

Andrew M Glazer

List of Publications by Year in descending order

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Version: 2024-02-01

41
papers

1,721
citations

331538

21
h-index

395590

33
g-index

49
all docs

49
docs citations

49
times ranked

3763
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | Common Ancestry-Specific Ion Channel Variants Predispose to Drug-Induced Arrhythmias. <i>Circulation</i> , 2022, 145, 299-308. | 1.6 | 12 |
| 2 | Veratridine Can Bind to a Site at the Mouth of the Channel Pore at Human Cardiac Sodium Channel NaV1.5. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2225. | 1.8 | 2 |
| 3 | Arrhythmia Variant Associations and Reclassifications in the eMERGE-III Sequencing Study. <i>Circulation</i> , 2022, 145, 877-891. | 1.6 | 18 |
| 4 | Dominant negative effects of SCN5A missense variants. <i>Genetics in Medicine</i> , 2022, 24, 1238-1248. | 1.1 | 9 |
| 5 | Mortality Among Patients With Early-Onset Atrial Fibrillation and Rare Variants in Cardiomyopathy and Arrhythmia Genes. <i>JAMA Cardiology</i> , 2022, 7, 733. | 3.0 | 14 |
| 6 | Estimating the Posttest Probability of Long QT Syndrome Diagnosis for Rare <i>KCNH2</i> Variants. <i>Circulation Genomic and Precision Medicine</i> , 2021, 14, e003289. | 1.6 | 10 |
| 7 | Incessant atrial and ventricular tachycardias associated with an SCN5A mutation. <i>HeartRhythm Case Reports</i> , 2021, 7, 806-811. | 0.2 | 0 |
| 8 | Early-Onset Atrial Fibrillation and the Prevalence of Rare Variants in Cardiomyopathy and Arrhythmia Genes. <i>JAMA Cardiology</i> , 2021, 6, 1371. | 3.0 | 66 |
| 9 | <i>KCNQ1</i> and Long QT Syndrome in 1/45 Amish. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e003133. | 1.6 | 7 |
| 10 | High-Throughput Reclassification of SCN5A Variants. <i>American Journal of Human Genetics</i> , 2020, 107, 111-123. | 2.6 | 88 |
| 11 | A Bayesian method to estimate variant-induced disease penetrance. <i>PLoS Genetics</i> , 2020, 16, e1008862. | 1.5 | 11 |
| 12 | High-throughput discovery of trafficking-deficient variants in the cardiac potassium channel KV11.1. <i>Heart Rhythm</i> , 2020, 17, 2180-2189. | 0.3 | 42 |
| 13 | Deep Mutational Scan of an <i>SCN5A</i> Voltage Sensor. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002786. | 1.6 | 33 |
| 14 | A Bayesian method to estimate variant-induced disease penetrance. , 2020, 16, e1008862. | | 0 |
| 15 | A Bayesian method to estimate variant-induced disease penetrance. , 2020, 16, e1008862. | | 0 |
| 16 | A Bayesian method to estimate variant-induced disease penetrance. , 2020, 16, e1008862. | | 0 |
| 17 | A Bayesian method to estimate variant-induced disease penetrance. , 2020, 16, e1008862. | | 0 |
| 18 | A Bayesian method to estimate variant-induced disease penetrance. , 2020, 16, e1008862. | | 0 |

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|----|--|-----|-----------|
| 19 | A Bayesian method to estimate variant-induced disease penetrance. , 2020, 16, e1008862. | | 0 |
| 20 | Androgenic Effects on Ventricular Repolarization. <i>Circulation</i> , 2019, 140, 1070-1080. | 1.6 | 67 |
| 21 | Harmonizing Clinical Sequencing and Interpretation for the eMERGE III Network. <i>American Journal of Human Genetics</i> , 2019, 105, 588-605. | 2.6 | 99 |
| 22 | Association of Thyroid Function Genetic Predictors With Atrial Fibrillation. <i>JAMA Cardiology</i> , 2019, 4, 136. | 3.0 | 23 |
| 23 | Patient-independent human induced pluripotent stem cell model: A new tool for rapid determination of genetic variant pathogenicity in long QT syndrome. <i>Heart Rhythm</i> , 2019, 16, 1686-1695. | 0.3 | 32 |
| 24 | A Mechanism of Calmodulin Modulation of the Human Cardiac Sodium Channel. <i>Structure</i> , 2018, 26, 683-694.e3. | 1.6 | 43 |
| 25 | Phenotype risk scores identify patients with unrecognized Mendelian disease patterns. <i>Science</i> , 2018, 359, 1233-1239. | 6.0 | 164 |
| 26 | <i>SCN5A</i> (Na ^V 1.5) Variant Functional Perturbation and Clinical Presentation. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e002095. | 1.6 | 36 |
| 27 | Hypogonadism as a Reversible Cause of Torsades de Pointes in Men. <i>Circulation</i> , 2018, 138, 110-113. | 1.6 | 57 |
| 28 | Arrhythmia genetics: Not dark and lite, but 50 shades of gray. <i>Heart Rhythm</i> , 2018, 15, 1231-1232. | 0.3 | 2 |
| 29 | Increased long QT and torsade de pointes reporting on tamoxifen compared with aromatase inhibitors. <i>Heart</i> , 2018, 104, 1859-1863. | 1.2 | 37 |
| 30 | Phenome-wide scanning identifies multiple diseases and disease severity phenotypes associated with HLA variants. <i>Science Translational Medicine</i> , 2017, 9, . | 5.8 | 105 |
| 31 | Comparison of HLA allelic imputation programs. <i>PLoS ONE</i> , 2017, 12, e0172444. | 1.1 | 58 |
| 32 | Genome-wide association and pathway analysis of left ventricular function after anthracycline exposure in adults. <i>Pharmacogenetics and Genomics</i> , 2017, 27, 247-254. | 0.7 | 54 |
| 33 | Partially repeatable genetic basis of benthic adaptation in threespine sticklebacks. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 887-902. | 1.1 | 33 |
| 34 | Clinical and Biological Insights Into Combined Post- and Pre-Capillary Pulmonary Hypertension. <i>Journal of the American College of Cardiology</i> , 2016, 68, 2525-2536. | 1.2 | 160 |
| 35 | Distinct developmental and genetic mechanisms underlie convergently evolved tooth gain in sticklebacks. <i>Development (Cambridge)</i> , 2015, 142, 2442-51. | 1.2 | 53 |
| 36 | Genome Assembly Improvement and Mapping Convergently Evolved Skeletal Traits in Sticklebacks with Genotyping-by-Sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1463-1472. | 0.8 | 112 |

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|----|--|-----|-----------|
| 37 | Two developmentally temporal quantitative trait loci underlie convergent evolution of increased branchial bone length in sticklebacks. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20140822. | 1.2 | 17 |
| 38 | Modular Skeletal Evolution in Sticklebacks Is Controlled by Additive and Clustered Quantitative Trait Loci. <i>Genetics</i> , 2014, 197, 405-420. | 1.2 | 122 |
| 39 | Parallel developmental genetic features underlie stickleback gill raker evolution. <i>EvoDevo</i> , 2014, 5, 19. | 1.3 | 36 |
| 40 | Exploring the Genetic Basis of Variation in Gene Predictions with a Synthetic Association Study. <i>PLoS ONE</i> , 2010, 5, e11645. | 1.1 | 0 |
| 41 | The Zn Finger protein Iguana impacts Hedgehog signaling by promoting ciliogenesis. <i>Developmental Biology</i> , 2010, 337, 148-156. | 0.9 | 87 |