

Stephanie M Gogarten

List of Publications by Year in descending order

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Version: 2024-02-01

64
papers

9,090
citations

101384

36
h-index

114278

63
g-index

75
all docs

75
docs citations

75
times ranked

19049
citing authors

#	ARTICLE	IF	CITATIONS
1	Association of clonal hematopoiesis with chronic obstructive pulmonary disease. <i>Blood</i> , 2022, 139, 357-368.	0.6	106
2	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. <i>Cell Genomics</i> , 2022, 2, 100084.	3.0	29
3	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. <i>Nature Genetics</i> , 2022, 54, 263-273.	9.4	156
4	Ancestral diversity improves discovery and fine-mapping of genetic loci for anthropometric traits. The Hispanic/Latino Anthropometry Consortium. <i>Human Genetics and Genomics Advances</i> , 2022, 3, 100099.	1.0	3
5	Accounting for population structure in genetic studies of cystic fibrosis. <i>Human Genetics and Genomics Advances</i> , 2022, 3, 100117.	1.0	1
6	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. <i>Nature</i> , 2021, 590, 290-299.	13.7	1,069
7	Identification of putative causal loci in whole-genome sequencing data via knockoff statistics. <i>Nature Communications</i> , 2021, 12, 3152.	5.8	17
8	Genome sequencing unveils a regulatory landscape of platelet reactivity. <i>Nature Communications</i> , 2021, 12, 3626.	5.8	29
9	Variant-specific inflation factors for assessing population stratification at the phenotypic variance level. <i>Nature Communications</i> , 2021, 12, 3506.	5.8	1
10	Genome-wide association study of body fat distribution traits in Hispanics/Latinos from the HCHS/SOL. <i>Human Molecular Genetics</i> , 2021, 30, 2190-2204.	1.4	8
11	BinomiRare: A robust test for association of a rare genetic variant with a binary outcome for mixed models and any case-control proportion. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100040.	1.0	2
12	Identification of novel and rare variants associated with handgrip strength using whole genome sequence data from the NHLBI Trans-Omics in Precision Medicine (TOPMed) Program. <i>PLoS ONE</i> , 2021, 16, e0253611.	1.1	4
13	Whole-genome association analyses of sleep-disordered breathing phenotypes in the NHLBI TOPMed program. <i>Genome Medicine</i> , 2021, 13, 136.	3.6	16
14	A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. <i>Nature Genetics</i> , 2021, 53, 1504-1516.	9.4	69
15	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. <i>Nature</i> , 2020, 586, 763-768.	13.7	376
16	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. <i>Nature Genetics</i> , 2020, 52, 969-983.	9.4	146
17	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. <i>Nature Communications</i> , 2020, 11, 2542.	5.8	59
18	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. <i>Journal of the National Cancer Institute</i> , 2019, 111, 146-157.	3.0	129

