Sarah Pendergrass

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/2665404/publications.pdf

Version: 2024-02-01

44	4,582	159585	243625
papers	citations	30 h-index	44 g-index

46	46	46	9982
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Systematic comparison of phenome-wide association study of electronic medical record data and genome-wide association study data. Nature Biotechnology, 2013, 31, 1102-1111.	17.5	846
2	Methods of integrating data to uncover genotypeâ€“phenotype interactions. Nature Reviews Genetics, 2015, 16, 85-97.	16.3	803
3	Molecular Subsets in the Gene Expression Signatures of Scleroderma Skin. PLoS ONE, 2008, 3, e2696.	2.5	334
4	Phenome-Wide Association Study (PheWAS) for Detection of Pleiotropy within the Population Architecture using Genomics and Epidemiology (PAGE) Network. PLoS Genetics, 2013, 9, e1003087.	3.5	171
5	Meta-Analysis of Genome-Wide Association Studies for Abdominal Aortic Aneurysm Identifies Four New Disease-Specific Risk Loci. Circulation Research, 2017, 120, 341-353.	4.5	166
6	The use of phenome-wide association studies (PheWAS) for exploration of novel genotype-phenotype relationships and pleiotropy discovery. Genetic Epidemiology, 2011, 35, 410-422.	1.3	161
7	Genetic Determinants of Lipid Traits in Diverse Populations from the Population Architecture using Genomics and Epidemiology (PAGE) Study. PLoS Genetics, 2011, 7, e1002138.	3.5	146
8	Intrinsic Gene Expression Subsets of Diffuse Cutaneous Systemic Sclerosis Are Stable in Serial Skin Biopsies. Journal of Investigative Dermatology, 2012, 132, 1363-1373.	0.7	138
9	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	12.8	133
10	Limited Systemic Sclerosis Patients with Pulmonary Arterial Hypertension Show Biomarkers of Inflammation and Vascular Injury. PLoS ONE, 2010, 5, e12106.	2.5	133
11	A Core MYC Gene Expression Signature Is Prominent in Basal-Like Breast Cancer but Only Partially Overlaps the Core Serum Response. PLoS ONE, 2009, 4, e6693.	2.5	126
12	Interferon and alternative activation of monocyte/macrophages in systemic sclerosis-associated pulmonary arterial hypertension. Arthritis and Rheumatism, 2011, 63, 1718-1728.	6.7	125
13	Pleiotropic genes for metabolic syndrome and inflammation. Molecular Genetics and Metabolism, 2014, 112, 317-338.	1.1	107
14	Characterizing and Managing Missing Structured Data in Electronic Health Records: Data Analysis. JMIR Medical Informatics, 2018, 6, e11.	2.6	104
15	A Phenomics-Based Strategy Identifies Loci on APOC1, BRAP, and PLCG1 Associated with Metabolic Syndrome Phenotype Domains. PLoS Genetics, 2011, 7, e1002322.	3.5	92
16	Using Electronic Health Records To Generate Phenotypes For Research. Current Protocols in Human Genetics, 2019, 100, e80.	3.5	74
17	Genome-wide analysis of mRNAs bound to the histone stem-loop binding protein. Rna, 2006, 12, 1853-1867.	3.5	66
18	Phenome-wide association studies demonstrating pleiotropy of genetic variants within FTO with and without adjustment for body mass index. Frontiers in Genetics, 2014, 5, 250.	2.3	66

