Yogasudha Veturi

List of Publications by Year
in descending order

		1040056	1058476
15 papers	**615** citations	**9** h-index	**14** g-index
18 all docs	**18** docs citations	**18** times ranked	**794** citing authors

#	Article	IF	Citations
1	Characterizing Heterogeneity in Neuroimaging, Cognition, Clinical Symptoms, and Genetics Among Patients With Late-Life Depression. JAMA Psychiatry, 2022, 79, 464.	11.0	47
2	Tissue specificity-aware TWAS (TSA-TWAS) framework identifies novel associations with metabolic, immunologic, and virologic traits in HIV-positive adults. PLoS Genetics, 2021, 17, e1009464.	3.5	11
3	A unified framework identifies new links between plasma lipids and diseases from electronic medical records across large-scale cohorts. Nature Genetics, 2021, 53, 972-981.	21.4	17
4	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
5	Innovative strategies for annotating the â€œrelationSNPâ€•between variants and molecular phenotypes. BioData Mining, 2019, 12, 10.	4.0	6
6	Modeling Heterogeneity in the Genetic Architecture of Ethnically Diverse Groups Using Random Effect Interaction Models. Genetics, 2019, 211, 1395-1407.	2.9	35
7	Influence of tissue context on gene prioritization for predicted transcriptome-wide association studies. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2019, 24, 296-307.	0.7	3
8	Rare variants in drug target genes contributing to complex diseases, phenome-wide. Scientific Reports, 2018, 8, 4624.	3.3	13
9	Influence of tissue context on gene prioritization for predicted transcriptome-wide association studies. , 2018, , .		4
10	Detecting potential pleiotropy across cardiovascular and neurological diseases using univariate, bivariate, and multivariate methods on 43,870 individuals from the eMERGE network. , 2018, , .		6
11	How powerful are summary-based methods for identifying expression-trait associations under different genetic architectures?. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 228-239.	0.7	14
12	Increased Proportion of Variance Explained and Prediction Accuracy of Survival of Breast Cancer Patients with Use of Whole-Genome Multiomic Profiles. Genetics, 2016, 203, 1425-1438.	2.9	49
13	Incorporating Genetic Heterogeneity in Whole-Genome Regressions Using Interactions. Journal of Agricultural, Biological, and Environmental Statistics, 2015, 20, 467-490.	1.4	32
14	Effectiveness of Shrinkage and Variable Selection Methods for the Prediction of Complex Human Traits using Data from Distantly Related Individuals. Annals of Human Genetics, 2015, 79, 122-135.	0.8	14
15	Multivariate Mixed Linear Model Analysis of Longitudinal Data: An Information-Rich Statistical Technique for Analyzing Plant Disease Resistance. Phytopathology, 2012, 102, 1016-1025.	2.2	8