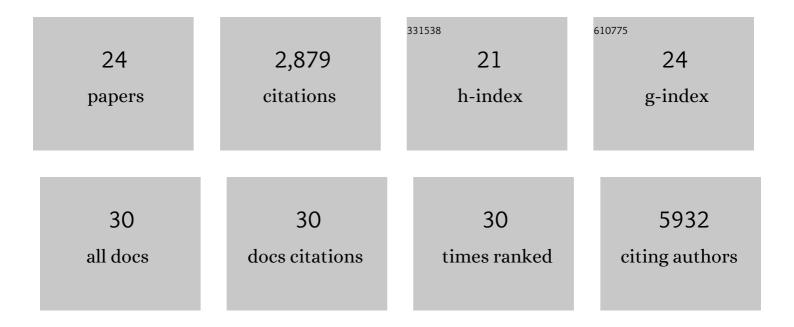
## Karla Sandoval

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/9820047/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Genetic analyses of diverse populations improves discovery for complex traits. Nature, 2019, 570, 514-518.	13.7	679
2	The genetics of Mexico recapitulates Native American substructure and affects biomedical traits. Science, 2014, 344, 1280-1285.	6.0	420
3	Reconstructing the Population Genetic History of the Caribbean. PLoS Genetics, 2013, 9, e1003925.	1.5	296
4	Pulling out the 1%: Whole-Genome Capture for the Targeted Enrichment of Ancient DNA Sequencing Libraries. American Journal of Human Genetics, 2013, 93, 852-864.	2.6	284
5	Reconstructing Native American Migrations from Whole-Genome and Whole-Exome Data. PLoS Genetics, 2013, 9, e1004023.	1.5	185
6	Latin Americans show wide-spread Converso ancestry and imprint of local Native ancestry on physical appearance. Nature Communications, 2018, 9, 5388.	5.8	123
7	Genetic ancestry influences asthma susceptibility and lung function among Latinos. Journal of Allergy and Clinical Immunology, 2015, 135, 228-235.	1.5	113
8	A genome-wide association study of bronchodilator response in Latinos implicates rare variants. Journal of Allergy and Clinical Immunology, 2014, 133, 370-378.e15.	1.5	105
9	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.	2.5	102
10	Genetic origin, admixture, and asymmetry in maternal and paternal human lineages in Cuba. BMC Evolutionary Biology, 2008, 8, 213.	3.2	101
11	Native American gene flow into Polynesia predating Easter Island settlement. Nature, 2020, 583, 572-577.	13.7	64
12	A genome-wide association and admixture mapping study of bronchodilator drug response in African Americans with asthma. Pharmacogenomics Journal, 2019, 19, 249-259.	0.9	54
13	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.	1.5	52
14	Population History and Gene Divergence in Native Mexicans Inferred from 76 Human Exomes. Molecular Biology and Evolution, 2020, 37, 994-1006.	3.5	43
15	Linguistic and maternal genetic diversity are not correlated in Native Mexicans. Human Genetics, 2009, 126, 521-531.	1.8	40
16	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.	1.5	33
17	Paths and timings of the peopling of Polynesia inferred from genomic networks. Nature, 2021, 597, 522-526.	13.7	31
18	Demographic History of Indigenous Populations in Mesoamerica Based on mtDNA Sequence Data. PLoS ONE, 2015, 10, e0131791.	1.1	29

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#	Article	IF	CITATIONS
19	A loss-of-function <i>IFNAR1</i> allele in Polynesia underlies severe viral diseases in homozygotes. Journal of Experimental Medicine, 2022, 219, .	4.2	28
20	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.	1.5	27
21	Yâ€chromosome diversity in Native Mexicans reveals continental transition of genetic structure in the Americas. American Journal of Physical Anthropology, 2012, 148, 395-405.	2.1	26
22	Development of a small panel of SNPs to infer ancestry in Chileans that distinguishes Aymara and Mapuche components. Biological Research, 2020, 53, 15.	1.5	18
23	SNPlexing the human Y-chromosome: A single-assay system for major haplogroup screening. Electrophoresis, 2007, 28, 3201-3206.	1.3	10
24	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.	2.6	10