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19	PheWAS and Beyond: The Landscape of Associations with Medical Diagnoses and Clinical Measures across 38,662 Individuals from Geisinger. American Journal of Human Genetics, 2018, 102, 592-608.	6.2	66
20	Detection of Pleiotropy through a Phenome-Wide Association Study (PheWAS) of Epidemiologic Data as Part of the Environmental Architecture for Genes Linked to Environment (EAGLE) Study. PLoS Genetics, 2014, 10, e1004678.	3.5	64
21	Characterization of mitochondrial haplogroups in a large population-based sample from the United States. Human Genetics, 2014, 133, 861-868.	3.8	60
22	Association of the FTO Obesity Risk Variant rs8050136 With Percentage of Energy Intake From Fat in Multiple Racial/Ethnic Populations. American Journal of Epidemiology, 2013, 178, 780-790.	3.4	59
23	Consistent Directions of Effect for Established Type 2 Diabetes Risk Variants Across Populations. Diabetes, 2012, 61, 1642-1647.	0.6	49
24	Antagonistic Effect of the Matricellular Signaling Protein CCN3 on TGF-Î²- and Wnt-Mediated Fibrillinogenesis in Systemic Sclerosis and Marfan Syndrome. Journal of Investigative Dermatology, 2010, 130, 1514-1523.	0.7	47
25	The detection and characterization of pleiotropy: discovery, progress, and promise. Briefings in Bioinformatics, 2016, 17, 13-22.	6.5	43
26	Electronic health record phenotype in subjects with genetic variants associated with arrhythmogenic right ventricular cardiomyopathy: a study of 30,716 subjects with exome sequencing. Genetics in Medicine, 2017, 19, 1245-1252.	2.4	43
27	The joint effect of air pollution exposure and copy number variation on risk for autism. Autism Research, 2017, 10, 1470-1480.	3.8	38
28	Low Frequency Variants, Collapsed Based on Biological Knowledge, Uncover Complexity of Population Stratification in 1000 Genomes Project Data. PLoS Genetics, 2013, 9, e1003959.	3.5	35
29	Leveraging Epidemiologic and Clinical Collections for Genomic Studies of Complex Traits. Human Heredity, 2015, 79, 137-146.	0.8	34
30	Polygenic inheritance of paclitaxel-induced sensory peripheral neuropathy driven by axon outgrowth gene sets in CALGB 40101 (Alliance). Pharmacogenomics Journal, 2014, 14, 336-342.	2.0	33
31	Multiancestral Analysis of Inflammation-Related Genetic Variants and C-Reactive Protein in the Population Architecture Using Genomics and Epidemiology Study. Circulation: Cardiovascular Genetics, 2014, 7, 178-188.	5.1	31
32	First Trimester Plasma Glucose Values in Women without Diabetes are Associated with Risk for Congenital Heart Disease in Offspring. Journal of Pediatrics, 2018, 195, 275-278.	1.8	29
33	Phenome-Wide Association Study to Explore Relationships between Immune System Related Genetic Loci and Complex Traits and Diseases. PLoS ONE, 2016, 11, e0160573.	2.5	23
34	Genomic architecture of pharmacological efficacy and adverse events. Pharmacogenomics, 2014, 15, 2025-2048.	1.3	21
35	Biologyâ€Driven Geneâ€Gene Interaction Analysis of Ageâ€Related Cataract in the eMERGE Network. Genetic Epidemiology, 2015, 39, 376-384.	1.3	20
36	Phenome-Wide Association Studies: Embracing Complexity for Discovery. Human Heredity, 2015, 79, 111-123.	0.8	20

#	Article	IF	Citations
37	A phenome-wide association study (PheWAS) in the Population Architecture using Genomics and Epidemiology (PAGE) study reveals potential pleiotropy in African Americans. PLoS ONE, 2019, 14, e0226771.	2.5	15
38	Rare variants in drug target genes contributing to complex diseases, phenome-wide. Scientific Reports, 2018, 8, 4624.	3.3	13
39	The importance of buprenorphine research in the opioid crisis. Molecular Psychiatry, 2019, 24, 626-632.	7.9	13
40	Evidence for extensive pleiotropy among pharmacogenes. Pharmacogenomics, 2016, 17, 853-866.	1.3	10
41	A Phenome-Wide Association Study Uncovers a Role for Autoimmunity in the Development of Chronic Obstructive Pulmonary Disease. American Journal of Respiratory Cell and Molecular Biology, 2018, 58, 777-779.	2.9	8
42	Understanding systemic sclerosis through gene expression profiling. Current Opinion in Rheumatology, 2007, 19, 561-567.	4.3	6
43	Novel EDGE encoding method enhances ability to identify genetic interactions. PLoS Genetics, 2021, 17, e1009534.	3.5	5
44	Using Adipose Measures from Health Care Provider-Based Imaging Data for Discovery. Journal of Obesity, 2018, 2018, 1-15.	2.7	4