Timothy P York

List of Publications by Year
in descending order

45 papers	1,283 citations

331259

21 h-index	

377514

34 g-index	

51 all docs	51 docs citations

51 times ranked	2427 citing authors

#	Article	IF	Citations
1	Study protocol to quantify the genetic architecture of sonographic cervical length and its relationship to spontaneous preterm birth. BMJ Open, 2022, 12, e053631.	0.8	3
2	Large-scale integration of DNA methylation and gene expression array platforms identifies both <i>cis</i> and <i>trans</i> relationships. Epigenetics, 2022, 17, 1753-1773.	1.3	2
3	Epigenomeâ€Wide Study of Posttraumatic Stress Disorder Symptom Severity in a Treatmentâ€Seeking Adolescent Sample. Journal of Traumatic Stress, 2021, 34, 607-615.	1.0	6
4	Maternal biological age assessed in early pregnancy is associated with gestational age at birth. Scientific Reports, 2021, 11, 15440.	1.6	6
5	Vaginal microbiome Lactobacillus crispatus is heritable among European American women. Communications Biology, 2021, 4, 872.	2.0	7
6	An epigenome-wide association study of early-onset major depression in monozygotic twins. Translational Psychiatry, 2020, 10, 301.	2.4	30
7	Replicated umbilical cord blood DNA methylation loci associated with gestational age at birth. Epigenetics, 2020, 15, 1243-1258.	1.3	10
8	osfr: An R Interface to the Open Science Framework. Journal of Open Source Software, 2020, 5, 2071.	2.0	10
9	Time course of panic disorder and posttraumatic stress disorder onsets. Social Psychiatry and Psychiatric Epidemiology, 2019, 54, 639-647.	1.6	14
10	Familial support following childhood sexual abuse is associated with longer telomere length in adult females. Journal of Behavioral Medicine, 2019, 42, 911-923.	1.1	6
11	Heritability, stability, and prevalence of tonic and phasic irritability as indicators of disruptive mood dysregulation disorder. Journal of Child Psychology and Psychiatry and Allied Disciplines, 2019, 60, 1032-1041.	3.1	34
12	DNA methylation studies of depression with onset in the peripartum: A critical systematic review. Neuroscience and Biobehavioral Reviews, 2019, 102, 106-122.	2.9	4
13	DNA methylation associated with postpartum depressive symptoms overlaps findings from a genome-wide association meta-analysis of depression. Clinical Epigenetics, 2019, 11, 169.	1.8	7
14	The Changing Age of Individuals Seeking Presymptomatic Genetic Testing for Huntington Disease. Journal of Genetic Counseling, 2018, 27, 1157-1166.	0.9	8
15	The role of endoplasmic reticulum aminopeptidase 2 in modulating immune detection of choriocarcinomaâ€. Biology of Reproduction, 2018, 98, 309-322.	1.2	13
16	Maternal prenatal stress and infant DNA methylation: A systematic review. Developmental Psychobiology, 2018, 60, 127-139.	0.9	82
17	Depressive Symptom Prevalence and Predictors in the First Half of Pregnancy. Journal of Women's Health, 2018, 27, 369-376.	1.5	29
18	Spontaneous preterm birth: advances toward the discovery of genetic predisposition. American Journal of Obstetrics and Gynecology, 2018, 218, 294-314.e2.	0.7	111

