

# Adam S Gordon

## List of Publications by Year in descending order

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Version: 2024-02-01

41  
papers

2,454  
citations

394421

19  
h-index

276875

41  
g-index

43  
all docs

43  
docs citations

43  
times ranked

5038  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic association of primary nonresponse to anti-TNF $\pm$ therapy in patients with inflammatory bowel disease. <i>Pharmacogenetics and Genomics</i> , 2022, 32, 1-9.	1.5	2
2	Enhancing the Quality of Care in Long-Term Care Settings. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 1409.	2.6	1
3	The reckoning: The return of genomic results to 1444 participants across the eMERGE3 Network. <i>Genetics in Medicine</i> , 2022, 24, 1130-1138.	2.4	12
4	Arrhythmia Variant Associations and Reclassifications in the eMERGE-III Sequencing Study. <i>Circulation</i> , 2022, 145, 877-891.	1.6	18
5	Practitioners'™ Confidence and Desires for Education in Cardiovascular and Sudden Cardiac Death Genetics. <i>Journal of the American Heart Association</i> , 2022, 11, e023763.	3.7	7
6	Loci identified by a genome-wide association study of carotid artery stenosis in the eMERGE network. <i>Genetic Epidemiology</i> , 2021, 45, 4-15.	1.3	6
7	Association between triglycerides, known risk SNVs and conserved rare variation in SLC25A40 in a multi-ancestry cohort. <i>BMC Medical Genomics</i> , 2021, 14, 11.	1.5	4
8	Multiplexing mutation rate assessment: determining pathogenicity of Msh2 variants in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2021, 218, .	2.9	12
9	Penetrance of Breast Cancer Susceptibility Genes from the eMERGE III Network. <i>JNCI Cancer Spectrum</i> , 2021, 5, pkab044.	2.9	14
10	Recommendations for reporting of secondary findings in clinical exome and genome sequencing, 2021 update: a policy statement of the American College of Medical Genetics and Genomics (ACMG). <i>Genetics in Medicine</i> , 2021, 23, 1391-1398.	2.4	145
11	Practice Patterns After Return of Rare Variants Associated With Cardiomyopathy in the Electronic Medical Records and Genomics Network. <i>Circulation: Heart Failure</i> , 2021, 14, e008155.	3.9	1
12	ACMG SF v3.0 list for reporting of secondary findings in clinical exome and genome sequencing: a policy statement of the American College of Medical Genetics and Genomics (ACMG). <i>Genetics in Medicine</i> , 2021, 23, 1381-1390.	2.4	356
13	Pleiotropy of systemic lupus erythematosus risk alleles and cardiometabolic disorders: A phenome-wide association study and inverse-variance weighted meta-analysis. <i>Lupus</i> , 2021, 30, 1264-1272.	1.6	2
14	Quantitative disease risk scores from EHR with applications to clinical risk stratification and genetic studies. <i>Npj Digital Medicine</i> , 2021, 4, 116.	10.9	7
15	Genome-wide Approach to Measure Variant-based Heritability of Drug Outcome Phenotypes. <i>Clinical Pharmacology and Therapeutics</i> , 2021, 110, 714-722.	4.7	7
16	Response to McGurk et al. <i>Genetics in Medicine</i> , 2021, , .	2.4	0
17	Association of Genetic Risk of Obesity with Postoperative Complications Using Mendelian Randomization. <i>World Journal of Surgery</i> , 2020, 44, 84-94.	1.6	4
18	Uptake and use of a minimum data set (MDS) for older people living and dying in care homes in England: a realist review protocol. <i>BMJ Open</i> , 2020, 10, e040397.	1.9	10

