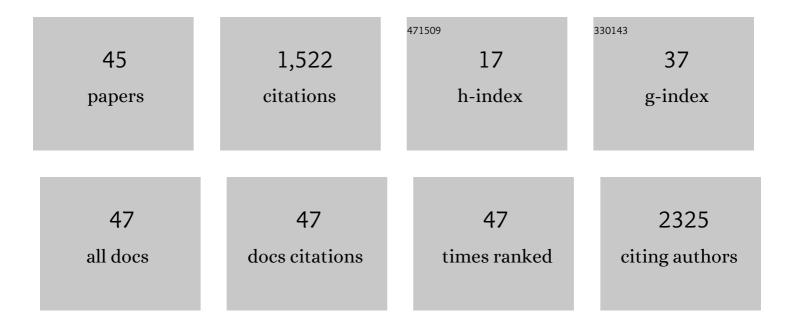
## Mahlet G Tadesse

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8459918/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Maternal-fetal genetic interactions, imprinting, and risk of placental abruption. Journal of Maternal-Fetal and Neonatal Medicine, 2022, 35, 3473-3482.	1.5	3
2	Race and Patient-reported Symptoms in Adherence to Adjuvant Endocrine Therapy: A Report from the Women's Hormonal Initiation and Persistence Study. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 699-709.	2.5	16
3	Bayesian statistics and modelling. Nature Reviews Methods Primers, 2021, 1, .	21.2	419
4	Integrative Analysis of DNA Methylation and microRNA Expression Reveals Mechanisms of Racial Heterogeneity in Hepatocellular Carcinoma. Frontiers in Genetics, 2021, 12, 708326.	2.3	5
5	Bayesian variable selection for high dimensional predictors and self-reported outcomes. BMC Medical Informatics and Decision Making, 2020, 20, 212.	3.0	0
6	Identification of miRNA-mRNA associations in hepatocellular carcinoma using hierarchical integrative model. BMC Medical Genomics, 2020, 13, 56.	1.5	6
7	Adherence to Adjuvant Endocrine Therapy in Insured Black and White Breast Cancer Survivors: Exploring Adherence Measures in Patient Data. Journal of Managed Care & Specialty Pharmacy, 2019, 25, 578-586.	0.9	16
8	Initiation of Adjuvant Endocrine Therapy in Black and White Women With Breast Cancer. Clinical Breast Cancer, 2018, 18, 337-346.e1.	2.4	13
9	Physical activity and epigenetic biomarkers in maternal blood during pregnancy. Epigenomics, 2018, 10, 1383-1395.	2.1	8
10	Identification of race-associated metabolite biomarkers for hepatocellular carcinoma in patients with liver cirrhosis and hepatitis C virus infection. PLoS ONE, 2018, 13, e0192748.	2.5	19
11	Bayesian Variable Selection Methods for Matched Case-Control Studies. International Journal of Biostatistics, 2017, 13, .	0.7	5
12	Metabolomic Characterization of Hepatocellular Carcinoma in Patients with Liver Cirrhosis for Biomarker Discovery. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 675-683.	2.5	40
13	Multivariate Bayesian Variable Selection Exploiting Dependence Structure Among Outcomes: Application to Air Pollution Effects on DNA Methylation. Biometrics, 2017, 73, 232-241.	1.4	10
14	Circulating early- and mid-pregnancy microRNAs and risk of gestational diabetes. Diabetes Research and Clinical Practice, 2017, 132, 1-9.	2.8	89
15	Maternal pre-pregnancy body mass index and circulating microRNAs in pregnancy. Obesity Research and Clinical Practice, 2017, 11, 464-474.	1.8	15
16	Genetic variations related to maternal whole blood mitochondrial DNA copy number: a genome-wide and candidate gene study. Journal of Maternal-Fetal and Neonatal Medicine, 2017, 30, 2433-2439.	1.5	15
17	Assessment of GC-MS in Detecting Changes in the Levels of Metabolites Using a Spike-in Experiment in Human Plasma. Metabolomics: Open Access, 2016, 6, .	0.1	0
18	Evaluation of hierarchical models for integrative genomic analyses. Bioinformatics, 2016, 32, 738-746.	4.1	6

