

Using NIH Figshare to collect supplementary material associated with a publication

A case study of Yosuke Tanigawa

Yosuke Tanigawa and his colleagues at Stanford University have used NIH Figshare to share supplementary data relating to a recent publication in PLoS Genetics¹ and grouped it into a collection². Because PLoS uses Figshare to store supplementary material from its publications and this research was funded by the National Human Genome Research, Yosuke was able to create a collection combining his PLoS supplementary material with the additional datasets he made available in NIH Figshare.

They analyzed large-scale population datasets consisting of more than 500,000 individuals and identified rare protein-altering variants that significantly reduce the risk of glaucoma. "We used the comprehensive health information in the two population cohorts in our study," said Yosuke. "While we are not allowed to share those individual-level data, we can make the aggregated summary-level association data publicly available, ensuring it's useful to other researchers."

Yosuke also has a keen interest in ensuring that the research he conducts is as FAIR as possible: findable, accessible, interoperable, and reusable³. “At the very least, I’m trying to make sure my research and accompanying datasets are findable by others,” said Yosuke. “It took very little time and effort to make this collection on Figshare, and if it makes it easier for people to find the data, that’s great.”

For more information on NIH Figshare, visit nih.figshare.com or email nihsupport@figshare.com.



Datasets described in 'Rare protein-altering variants in ANGPTL7 lower intraocular pressure and protect against glaucoma'

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This collection contains main and supplementary figures, tables, and datasets, as well as other datasets (the genome-wide summary statistics and the results of gene-based burden and dispersion tests) described in 'Rare protein-altering variants in ANGPTL7 lower intraocular pressure and protect against glaucoma'. Please see our publication for more details.

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Yosuke Tanigawa is a PhD student in Biomedical Informatics in the Department of Biomedical Data Science at Stanford University specializing in population genomics and analysis of large-scale datasets. To find out more about Yosuke’s research, check out his personal website⁴ and his profile on NIH Figshare⁵.

References:

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