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19	Frequency of genomic secondary findings among 21,915 eMERGE network participants. <i>Genetics in Medicine</i> , 2020, 22, 1470-1477.	2.4	61
20	Pleiotropy in the Genetic Predisposition to Rheumatoid Arthritis: A Phenome-Wide Association Study and Inverse Variance-Weighted Meta-Analysis. <i>Arthritis and Rheumatology</i> , 2020, 72, 1483-1492.	5.6	10
21	Rates of Actionable Genetic Findings in Individuals with Colorectal Cancer or Polyps Ascertained from a Community Medical Setting. <i>American Journal of Human Genetics</i> , 2019, 105, 526-533.	6.2	4
22	Harmonizing Clinical Sequencing and Interpretation for the eMERGE III Network. <i>American Journal of Human Genetics</i> , 2019, 105, 588-605.	6.2	99
23	Heritability and genome-wide association study of benign prostatic hyperplasia (BPH) in the eMERGE network. <i>Scientific Reports</i> , 2019, 9, 6077.	3.3	21
24	Effects of care assistant communication style on communicative behaviours of residents with dementia: a systematic multiple case study. <i>Scandinavian Journal of Caring Sciences</i> , 2019, 33, 207-214.	2.1	4
25	The eMERGE genotype set of 83,717 subjects imputed to ~40 million variants genome wide and association with the herpes zoster medical record phenotype. <i>Genetic Epidemiology</i> , 2019, 43, 63-81.	1.3	63
26	Probing the Virtual Proteome to Identify Novel Disease Biomarkers. <i>Circulation</i> , 2018, 138, 2469-2481.	1.6	42
27	A study paradigm integrating prospective epidemiologic cohorts and electronic health records to identify disease biomarkers. <i>Nature Communications</i> , 2018, 9, 3522.	12.8	13
28	Concordance between Research Sequencing and Clinical Pharmacogenetic Genotyping in the eMERGE-PGx Study. <i>Journal of Molecular Diagnostics</i> , 2017, 19, 561-566.	2.8	18
29	Building a family network from genetic testing. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2017, 5, 122-129.	1.2	4
30	Clinical Sequencing Exploratory Research Consortium: Accelerating Evidence-Based Practice of Genomic Medicine. <i>American Journal of Human Genetics</i> , 2016, 98, 1051-1066.	6.2	137
31	Genetic variation among 82 pharmacogenes: The PGRNseq data from the eMERGE network. <i>Clinical Pharmacology and Therapeutics</i> , 2016, 100, 160-169.	4.7	163
32	PGRNseq. <i>Pharmacogenetics and Genomics</i> , 2016, 26, 161-168.	1.5	93
33	Association of Arrhythmia-Related Genetic Variants With Phenotypes Documented in Electronic Medical Records. <i>JAMA - Journal of the American Medical Association</i> , 2016, 315, 47.	7.4	148
34	Medical students' and doctors' attitudes towards older patients and their care in hospital settings: a conceptualisation. <i>Age and Ageing</i> , 2015, 44, 776-783.	1.6	41
35	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. <i>American Journal of Human Genetics</i> , 2014, 94, 233-245.	6.2	193
36	Quantifying rare, deleterious variation in 12 human cytochrome P450 drug-metabolism genes in a large-scale exome dataset. <i>Human Molecular Genetics</i> , 2014, 23, 1957-1963.	2.9	82

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37	Design and Anticipated Outcomes of the eMERGE-PCx Project: A Multicenter Pilot for Preemptive Pharmacogenomics in Electronic Health Record Systems. <i>Clinical Pharmacology and Therapeutics</i> , 2014, 96, 482-489.	4.7	223
38	Pathogenic Variants for Mendelian and Complex Traits in Exomes of 6,517 European and African Americans: Implications for the Return of Incidental Results. <i>American Journal of Human Genetics</i> , 2014, 95, 183-193.	6.2	78
39	Rare coding variation in paraoxonase-1 is associated with ischemic stroke in the NHLBI Exome Sequencing Project. <i>Journal of Lipid Research</i> , 2014, 55, 1173-1178.	4.2	23
40	Exome Sequencing Reveals Novel Rare Variants in the Ryanodine Receptor and Calcium Channel Genes in Malignant Hyperthermia Families. <i>Anesthesiology</i> , 2013, 119, 1054-1065.	2.5	56
41	Adaptations to Climate in Candidate Genes for Common Metabolic Disorders. <i>PLoS Genetics</i> , 2008, 4, e32.	3.5	238