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19	Does Parenting Influence the Enduring Impact of Severe Childhood Sexual Abuse on Psychiatric Resilience in Adulthood?. Child Psychiatry and Human Development, 2018, 49, 33-41.	1.1	26
20	Prospective longitudinal study of the pregnancy DNA methylome: the US Pregnancy, Race, Environment, Genes (PREG) study. BMJ Open, 2018, 8, e019721.	0.8	19
21	Discovery of rare ancestry-specific variants in the fetal genome that confer risk of preterm premature rupture of membranes (PPROM) and preterm birth. BMC Medical Genetics, 2018, 19, 181.	2.1	14
22	Mutations in fetal genes involved in innate immunity and host defense against microbes increase risk of preterm premature rupture of membranes (<scp>PPROM</scp>). Molecular Genetics & Genomic Medicine, 2017, 5, 720-729.	0.6	53
23	Rare mutations and potentially damaging missense variants in genes encoding fibrillar collagens and proteins involved in their production are candidates for risk for preterm premature rupture of membranes. PLoS ONE, 2017, 12, e0174356.	1.1	14
24	An epidemiologic study of childhood sexual abuse and adult sleep disturbances.. Psychological Trauma: Theory, Research, Practice, and Policy, 2016, 8, 198-205.	1.4	52
25	Establishing an analytic pipeline for genome-wide DNA methylation. Clinical Epigenetics, 2016, 8, 45.	1.8	36
26	Associations Between Gestational Age at Birth and Alcohol Use in the Avon Longitudinal Study of Parents and Children. Alcoholism: Clinical and Experimental Research, 2016, 40, 1328-1338.	1.4	1
27	A narrow heritability evaluation of gestational age at birth. Human Genetics, 2015, 134, 809-811.	1.8	3
28	The contribution of genetic and environmental factors toÂtheÂduration of pregnancy. American Journal of Obstetrics and Gynecology, 2014, 210, 398-405.	0.7	71
29	The impact of childhood parental loss on risk for mood, anxiety and substance use disorders in a population-based sample of male twins. Psychiatry Research, 2014, 220, 404-409.	1.7	44
30	Resolving the Effects of Maternal and Offspring Genotype on Dyadic Outcomes in Genome Wide Complex Trait Analysis (â€œM-GCTAâ€. Behavior Genetics, 2014, 44, 445-455.	1.4	67
31	Epigenetic Alterations and an Increased Frequency of Micronuclei in Women with Fibromyalgia. Nursing Research and Practice, 2013, 2013, 1-12.	0.4	43
32	Fetal and Maternal Genesâ€™ Influence on Gestational Age in a Quantitative Genetic Analysis of 244,000 Swedish Births. American Journal of Epidemiology, 2013, 178, 543-550.	1.6	62
33	Increased Frequency of Micronuclei in Adults with a History of Childhood Sexual Abuse: A Discordant Monozygotic Twin Study. PLoS ONE, 2013, 8, e55337.	1.1	8
34	Epistasis between COMT and MTHFR in Maternal-Fetal Dyads Increases Risk for Preeclampsia. PLoS ONE, 2011, 6, e16681.	1.1	49
35	Genetic and environmental influences on spontaneous micronuclei frequencies in children and adults: a twin study. Mutagenesis, 2011, 26, 745-752.	1.0	16
36	Racial Differences in Genetic and Environmental Risk to Preterm Birth. PLoS ONE, 2010, 5, e12391.	1.1	47

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37	High-resolution mass spectrometry proteomics for the identification of candidate plasma protein biomarkers for chronic obstructive pulmonary disease. Biomarkers, 2010, 15, 367-377.	0.9	10
38	Estimating Fetal and Maternal Genetic Contributions to Premature Birth From Multiparous Pregnancy Histories of Twins Using MCMC and Maximum-Likelihood Approaches. Twin Research and Human Genetics, 2009, 12, 333-342.	0.3	28
39	Asthma pharmacogenetic study using finite mixture models to handle drug-response heterogeneity. Pharmacogenomics, 2009, 10, 753-767.	0.6	11
40	Comparison of multivariate adaptive regression splines and logistic regression in detecting SNP–SNP interactions and their application in prostate cancer. Journal of Human Genetics, 2008, 53, 802-811.	1.1	32
41	Pharmacogenetics of the 5-lipoxygenase biosynthetic pathway and variable clinical response to montelukast. Pharmacogenetics and Genomics, 2007, 17, 189-196.	0.7	101
42	Multivariate adaptive regression splines: a powerful method for detecting disease–risk relationship differences among subgroups. Statistics in Medicine, 2006, 25, 1355-1367.	0.8	29
43	Epistatic and Environmental Control of Genome-Wide Gene Expression. Twin Research and Human Genetics, 2005, 8, 5-15.	0.3	14
44	Epistatic and environmental control of genome-wide gene expression. Twin Research and Human Genetics, 2005, 8, 5-15.	0.3	7
45	Common Disease Analysis Using Multivariate Adaptive Regression Splines (MARS): Genetic Analysis Workshop 12 Simulated Sequence Data. Genetic Epidemiology, 2001, 21, S649-54.	0.6	31