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19	Genetic association testing using the GENESIS R/Bioconductor package. <i>Bioinformatics</i> , 2019, 35, 5346-5348.	1.8	260
20	A fully adjusted two-stage procedure for rank-normalization in genetic association studies. <i>Genetic Epidemiology</i> , 2019, 43, 263-275.	0.6	60
21	Efficient Variant Set Mixed Model Association Tests for Continuous and Binary Traits in Large-Scale Whole-Genome Sequencing Studies. <i>American Journal of Human Genetics</i> , 2019, 104, 260-274.	2.6	103
22	Genome-wide association study and meta-analysis identify loci associated with ventricular and supraventricular ectopy. <i>Scientific Reports</i> , 2018, 8, 5675.	1.6	4
23	Genome-Wide Association Study of Heavy Smoking and Daily/Nondaily Smoking in the Hispanic Community Health Study/Study of Latinos (HCHS/SOL). <i>Nicotine and Tobacco Research</i> , 2018, 20, 448-457.	1.4	21
24	Genome-wide association study of depressive symptoms in the Hispanic Community Health Study/Study of Latinos. <i>Journal of Psychiatric Research</i> , 2018, 99, 167-176.	1.5	15
25	Genome-wide association study of PR interval in Hispanics/Latinos identifies novel locus at <i>ID2</i> . <i>Heart</i> , 2018, 104, 904-911.	1.2	12
26	Association Between Titin Loss-of-Function Variants and Early-Onset Atrial Fibrillation. <i>JAMA - Journal of the American Medical Association</i> , 2018, 320, 2354.	3.8	144
27	Multi-Omics Analysis Reveals a HIF Network and Hub Gene <i>EPAS1</i> Associated with Lung Adenocarcinoma. <i>EBioMedicine</i> , 2018, 32, 93-101.	2.7	35
28	Genome-wide association study of generalized anxiety symptoms in the Hispanic Community Health Study/Study of Latinos. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2017, 174, 132-143.	1.1	37
29	A genome-wide interaction analysis of tricyclic/tetracyclic antidepressants and RR and QT intervals: a pharmacogenomics study from the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium. <i>Journal of Medical Genetics</i> , 2017, 54, 313-323.	1.5	9
30	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. <i>Nature Communications</i> , 2017, 8, 15805.	5.8	95
31	Genome-wide association study of heart rate and its variability in Hispanic/Latino cohorts. <i>Heart Rhythm</i> , 2017, 14, 1675-1684.	0.3	18
32	SeqArray—a storage-efficient high-performance data format for WGS variant calls. <i>Bioinformatics</i> , 2017, 33, 2251-2257.	1.8	127
33	Analysis commons, a team approach to discovery in a big-data environment for genetic epidemiology. <i>Nature Genetics</i> , 2017, 49, 1560-1563.	9.4	93
34	GWAS of the electrocardiographic QT interval in Hispanics/Latinos generalizes previously identified loci and identifies population-specific signals. <i>Scientific Reports</i> , 2017, 7, 17075.	1.6	23
35	Meta-Analysis of Genome-Wide Association Studies with Correlated Individuals: Application to the Hispanic Community Health Study/Study of Latinos (HCHS/SOL). <i>Genetic Epidemiology</i> , 2016, 40, 492-501.	0.6	16
36	GENOME-WIDE ASSOCIATION STUDY (GWAS) AND GENOME-WIDE BY ENVIRONMENT INTERACTION STUDY (GWEIS) OF DEPRESSIVE SYMPTOMS IN AFRICAN AMERICAN AND HISPANIC/LATINA WOMEN. <i>Depression and Anxiety</i> , 2016, 33, 265-280.	2.0	99

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37	Local Ancestry Inference in a Large US-Based Hispanic/Latino Study: Hispanic Community Health Study/Study of Latinos (HCHS/SOL). <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1525-1534.	0.8	51
38	Genetic variation near <i>IRS1</i> is associated with adiposity and a favorable metabolic profile in <i>UKS</i> . <i>SCHL</i> . <i>Obesity</i> , 2016, 24, 2407-2413.	1.5	5
39	Genome-wide Association Study of Platelet Count Identifies Ancestry-Specific Loci in Hispanic/Latino Americans. <i>American Journal of Human Genetics</i> , 2016, 98, 229-242.	2.6	71
40	Shared genetic susceptibility of vascular-related biomarkers with ischemic and recurrent stroke. <i>Neurology</i> , 2016, 86, 351-359.	1.5	33
41	Genetic Diversity and Association Studies in US Hispanic/Latino Populations: Applications in the Hispanic Community Health Study/Study of Latinos. <i>American Journal of Human Genetics</i> , 2016, 98, 165-184.	2.6	266
42	Genome-wide association study of colorectal cancer identifies six new susceptibility loci. <i>Nature Communications</i> , 2015, 6, 7138.	5.8	138
43	Genetic Associations with Plasma B12, B6, and Folate Levels in an Ischemic Stroke Population from the Vitamin Intervention for Stroke Prevention (VISP) Trial. <i>Frontiers in Public Health</i> , 2014, 2, 112.	1.3	23
44	Genome-Wide Meta-Analysis of Homocysteine and Methionine Metabolism Identifies Five One Carbon Metabolism Loci and a Novel Association of <i>ALDH1L1</i> with Ischemic Stroke. <i>PLoS Genetics</i> , 2014, 10, e1004214.	1.5	69
45	<code>VariantAnnotation</code> : a <code>Bioconductor</code> package for exploration and annotation of genetic variants. <i>Bioinformatics</i> , 2014, 30, 2076-2078.	1.8	293
46	Identification of Genetic Susceptibility Loci for Colorectal Tumors in a Genome-Wide Meta-analysis. <i>Gastroenterology</i> , 2013, 144, 799-807.e24.	0.6	292
47	THE PANCHROMATIC HUBBLE ANDROMEDA TREASURY. <i>Astrophysical Journal, Supplement Series</i> , 2012, 200, 18.	3.0	269
48	A high-performance computing toolset for relatedness and principal component analysis of SNP data. <i>Bioinformatics</i> , 2012, 28, 3326-3328.	1.8	1,939
49	GWASTools: an R/Bioconductor package for quality control and analysis of genome-wide association studies. <i>Bioinformatics</i> , 2012, 28, 3329-3331.	1.8	177
50	Detectable clonal mosaicism from birth to old age and its relationship to cancer. <i>Nature Genetics</i> , 2012, 44, 642-650.	9.4	511
51	Interplay of Genetic Risk Factors (<i>CHRNA5</i> - <i>CHRNA3</i> - <i>CHRNA4</i>) and Cessation Treatments in Smoking Cessation Success. <i>American Journal of Psychiatry</i> , 2012, 169, 735-742.	4.0	138
52	THE HISTORY OF STAR FORMATION IN GALAXY DISKS IN THE LOCAL VOLUME AS MEASURED BY THE ADVANCED CAMERA FOR SURVEYS NEARBY GALAXY SURVEY TREASURY. <i>Astrophysical Journal Letters</i> , 2011, 734, L22.	3.0	18
53	HOW TYPICAL ARE THE LOCAL GROUP DWARF GALAXIES?. <i>Astrophysical Journal</i> , 2011, 743, 8.	1.6	49
54	THE ACS NEARBY GALAXY SURVEY TREASURY. VIII. THE GLOBAL STAR FORMATION HISTORIES OF 60 DWARF GALAXIES IN THE LOCAL VOLUME. <i>Astrophysical Journal</i> , 2011, 739, 5.	1.6	295

