids. Allergy: European Journal of Allergy and Clinical Immunology, 2020, 75, 984-989.	5.7	14
123	Multiâ€ancestry genomeâ€wide association study of asthma exacerbations. Pediatric Allergy and Immunology, 2022, 33, .	2.6	14
124	Genomeâ€wide association studies of exacerbations in children using longâ€acting beta2â€agonists. Pediatric Allergy and Immunology, 2021, 32, 1197-1207.	2.6	13
125	Racial Differences in Left Atrial Size: Results from the Coronary Artery Risk Development in Young Adults (CARDIA) Study. PLoS ONE, 2016, 11, e0151559.	2.5	13
126	Adapt-Mix: learning local genetic correlation structure improves summary statistics-based analyses. Bioinformatics, 2015, 31, i181-i189.	4.1	12

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127	Epigenome-wide association study of lung function in Latino children and youth with asthma. Clinical Epigenetics, 2022, 14, 9.	4.1	12
128	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
129	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
130	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
131	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
132	Variants in genes coding for glutathione S-transferases and asthma outcomes in children. Pharmacogenomics, 2018, 19, 707-713.	1.3	10
133	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
134	Lymph node–resident dendritic cells drive T _H 2 cell development involving MARCH1. Science Immunology, 2021, 6, eabh0707.	11.9	10
135	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
136	Clotting factor genes are associated with preeclampsia in high-altitude pregnant women in the Peruvian Andes. American Journal of Human Genetics, 2022, 109, 1117-1139.	6.2	10
137	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
138	Maternal age and asthma in Latino populations. Clinical and Experimental Allergy, 2016, 46, 1398-1406.	2.9	8
139	Differential asthma odds following respiratory infection in children from three minority populations. PLoS ONE, 2020, 15, e0231782.	2.5	8
140	Towards Equity in Health: Researchers Take Stock. PLoS Medicine, 2016, 13, e1002186.	8.4	8
141	Breastfeeding associated with higher lung function in African American youths with asthma. Journal of Asthma, 2017, 54, 856-865.	1.7	7
142	Novel locus for atopic dermatitis in African Americans and replication in European Americans. Journal of Allergy and Clinical Immunology, 2019, 143, 1229-1231.	2.9	7
143	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
144	Robust, flexible, and scalable tests for Hardy–Weinberg equilibrium across diverse ancestries. Genetics, 2021, 218, .	2.9	6

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145	<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
146	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
147	LTA4H rs2660845 association with montelukast response in early and late-onset asthma. PLoS ONE, 2021, 16, e0257396.	2.5	6
148	Race- and Ethnicity-Based Spirometry Reference Equations. Chest, 2022, 162, 184-195.	0.8	6
149	Multiomics analysis identifies BIRC3 as a novel glucocorticoid response–associated gene. Journal of Allergy and Clinical Immunology, 2022, 149, 1981-1991.	2.9	6
150	Origins of Cancer Disparities in Young Adults: Logic Models to Guide Research. American Journal of Preventive Medicine, 2017, 53, S95-S102.	3.0	5
151	Whole Genome Sequencing Identifies CRISPLD2 as a Lung Function Gene in Children With Asthma. Chest, 2019, 156, 1068-1079.	0.8	5
152	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
153	Atopic dermatitis, race, and genetics. Journal of Allergy and Clinical Immunology, 2020, 145, 108-110.	2.9	5
154	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
155	Optimized distributed systems achieve significant performance improvement on sorted merging of massive VCF files. GigaScience, 2018, 7, .	6.4	4
156	An epistatic interaction between pre-natal smoke exposure and socioeconomic status has a significant impact on bronchodilator drug response in African American youth with asthma. BioData Mining, 2020, 13, 7.	4.0	4
157	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
158	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
159	<scp>PAI</scp> â€l gainâ€ofâ€function genotype, factors increasing <scp>PAI</scp> â€l levels, and airway obstruction: The <scp>GALA II</scp> Cohort. Clinical and Experimental Allergy, 2017, 47, 1150-1158.	2.9	2
160	Genetic loci determining total immunoglobulin E levels from birth through adulthood. Allergy: European Journal of Allergy and Clinical Immunology, 2019, 74, 621-625.	5.7	2
161	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
162	Impact of Moderate Alcohol Discontinuation on InsulinÂAction and Secretion in Latinos With and Without Hepatitis C. Alcoholism: Clinical and Experimental Research, 2018, 42, 492-499.	2.4	1

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163	Powerful Tests for Multi-Marker Association Analysis Using Ensemble Learning. PLoS ONE, 2015, 10, e0143489.	2.5	0
164	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
165	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
166	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
167	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
168	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
169	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
170	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
171	Title is missing!. , 2020, 15, e0231782.		0
172	Title is missing!. , 2020, 15, e0231782.		0
173	Title is missing!. , 2020, 15, e0231782.		0
174	Title is missing!. , 2020, 15, e0231782.		0