

# Kathryn E Kemper

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3758688/publications.pdf>

Version: 2024-02-01

32  
papers

6,503  
citations

236925

25  
h-index

414414

32  
g-index

35  
all docs

35  
docs citations

35  
times ranked

11790  
citing authors

#	ARTICLE	IF	CITATIONS
1	Correlates of cervical cancer screening among women living with HIV in Kenya: A cross-sectional study. <i>International Journal of Gynecology and Obstetrics</i> , 2022, 156, 151-158.	2.3	3
2	Phenotypic covariance across the entire spectrum of relatedness for 86 billion pairs of individuals. <i>Nature Communications</i> , 2021, 12, 1050.	12.8	19
3	Genome-wide association study of dietary intake in the UK biobank study and its associations with schizophrenia and other traits. <i>Translational Psychiatry</i> , 2020, 10, 51.	4.8	33
4	Genome-wide association study identifies 143 loci associated with 25 hydroxyvitamin D concentration. <i>Nature Communications</i> , 2020, 11, 1647.	12.8	211
5	Genotype-by-environment interactions inferred from genetic effects on phenotypic variability in the UK Biobank. <i>Science Advances</i> , 2019, 5, eaaw3538.	10.3	123
6	The effect of X-linked dosage compensation on complex trait variation. <i>Nature Communications</i> , 2019, 10, 3009.	12.8	44
7	Genetic correlates of social stratification in Great Britain. <i>Nature Human Behaviour</i> , 2019, 3, 1332-1342.	12.0	177
8	Quantifying between-cohort and between-sex genetic heterogeneity in major depressive disorder. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2019, 180, 439-447.	1.7	35
9	Genome-wide association study of medication-use and associated disease in the UK Biobank. <i>Nature Communications</i> , 2019, 10, 1891.	12.8	140
10	Complex Trait Prediction from Genome Data: Contrasting EBV in Livestock to PRS in Humans. <i>Genetics</i> , 2019, 211, 1131-1141.	2.9	99
11	Improved polygenic prediction by Bayesian multiple regression on summary statistics. <i>Nature Communications</i> , 2019, 10, 5086.	12.8	291
12	A resource-efficient tool for mixed model association analysis of large-scale data. <i>Nature Genetics</i> , 2019, 51, 1749-1755.	21.4	294
13	Effectiveness and cost of multilayered colorectal cancer screening promotion interventions at federally qualified health centers in Washington State. <i>Cancer</i> , 2018, 124, 4121-4129.	4.1	31
14	Imprint of assortative mating on the human genome. <i>Nature Human Behaviour</i> , 2018, 2, 948-954.	12.0	97
15	Dissection of genetic variation and evidence for pleiotropy in male pattern baldness. <i>Nature Communications</i> , 2018, 9, 5407.	12.8	65
16	Association Between Population Density and Genetic Risk for Schizophrenia. <i>JAMA Psychiatry</i> , 2018, 75, 901.	11.0	67
17	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals. <i>Nature Genetics</i> , 2018, 50, 1112-1121.	21.4	1,835
18	Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. <i>Nature Communications</i> , 2018, 9, 2941.	12.8	570

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19	A multi-trait Bayesian method for mapping QTL and genomic prediction. <i>Genetics Selection Evolution</i> , 2018, 50, 10.	3.0	32
20	Comparison of Genotypic and Phenotypic Correlations: Cheverud's Conjecture in Humans. <i>Genetics</i> , 2018, 209, 941-948.	2.9	117
21	Meta-analysis of genome-wide association studies for height and body mass index in ~700000 individuals of European ancestry. <i>Human Molecular Genetics</i> , 2018, 27, 3641-3649.	2.9	1,541
22	Differentially Expressed Genes in Endometrium and Corpus Luteum of Holstein Cows Selected for High and Low Fertility Are Enriched for Sequence Variants Associated with Fertility1. <i>Biology of Reproduction</i> , 2016, 94, 19.	2.7	53
23	Targeted imputation of sequence variants and gene expression profiling identifies twelve candidate genes associated with lactation volume, composition and calving interval in dairy cattle. <i>Mammalian Genome</i> , 2016, 27, 81-97.	2.2	75
24	A computationally efficient algorithm for genomic prediction using a Bayesian model. <i>Genetics Selection Evolution</i> , 2015, 47, 34.	3.0	23
25	Improved precision of QTL mapping using a nonlinear Bayesian method in a multi-breed population leads to greater accuracy of across-breed genomic predictions. <i>Genetics Selection Evolution</i> , 2015, 47, 29.	3.0	113
26	Selection for complex traits leaves little or no classic signatures of selection. <i>BMC Genomics</i> , 2014, 15, 246.	2.8	124
27	Adaptation of gastrointestinal nematode parasites to host genotype: single locus simulation models. <i>Genetics Selection Evolution</i> , 2013, 45, 14.	3.0	21
28	Detection of quantitative trait loci in <i>Bos indicus</i> and <i>Bos taurus</i> cattle using genome-wide association studies. <i>Genetics Selection Evolution</i> , 2013, 45, 43.	3.0	44
29	Comparing linkage and association analyses in sheep points to a better way of doing GWAS. <i>Genetical Research</i> , 2012, 94, 191-203.	0.9	22
30	Genetic architecture of body size in mammals. <i>Genome Biology</i> , 2012, 13, 244.	9.6	68
31	Understanding and predicting complex traits: knowledge from cattle. <i>Human Molecular Genetics</i> , 2012, 21, R45-R51.	2.9	64
32	The distribution of SNP marker effects for faecal worm egg count in sheep, and the feasibility of using these markers to predict genetic merit for resistance to worm infections. <i>Genetical Research</i> , 2011, 93, 203-219.	0.9	67