# Kelsey E Grinde

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1584253/publications.pdf

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| 12 | 281 | 1307594 7 | 1281871 11 |
|---|---|---|---|
| papers | citations | h-index | g-index |

| 12 | 12 | 12 | 1110 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Circular RNA Profiles in Viremia and ART Suppression Predict Competing circRNAâ€“miRNAâ€“mRNA Networks Exclusive to HIV-1 Viremic Patients. Viruses, 2022, 14, 683. | 3.3 | 3 |
| 2 | Whole genome sequence analyses of eGFR in 23,732 people representing multiple ancestries in the NHLBI trans-omics for precision medicine (TOPMed) consortium. EBioMedicine, 2021, 63, 103157. | 6.1 | 14 |
| 3 | Coagulation factor VIII: Relationship to cardiovascular disease risk and whole genome sequence and epigenomeâ€wide analysis in African Americans. Journal of Thrombosis and Haemostasis, 2020, 18, 1335-1347. | 3.8 | 17 |
| 4 | A fully adjusted twoâ€stage procedure for rankâ€normalization in genetic association studies. Genetic Epidemiology, 2019, 43, 263-275. | 1.3 | 60 |
| 5 | Genome-wide Significance Thresholds for Admixture Mapping Studies. American Journal of Human Genetics, 2019, 104, 454-465. | 6.2 | 25 |
| 6 | Generalizing polygenic risk scores from Europeans to Hispanics/Latinos. Genetic Epidemiology, 2019, 43, 50-62. | 1.3 | 89 |
| 7 | Mo1146 ANESTHESIA PROFESSIONAL-DELIVERED SEDATION IS ASSOCIATED WITH SIMILAR OUTCOMES COMPARED TO NURSE ADMINISTERED SEDATION IN PATIENTS WITH ACUTE UPPER GASTROINTESTINAL BLEEDING. Gastrointestinal Endoscopy, 2018, 87, AB418-AB419. | 1.0 | 0 |
| 8 | Illustrating, Quantifying, and Correcting for Bias in Post-hoc Analysis of Gene-Based Rare Variant Tests of Association. Frontiers in Genetics, 2017, 8, 117. | 2.3 | 4 |
| 9 | Local Ancestry Inference in a Large US-Based Hispanic/Latino Study: Hispanic Community Health Study/Study of Latinos (HCHS/SOL). G3: Genes, Genomes, Genetics, 2016, 6, 1525-1534. | 1.8 | 51 |
| 10 | A general method for combining different family-based rare-variant tests of association to improve power and robustness of a wide range of genetic architectures. BMC Proceedings, 2016, 10, 165-170. | 1.6 | 4 |
| 11 | A multistep approach to single nucleotide polymorphismâ€“set analysis: an evaluation of power and type I error of gene-based tests of association after pathway-based association tests. BMC Proceedings, 2016, 10, 349-355. | 1.6 | 2 |
| 12 | A general approach for combining diverse rare variant association tests provides improved robustness across a wider range of genetic architectures. European Journal of Human Genetics, 2016, 24, 767-773. | 2.8 | 12 |