

# Paula S Ramos

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6909259/publications.pdf>

Version: 2024-02-01

39  
papers

2,668  
citations

361413

20  
h-index

315739

38  
g-index

43  
all docs

43  
docs citations

43  
times ranked

5569  
citing authors

#	ARTICLE	IF	CITATIONS
1	Antifibrotic factor KLF4 is repressed by the miR-10/TFAP2A/TBX5 axis in dermal fibroblasts: insights from twins discordant for systemic sclerosis. <i>Annals of the Rheumatic Diseases</i> , 2022, 81, 268-277.	0.9	19
2	GPA-Tree: statistical approach for functional-annotation-tree-guided prioritization of GWAS results. <i>Bioinformatics</i> , 2022, 38, 1067-1074.	4.1	4
3	A pragmatic implementation research study for In Our DNA SC: a protocol to identify multi-level factors that support the implementation of a population-wide genomic screening initiative in diverse populations. <i>Implementation Science Communications</i> , 2022, 3, 48.	2.2	8
4	Social Factors, Epigenomics and Lupus in African American Women (SELA) Study: protocol for an observational mechanistic study examining the interplay of multiple individual and social factors on lupus outcomes in a health disparity population. <i>Lupus Science and Medicine</i> , 2022, 9, e000698.	2.7	0
5	Unravelling the complex genetic regulation of immune cells. <i>Nature Reviews Rheumatology</i> , 2021, 17, 131-132.	8.0	2
6	Genetic landscape of Gullah African Americans. <i>American Journal of Physical Anthropology</i> , 2021, 175, 905-919.	2.1	9
7	Integrating genetic and social factors to understand health disparities in lupus. <i>Current Opinion in Rheumatology</i> , 2021, 33, 598-604.	4.3	9
8	Differential DNA Methylation Landscape in Skin Fibroblasts from African Americans with Systemic Sclerosis. <i>Genes</i> , 2021, 12, 129.	2.4	12
9	Nucleic Acid-Sensing and Interferon-Inducible Pathways Show Differential Methylation in MZ Twins Discordant for Lupus and Overexpression in Independent Lupus Samples: Implications for Pathogenic Mechanism and Drug Targeting. <i>Genes</i> , 2021, 12, 1898.	2.4	6
10	<i>HLA</i> and autoantibodies define scleroderma subtypes and risk in African and European Americans and suggest a role for molecular mimicry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 552-562.	7.1	52
11	GAIL: An interactive webserver for inference and dynamic visualization of gene-gene associations based on gene ontology guided mining of biomedical literature. <i>PLoS ONE</i> , 2019, 14, e0219195.	2.5	5
12	Epigenetics of scleroderma: Integrating genetic, ethnic, age, and environmental effects. <i>Journal of Scleroderma and Related Disorders</i> , 2019, 4, 238-250.	1.7	8
13	Integrative analysis of DNA methylation in discordant twins unveils distinct architectures of systemic sclerosis subsets. <i>Clinical Epigenetics</i> , 2019, 11, 58.	4.1	32
14	An Analytic Approach Using Candidate Gene Selection and Logic Forest to Identify Gene by Environment Interactions (G Å E) for Systemic Lupus Erythematosus in African Americans. <i>Genes</i> , 2018, 9, 496.	2.4	7
15	Brief Report: Whole-Exome Sequencing to Identify Rare Variants and Gene Networks That Increase Susceptibility to Scleroderma in African Americans. <i>Arthritis and Rheumatology</i> , 2018, 70, 1654-1660.	5.6	10
16	ShinyGPA: An interactive visualization toolkit for investigating pleiotropic architecture using GWAS datasets. <i>PLoS ONE</i> , 2018, 13, e0190949.	2.5	3
17	Transancestral mapping and genetic load in systemic lupus erythematosus. <i>Nature Communications</i> , 2017, 8, 16021.	12.8	314
18	Population Genetics and Natural Selection in Rheumatic Disease. <i>Rheumatic Disease Clinics of North America</i> , 2017, 43, 313-326.	1.9	10