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#	Article	IF	CITATIONS
19	Candidate Gene and MicroRNA Expression in Fetal Membranes and Preterm Delivery Risk. Reproductive Sciences, 2016, 23, 731-737.	2.5	28
20	Placental genetic variations in circadian clock-related genes increase the risk of placental abruption. International Journal of Molecular Epidemiology and Genetics, 2016, 7, 32-40.	0.4	5
21	Circadian clock-related genetic risk scores and risk of placental abruption. Placenta, 2015, 36, 1480-1486.	1.5	10
22	Mixture of inhomogeneous matrix models for speciesâ€rich ecosystems. Environmetrics, 2015, 26, 39-51.	1.4	8
23	Pathway and Network Approaches for Identification of Cancer Signature Markers from Omics Data. Journal of Cancer, 2015, 6, 54-65.	2.5	44
24	Risk of Common Mental Disorders in Relation to Symptoms of Obstructive Sleep Apnea Syndrome among Ethiopian College Students. Journal of Sleep Disorders Treatment & Care, 2015, 04, .	0.1	2
25	GC-MS Based Plasma Metabolomics for Identification of Candidate Biomarkers for Hepatocellular Carcinoma in Egyptian Cohort. PLoS ONE, 2015, 10, e0127299.	2.5	60
26	LCâ€MS/MSâ€based serum proteomics for identification of candidate biomarkers for hepatocellular carcinoma. Proteomics, 2015, 15, 2369-2381.	2.2	66
27	Early Pregnancy Maternal Blood DNA Methylation in Repeat Pregnancies and Change in Gestational Diabetes Mellitus Status—A Pilot Study. Reproductive Sciences, 2015, 22, 904-910.	2.5	25
28	Psychometric properties and factor structure of the General Health Questionnaire as a screening tool for anxiety and depressive symptoms in a multi-national study of young adults. Journal of Affective Disorders, 2015, 187, 197-202.	4.1	43
29	Daytime sleepiness, circadian preference, caffeine consumption and use of other stimulants among Thai college students. Journal of Public Health and Epidemiology, 2014, 8, 202-210.	0.3	21
30	Daytime Sleepiness, Circadian Preference, Caffeine Consumption and Khat Use among College Students in Ethiopia. Journal of Sleep Disorders Treatment & Care, 2014, 03, .	0.1	22
31	Assessing validity of a depression screening instrument in the absence of a gold standard. Annals of Epidemiology, 2014, 24, 527-531.	1.9	28
32	Biological network inference using low order partial correlation. Methods, 2014, 69, 266-273.	3.8	35
33	Placental Genome and Maternal-Placental Genetic Interactions: A Genome-Wide and Candidate Gene Association Study of Placental Abruption. PLoS ONE, 2014, 9, e116346.	2.5	29
34	Construct Validity and Factor Structure of the Pittsburgh Sleep Quality Index and Epworth Sleepiness Scale in a Multi-National Study of African, South East Asian and South American College Students. PLoS ONE, 2014, 9, e116383.	2.5	69
35	An integrated pharmacogenomic analysis of doxorubicin response using genotype information on DMET genes. , 2013, , .		1
36	Evaluation of normalization methods for analysis of LC-MS data. , 2012, , .		7

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#	Article	IF	CITATIONS
37	Normalization of LC-MS data using Gaussian process. , 2012, , .		3
38	Integration of multiple data sources for identifying functional modules using Bayesian network. , 2012, , .		0
39	Variability assessment of LC-MS experiments and its application to experimental design and difference detection. , 2012, , .		0
40	Bayesian Alignment Model for LC-MS Data. , 2011, , .		0
41	Incorporating biological information into linear models: A Bayesian approach to the selection of pathways and genes. Annals of Applied Statistics, 2011, 5, 1978-2002.	1.1	119
42	Analysis of LC-MS Data Using probabilitic-based mixture regression modelsAnalyse von LC-MS-Daten mit wahrscheinlichkeitsbasierter Mischung von Regressionsmodellen. Automatisierungstechnik, 2009, 57, 453-465.	0.8	1
43	Bayesian Variable Selection in Clustering High-Dimensional Data. Journal of the American Statistical Association, 2005, 100, 602-617.	3.1	190
44	A Bayesian Hierarchical Model for the Analysis of Affymetrix Arrays. Annals of the New York Academy of Sciences, 2004, 1020, 41-48.	3.8	4
45	Identification of Differentially Expressed Genes in High-Density Oligonucleotide Arrays Accounting for the Quantification Limits of the Technology. Biometrics, 2003, 59, 542-554.	1.4	13