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55	Common variants near CAV1 and CAV2 are associated with primary open-angle glaucoma in Caucasians from the USA. <i>Human Molecular Genetics</i> , 2011, 20, 4707-4713.	1.4	156
56	THE ADVANCED CAMERA FOR SURVEYS NEARBY GALAXY SURVEY TREASURY. IV. THE STAR FORMATION HISTORY OF NGC 2976. <i>Astrophysical Journal</i> , 2010, 709, 135-148.	1.6	32
57	THE ADVANCED CAMERA FOR SURVEYS NEARBY GALAXY SURVEY TREASURY. V. RADIAL STAR FORMATION HISTORY OF NGC 300. <i>Astrophysical Journal</i> , 2010, 712, 858-874.	1.6	86
58	THE NGC 300 TRANSIENT: AN ALTERNATIVE METHOD FOR MEASURING PROGENITOR MASSES. <i>Astrophysical Journal</i> , 2009, 703, 300-310.	1.6	50
59	<i>SPITZER</i> OBSERVATIONS OF A GRAVITATIONALLY LENSED QUASAR, QSO 2237+0305. <i>Astrophysical Journal</i> , 2009, 697, 1010-1019.	1.6	27
60	THE ACS NEARBY GALAXY SURVEY TREASURY. II. YOUNG STARS AND THEIR RELATION TO H α AND UV EMISSION TIMESCALES IN THE M81 OUTER DISK. <i>Astrophysical Journal</i> , 2009, 691, 115-130.	1.6	45
61	THE ACS NEARBY GALAXY SURVEY TREASURY. I. THE STAR FORMATION HISTORY OF THE M81 OUTER DISK. <i>Astronomical Journal</i> , 2009, 137, 419-430.	1.9	57
62	THE ACS NEARBY GALAXY SURVEY TREASURY. <i>Astrophysical Journal</i> , Supplement Series, 2009, 183, 67-108.	3.0	435
63	The Size-Luminosity Relation of Disk Galaxies in EDisCS Clusters. <i>Proceedings of the International Astronomical Union</i> , 2006, 2, 201-201.	0.0	0
64	The Ultraviolet, Optical, and Infrared Properties of Sloan Digital Sky Survey Sources Detected byGALEX. <i>Astronomical Journal</i> , 2005, 130, 1022-1036.	1.9	31