#	ARTICLE	IF	CITATIONS
19	An evaluation of common methods for dichotomization of continuous variables to discriminate disease status. <i>Communications in Statistics - Theory and Methods</i> , 2017, 46, 10823-10834.	1.0	27
20	Clinical and serological features of systemic sclerosis in a multicenter African American cohort. <i>Medicine (United States)</i> , 2017, 96, e8980.	1.0	78
21	Impact of common genetic determinants of Hemoglobin A1c on type 2 diabetes risk and diagnosis in ancestrally diverse populations: A transethnic genome-wide meta-analysis. <i>PLoS Medicine</i> , 2017, 14, e1002383.	8.4	341
22	GPA-MDS: A Visualization Approach to Investigate Genetic Architecture among Phenotypes Using GWAS Results. <i>International Journal of Genomics</i> , 2016, 2016, 1-6.	1.6	3
23	Genetics of systemic sclerosis. <i>Current Opinion in Rheumatology</i> , 2015, 27, 521-529.	4.3	28
24	Genetics of autoimmune diseases: insights from population genetics. <i>Journal of Human Genetics</i> , 2015, 60, 657-664.	2.3	127
25	Genes Associated with SLE Are Targets of Recent Positive Selection. <i>Autoimmune Diseases</i> , 2014, 2014, 1-11.	0.6	33
26	Lupus Nephritis Susceptibility Loci in Women with Systemic Lupus Erythematosus. <i>Journal of the American Society of Nephrology: JASN</i> , 2014, 25, 2859-2870.	6.1	117
27	Variable Association of Reactive Intermediate Genes with Systemic Lupus Erythematosus in Populations with Different African Ancestry. <i>Journal of Rheumatology</i> , 2013, 40, 842-849.	2.0	15
28	Brief Report: Enrichment of associations in genes with fibrosis, apoptosis, and innate immunity functions with cardiac manifestations of neonatal lupus. <i>Arthritis and Rheumatism</i> , 2012, 64, 4060-4065.	6.7	13
29	Immune function genes CD99L2, JARID2 and TPO show association with autism spectrum disorder. <i>Molecular Autism</i> , 2012, 3, 4.	4.9	32
30	Genome-wide association analysis of juvenile idiopathic arthritis identifies a new susceptibility locus at chromosomal region 3q13. <i>Arthritis and Rheumatism</i> , 2012, 64, 2781-2791.	6.7	62
31	Identification of IRF8, TMEM39A, and IKZF3-ZPBP2 as Susceptibility Loci for Systemic Lupus Erythematosus in a Large-Scale Multiracial Replication Study. <i>American Journal of Human Genetics</i> , 2012, 90, 648-660.	6.2	161
32	Preferential transmission of genetic risk variants of candidate loci at 6p21 from asymptomatic grandparents to mothers of children with neonatal lupus. <i>Arthritis and Rheumatism</i> , 2012, 64, 931-939.	6.7	9
33	Genetic analyses of interferon pathway-related genes reveal multiple new loci associated with systemic lupus erythematosus. <i>Arthritis and Rheumatism</i> , 2011, 63, 2049-2057.	6.7	45
34	A Comprehensive Analysis of Shared Loci between Systemic Lupus Erythematosus (SLE) and Sixteen Autoimmune Diseases Reveals Limited Genetic Overlap. <i>PLoS Genetics</i> , 2011, 7, e1002406.	3.5	148
35	Identification of candidate loci at 6p21 and 21q22 in a genome-wide association study of cardiac manifestations of neonatal lupus. <i>Arthritis and Rheumatism</i> , 2010, 62, 3415-3424.	6.7	84
36	The susceptibility loci juvenile idiopathic arthritis shares with other autoimmune diseases extend to PTPN2, COG6, and ANGPT1. <i>Arthritis and Rheumatism</i> , 2010, 62, 3265-3276.	6.7	105

#	ARTICLE	IF	CITATIONS
37	Genetic Factors Predisposing to Systemic Lupus Erythematosus and Lupus Nephritis. <i>Seminars in Nephrology</i> , 2010, 30, 164-176.	1.6	81
38	Familial aggregation and linkage analysis of autoantibody traits in pedigrees multiplex for systemic lupus erythematosus. <i>Genes and Immunity</i> , 2006, 7, 417-432.	4.1	56
39	Genetic Association of the R620W Polymorphism of Protein Tyrosine Phosphatase PTPN22 with Human SLE. <i>American Journal of Human Genetics</i> , 2004, 75, 504-507.	6.2	591