# Sarah A Gagliano Taliun

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7806214/publications.pdf

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|---|---|---|---|
| 34<br>papers | 3,204<br>citations | 430874<br>18<br>h-index | 377865<br>34<br>g-index |
| 51<br>all docs | 51<br>docs citations | 51<br>times ranked | 7497<br>citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | GWAS of Hematuria. Clinical Journal of the American Society of Nephrology: CJASN, 2022, 17, 672-683. | 4.5 | 7 |
| 2 | Genome-wide meta-analysis of iron status biomarkers and the effect of iron on all-cause mortality in HUNT. Communications Biology, 2022, 5, . | 4.4 | 11 |
| 3 | Insights From a Large-Scale Whole-Genome Sequencing Study of Systolic Blood Pressure, Diastolic Blood Pressure, and Hypertension. Hypertension, 2022, 79, 1656-1667. | 2.7 | 12 |
| 4 | Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299. | 27.8 | 1,069 |
| 5 | Human-lineage-specific genomic elements are associated with neurodegenerative disease and APOE transcript usage. Nature Communications, 2021, 12, 2076. | 12.8 | 9 |
| 6 | One scientist coupleâ€™s five suggestions to solve the â€˜two body problemâ€™. Nature, 2021, , . | 27.8 | 1 |
| 7 | Genome-wide association study of cardiac troponin I in the general population. Human Molecular Genetics, 2021, 30, 2027-2039. | 2.9 | 11 |
| 8 | Cross-platform transcriptional profiling identifies common and distinct molecular pathologies in Lewy body diseases. Acta Neuropathologica, 2021, 142, 449-474. | 7.7 | 27 |
| 9 | Ten simple rules for conducting a mendelian randomization study. PLoS Computational Biology, 2021, 17, e1009238. | 3.2 | 33 |
| 10 | Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. Nature Communications, 2020, 11, 5182. | 12.8 | 32 |
| 11 | Neuronal intranuclear inclusion disease is genetically heterogeneous. Annals of Clinical and Translational Neurology, 2020, 7, 1716-1725. | 3.7 | 38 |
| 12 | Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. Nature Communications, 2020, 11, 6417. | 12.8 | 39 |
| 13 | Scalable generalized linear mixed model for region-based association tests in large biobanks and cohorts. Nature Genetics, 2020, 52, 634-639. | 21.4 | 124 |
| 14 | Exploring and visualizing large-scale genetic associations by using PheWeb. Nature Genetics, 2020, 52, 550-552. | 21.4 | 129 |
| 15 | Regulatory sites for splicing in human basal ganglia are enriched for disease-relevant information. Nature Communications, 2020, 11, 1041. | 12.8 | 22 |
| 16 | Ancestry-agnostic estimation of DNA sample contamination from sequence reads. Genome Research, 2020, 30, 185-194. | 5.5 | 51 |
| 17 | Informing disease modelling with brain-relevant functional genomic annotations. Brain, 2019, 142, 3694-3712. | 7.6 | 8 |
| 18 | Metaâ€MultiSKAT: Multiple phenotype metaâ€analysis for regionâ€based association test. Genetic Epidemiology, 2019, 43, 800-814. | 1.3 | 9 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Genetic determinants of low vitamin B12 levels in Alzheimer's disease risk. Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring, 2019, 11, 430-434. | 2.4 | 3 |
| 20 | Exploring various polygenic risk scores for skin cancer in the phenomes of the Michigan genomics initiative and the UK Biobank with a visual catalog: PRSWeb. PLoS Genetics, 2019, 15, e1008202. | 3.5 | 28 |
| 21 | Moving beyond neurons: the role of cell type-specific gene regulation in Parkinsonâ€™s disease heritability. Npj Parkinson's Disease, 2019, 5, 6. | 5.3 | 83 |
| 22 | The impact of donor and recipient common clinical and genetic variation on estimated glomerular filtration rate in a European renal transplant population. American Journal of Transplantation, 2019, 19, 2262-2273. | 4.7 | 13 |
| 23 | Relative impact of indels versus SNPs on complex disease. Genetic Epidemiology, 2019, 43, 112-117. | 1.3 | 9 |
| 24 | Picomolar concentrations of oligomeric alpha-synuclein sensitizes TLR4 to play an initiating role in Parkinsonâ€™s disease pathogenesis. Acta Neuropathologica, 2019, 137, 103-120. | 7.7 | 103 |
| 25 | Teaching at the university level is not a hassle. Nature, 2019, 574, 285-285. | 27.8 | 0 |
| 26 | Long- and short-term outcomes in renal allografts with deceased donors: A large recipient and donor genome-wide association study. American Journal of Transplantation, 2018, 18, 1370-1379. | 4.7 | 47 |
| 27 | Efficiently controlling for case-control imbalance and sample relatedness in large-scale genetic association studies. Nature Genetics, 2018, 50, 1335-1341. | 21.4 | 896 |
| 28 | Itâ€™s All in the Brain: A Review of Available Functional Genomic Annotations. Biological Psychiatry, 2017, 81, 478-483. | 1.3 | 14 |
| 29 | Genomics implicates adaptive and innate immunity in Alzheimer's and Parkinson's diseases. Annals of Clinical and Translational Neurology, 2016, 3, 924-933. | 3.7 | 84 |
| 30 | Allele-Skewed DNA Modification in the Brain: Relevance to a Schizophrenia GWAS. American Journal of Human Genetics, 2016, 98, 956-962. | 6.2 | 20 |
| 31 | Smoking Gun or Circumstantial Evidence? Comparison of Statistical Learning Methods using Functional Annotations for Prioritizing Risk Variants. Scientific Reports, 2015, 5, 13373. | 3.3 | 7 |
| 32 | A genome-wide association study of suicide severity scores in bipolar disorder. Journal of Psychiatric Research, 2015, 65, 23-29. | 3.1 | 36 |
| 33 | A Bayesian Method to Incorporate Hundreds of Functional Characteristics with Association Evidence to Improve Variant Prioritization. PLoS ONE, 2014, 9, e98122. | 2.5 | 29 |
| 34 | Protein kinase cAMP-dependent regulatory type II beta (PRKAR2B) gene variants in antipsychotic-induced weight gain. Human Psychopharmacology, 2014, 29, 330-335. | 1.5 | 10 |