

Yogasudha Veturi

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5209246/publications.pdf>

Version: 2024-02-01

15
papers

615
citations

1040056

9
h-index

1058476

14
g-index

18
all docs

18
docs citations

18
times ranked

794
citing authors

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