

Kathryn E Kemper

List of Publications by Year in descending order

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Version: 2024-02-01

29
papers

6,748
citations

304368

22
h-index

476904

29
g-index

35
all docs

35
docs citations

35
times ranked

12039
citing authors

#	ARTICLE	IF	CITATIONS
1	Widespread signatures of natural selection across human complex traits and functional genomic categories. <i>Nature Communications</i> , 2021, 12, 1164.	5.8	50
2	Phenotypic covariance across the entire spectrum of relatedness for 86 billion pairs of individuals. <i>Nature Communications</i> , 2021, 12, 1050.	5.8	19
3	A unified framework for association and prediction from vertex-wise grey-matter structure. <i>Human Brain Mapping</i> , 2020, 41, 4062-4076.	1.9	16
4	Genetic control of temperament traits across species: association of autism spectrum disorder risk genes with cattle temperament. <i>Genetics Selection Evolution</i> , 2020, 52, 51.	1.2	25
5	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.	2.4	33
6	Genome-wide association study identifies 143 loci associated with 25 hydroxyvitamin D concentration. <i>Nature Communications</i> , 2020, 11, 1647.	5.8	211
7	Genotype-by-environment interactions inferred from genetic effects on phenotypic variability in the UK Biobank. <i>Science Advances</i> , 2019, 5, eaaw3538.	4.7	123
8	The effect of X-linked dosage compensation on complex trait variation. <i>Nature Communications</i> , 2019, 10, 3009.	5.8	44
9	Genetic correlates of social stratification in Great Britain. <i>Nature Human Behaviour</i> , 2019, 3, 1332-1342.	6.2	177
10	Genome-wide association study of medication-use and associated disease in the UK Biobank. <i>Nature Communications</i> , 2019, 10, 1891.	5.8	140
11	Complex Trait Prediction from Genome Data: Contrasting EBV in Livestock to PRS in Humans. <i>Genetics</i> , 2019, 211, 1131-1141.	1.2	99
12	Improved polygenic prediction by Bayesian multiple regression on summary statistics. <i>Nature Communications</i> , 2019, 10, 5086.	5.8	291
13	A resource-efficient tool for mixed model association analysis of large-scale data. <i>Nature Genetics</i> , 2019, 51, 1749-1755.	9.4	294
14	Imprint of assortative mating on the human genome. <i>Nature Human Behaviour</i> , 2018, 2, 948-954.	6.2	97
15	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.	9.4	1,835
16	Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. <i>Nature Communications</i> , 2018, 9, 2941.	5.8	570
17	A multi-trait Bayesian method for mapping QTL and genomic prediction. <i>Genetics Selection Evolution</i> , 2018, 50, 10.	1.2	32
18	Meta-analysis of genome-wide association studies for height and body mass index in $\sim 700,000$ individuals of European ancestry. <i>Human Molecular Genetics</i> , 2018, 27, 3641-3649.	1.4	1,541

#	ARTICLE	IF	CITATIONS
19	Identifying gene targets for brain-related traits using transcriptomic and methylomic data from blood. <i>Nature Communications</i> , 2018, 9, 2282.	5.8	294
20	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.	1.0	75
21	A computationally efficient algorithm for genomic prediction using a Bayesian model. <i>Genetics Selection Evolution</i> , 2015, 47, 34.	1.2	23
22	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.	1.2	113
23	A Multi-Trait, