

# Kevin L Keys

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9520615/publications.pdf>

Version: 2024-02-01

24  
papers

370  
citations

1039880

9  
h-index

887953

17  
g-index

32  
all docs

32  
docs citations

32  
times ranked

978  
citing authors

#	ARTICLE	IF	CITATIONS
1	Epigenome-wide association study of lung function in Latino children and youth with asthma. <i>Clinical Epigenetics</i> , 2022, 14, 9.	1.8	12
2	Integrative genomic analysis in African American children with asthma finds three novel loci associated with lung function. <i>Genetic Epidemiology</i> , 2021, 45, 190-208.	0.6	4
3	A genome-wide study of DNA methylation in white blood cells and asthma in Latino children and youth. <i>Epigenetics</i> , 2021, 16, 577-585.	1.3	10
4	Genome-wide association study reveals a novel locus for asthma with severe exacerbations in diverse populations. <i>Pediatric Allergy and Immunology</i> , 2021, 32, 106-115.	1.1	17
5	OpenMendel: a cooperative programming project for statistical genetics. <i>Human Genetics</i> , 2020, 139, 61-71.	1.8	29
6	On the cross-population generalizability of gene expression prediction models. <i>PLoS Genetics</i> , 2020, 16, e1008927.	1.5	41
7	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. <i>Genetics</i> , 2020, 215, 869-886.	1.2	11
8	Whole-Genome Sequencing Identifies Novel Functional Loci Associated with Lung Function in Puerto Rican Youth. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020, 202, 962-972.	2.5	11
9	Iterative hard thresholding in genome-wide association studies: Generalized linear models, prior weights, and double sparsity. <i>GigaScience</i> , 2020, 9, .	3.3	10
10	Sequencing and imputation in GWAS: Cost-effective strategies to increase power and genomic coverage across diverse populations. <i>Genetic Epidemiology</i> , 2020, 44, 537-549.	0.6	30
11	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
12	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
13	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
14	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
15	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
16	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
17	Ambient air pollution, asthma drug response, and telomere length in African American youth. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 144, 839-845.e10.	1.5	24
18	Proximal Distance Algorithms: Theory and Practice. <i>Journal of Machine Learning Research</i> , 2019, 20, .	62.4	0

#	ARTICLE	IF	CITATIONS
19	Whole-Genome Sequencing of Pharmacogenetic Drug Response in Racially Diverse Children with Asthma. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2018, 197, 1552-1564.	2.5	102
20	Influence of pathway topology and functional class on the molecular evolution of human metabolic genes. <i>PLoS ONE</i> , 2018, 13, e0208782.	1.1	3
21	Genetic Determinants of Telomere Length in African American Youth. <i>Scientific Reports</i> , 2018, 8, 13265.	1.6	20
22	BioSimulator.jl: Stochastic simulation in Julia. <i>Computer Methods and Programs in Biomedicine</i> , 2018, 167, 23-35.	2.6	12
23	Iterative hard thresholding for model selection in genome-wide association studies. <i>Genetic Epidemiology</i> , 2017, 41, 756-768.	0.6	6
24	Ten Simple Rules for Getting Help from Online Scientific Communities. <i>PLoS Computational Biology</i> , 2011, 7, e1002202.	1.5	12