Adam S Gordon

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/3381390/publications.pdf

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	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). Genetics in Medicine, 2021, 23, 1381-1390.	2.4	356
2	Adaptations to Climate in Candidate Genes for Common Metabolic Disorders. PLoS Genetics, 2008, 4, e32.	3.5	238
3	Design and Anticipated Outcomes of the eMERGE-PGx Project: A Multicenter Pilot for Preemptive Pharmacogenomics in Electronic Health Record Systems. Clinical Pharmacology and Therapeutics, 2014, 96, 482-489.	4.7	223
4	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	6.2	193
5	Genetic variation among 82 pharmacogenes: The PGRNseq data from the eMERGE network. Clinical Pharmacology and Therapeutics, 2016, 100, 160-169.	4.7	163
6	Association of Arrhythmia-Related Genetic Variants With Phenotypes Documented in Electronic Medical Records. JAMA - Journal of the American Medical Association, 2016, 315, 47.	7.4	148
7	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). Genetics in Medicine, 2021, 23, 1391-1398.	2.4	145
8	Clinical Sequencing Exploratory Research Consortium: Accelerating Evidence-Based Practice of Genomic Medicine. American Journal of Human Genetics, 2016, 98, 1051-1066.	6.2	137
9	Harmonizing Clinical Sequencing and Interpretation for the eMERGE III Network. American Journal of Human Genetics, 2019, 105, 588-605.	6.2	99
10	PGRNseq. Pharmacogenetics and Genomics, 2016, 26, 161-168.	1.5	93
11	Quantifying rare, deleterious variation in 12 human cytochrome P450 drug-metabolism genes in a large-scale exome dataset. Human Molecular Genetics, 2014, 23, 1957-1963.	2.9	82
12	Pathogenic Variants for Mendelian and Complex Traits in Exomes of 6,517 European and African Americans: Implications for the Return of Incidental Results. American Journal of Human Genetics, 2014, 95, 183-193.	6.2	78
13	The eMERGE genotype set of 83,717 subjects imputed to ~40â€‰million variants genome wide and association with the herpes zoster medical record phenotype. Genetic Epidemiology, 2019, 43, 63-81.	1.3	63
14	Frequency of genomic secondaryÂfindings among 21,915 eMERGE network participants. Genetics in Medicine, 2020, 22, 1470-1477.	2.4	61
15	Exome Sequencing Reveals Novel Rare Variants in the Ryanodine Receptor and Calcium Channel Genes in Malignant Hyperthermia Families. Anesthesiology, 2013, 119, 1054-1065.	2.5	56
16	Probing the Virtual Proteome to Identify Novel Disease Biomarkers. Circulation, 2018, 138, 2469-2481.	1.6	42
17	Medical students' and doctors' attitudes towards older patients and their care in hospital settings: a conceptualisation. Age and Ageing, 2015, 44, 776-783.	1.6	41
18	Rare coding variation in paraoxonase-1 is associated with ischemic stroke in the NHLBI Exome Sequencing Project. Journal of Lipid Research, 2014, 55, 1173-1178.	4.2	23

#	Article	IF	Citations
19	Heritability and genome-wide association study of benign prostatic hyperplasia (BPH) in the eMERGE network. Scientific Reports, 2019, 9, 6077.	3.3	21
20	Concordance between Research Sequencing and Clinical Pharmacogenetic Genotyping in the eMERGE-PGx Study. Journal of Molecular Diagnostics, 2017, 19, 561-566.	2.8	18
21	Arrhythmia Variant Associations and Reclassifications in the eMERGE-III Sequencing Study. Circulation, 2022, 145, 877-891.	1.6	18
22	Penetrance of Breast Cancer Susceptibility Genes from the eMERGE III Network. JNCI Cancer Spectrum, 2021, 5, pkab044.	2.9	14
23	A study paradigm integrating prospective epidemiologic cohorts and electronic health records to identify disease biomarkers. Nature Communications, 2018, 9, 3522.	12.8	13
24	Multiplexing mutation rate assessment: determining pathogenicity of Msh2 variants in Saccharomyces cerevisiae. Genetics, 2021, 218, .	2.9	12
25	The reckoning: The return of genomic results to 1444 participants across the eMERGE3 Network. Genetics in Medicine, 2022, 24, 1130-1138.	2.4	12
26	Uptake and use of a minimum data set (MDS) for older people living and dying in care homes in England: a realist review protocol. BMJ Open, 2020, 10, e040397.	1.9	10
27	Pleiotropy in the Genetic Predisposition to Rheumatoid Arthritis: A Phenomeâ€Wide Association Study and Inverse Varianceâ€“Weighted Metaâ€Analysis. Arthritis and Rheumatology, 2020, 72, 1483-1492.	5.6	10
28	Quantitative disease risk scores from EHR with applications to clinical risk stratification and genetic studies. Npj Digital Medicine, 2021, 4, 116.	10.9	7
29	Genomeâ€Wide Approach to Measure Variantâ€Based Heritability of Drug Outcome Phenotypes. Clinical Pharmacology and Therapeutics, 2021, 110, 714-722.	4.7	7
30	Practitionersâ€™ Confidence and Desires for Education in Cardiovascular and Sudden Cardiac Death Genetics. Journal of the American Heart Association, 2022, 11, e023763.	3.7	7
31	Loci identified by a genomeâ€wide association study of carotid artery stenosis in the eMERGE network. Genetic Epidemiology, 2021, 45, 4-15.	1.3	6
32	Building a family network from genetic testing. Molecular Genetics & Genomic Medicine, 2017, 5, 122-129.	1.2	4
33	Rates of Actionable Genetic Findings in Individuals with Colorectal Cancer or Polyps Ascertained from a Community Medical Setting. American Journal of Human Genetics, 2019, 105, 526-533.	6.2	4
34	Effects of care assistant communication style on communicative behaviours of residents with dementia: a systematic multiple case study. Scandinavian Journal of Caring Sciences, 2019, 33, 207-214.	2.1	4
35	Association of Genetic Risk of Obesity with Postoperative Complications Using Mendelian Randomization. World Journal of Surgery, 2020, 44, 84-94.	1.6	4
36	Association between triglycerides, known risk SNVs and conserved rare variation in SLC25A40 in a multi-ancestry cohort. BMC Medical Genomics, 2021, 14, 11.	1.5	4

#	Article	IF	Citations
37	Pleiotropy of systemic lupus erythematosus risk alleles and cardiometabolic disorders: A phenome-wide association study and inverse-variance weighted meta-analysis. Lupus, 2021, 30, 1264-1272.	1.6	2
38	Genetic association of primary nonresponse to anti-TNFÎ± therapy in patients with inflammatory bowel disease. Pharmacogenetics and Genomics, 2022, 32, 1-9.	1.5	2
39	Practice Patterns After Return of Rare Variants Associated With Cardiomyopathy in the Electronic Medical Records and Genomics Network. Circulation: Heart Failure, 2021, 14, e008155.	3.9	1
40	Enhancing the Quality of Care in Long-Term Care Settings. International Journal of Environmental Research and Public Health, 2022, 19, 1409.	2.6	1
41	Response to McGurk etÂal. Genetics in Medicine, 2021, , .	2.4	0