

Yosuke Tanigawa

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

1,716
citations

759055

12
h-index

677027

22
g-index

59
all docs

59
docs citations

59
times ranked

3049
citing authors

#	ARTICLE	IF	CITATIONS
1	Fast Lasso method for large-scale and ultrahigh-dimensional Cox model with applications to UK Biobank. <i>Biostatistics</i> , 2022, 23, 522-540.	0.9	22
2	Significant sparse polygenic risk scores across 813 traits in UK Biobank. <i>PLoS Genetics</i> , 2022, 18, e1010105.	1.5	40
3	Integration of rare expression outlier-associated variants improves polygenic risk prediction. <i>American Journal of Human Genetics</i> , 2022, 109, 1055-1064.	2.6	8
4	Sex-specific genetic effects across biomarkers. <i>European Journal of Human Genetics</i> , 2021, 29, 154-163.	1.4	48
5	Genetics of 35 blood and urine biomarkers in the UK Biobank. <i>Nature Genetics</i> , 2021, 53, 185-194.	9.4	377
6	Survival analysis on rare events using group-regularized multi-response Cox regression. <i>Bioinformatics</i> , 2021, 37, 4437-4443.	1.8	3
7	Polygenic risk modeling with latent trait-related genetic components. <i>European Journal of Human Genetics</i> , 2021, 29, 1071-1081.	1.4	14
8	Fast numerical optimization for genome sequencing data in population biobanks. <i>Bioinformatics</i> , 2021, 37, 4148-4155.	1.8	9
9	A cross-population atlas of genetic associations for 220 human phenotypes. <i>Nature Genetics</i> , 2021, 53, 1415-1424.	9.4	560
10	APOC3 genetic variation, serum triglycerides, and risk of coronary artery disease in Asian Indians, Europeans, and other ethnic groups. <i>Lipids in Health and Disease</i> , 2021, 20, 113.	1.2	12
11	Bayesian model comparison for rare-variant association studies. <i>American Journal of Human Genetics</i> , 2021, 108, 2354-2367.	2.6	2
12	Significant shared heritability underlies suicide attempt and clinically predicted probability of attempting suicide. <i>Molecular Psychiatry</i> , 2020, 25, 2422-2430.	4.1	91
13	Rare protein-altering variants in ANGPTL7 lower intraocular pressure and protect against glaucoma. <i>PLoS Genetics</i> , 2020, 16, e1008682.	1.5	31
14	Assessing Digital Phenotyping to Enhance Genetic Studies of Human Diseases. <i>American Journal of Human Genetics</i> , 2020, 106, 611-622.	2.6	42
15	Cardiac Imaging of Aortic Valve Area From 34 287 UK Biobank Participants Reveals Novel Genetic Associations and Shared Genetic Comorbidity With Multiple Disease Phenotypes. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e003014.	1.6	16
16	A fast and scalable framework for large-scale and ultrahigh-dimensional sparse regression with application to the UK Biobank. <i>PLoS Genetics</i> , 2020, 16, e1009141.	1.5	75
17	Rare protein-altering variants in ANGPTL7 lower intraocular pressure and protect against glaucoma. , 2020, 16, e1008682.		0
18	Rare protein-altering variants in ANGPTL7 lower intraocular pressure and protect against glaucoma. , 2020, 16, e1008682.		0

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19	Rare protein-altering variants in ANGPTL7 lower intraocular pressure and protect against glaucoma. , 2020, 16, e1008682.		0
20	Rare protein-altering variants in ANGPTL7 lower intraocular pressure and protect against glaucoma. , 2020, 16, e1008682.		0
21	Title is missing!. , 2020, 16, e1009141.		0
22	Title is missing!. , 2020, 16, e1009141.		0
23	Title is missing!. , 2020, 16, e1009141.		0
24	Title is missing!. , 2020, 16, e1009141.		0
25	Title is missing!. , 2020, 16, e1009141.		0
26	Title is missing!. , 2020, 16, e1009141.		0
27	Components of genetic associations across 2,138 phenotypes in the UK Biobank highlight adipocyte biology. Nature Communications, 2019, 10, 4064.	5.8	48
28	Global Biobank Engine: enabling genotype-phenotype browsing for biobank summary statistics. Bioinformatics, 2019, 35, 2495-2497.	1.8	79
29	Collaborative environmental DNA sampling from petal surfaces of flowering cherry <i>Cerasus</i> — <i>â€%yedoensis</i> <i>â€~Somei-yoshino</i> â€™™ across the Japanese archipelago. Journal of Plant Research, 2018, 131, 709-717.		1
30	Medical relevance of protein-truncating variants across 337,205 individuals in the UK Biobank study. Nature Communications, 2018, 9, 1612.	5.8	95
31	SNPs2ChIP: Latent Factors of ChIP-seq to infer functions of non-coding SNPs. , 2018, , .		0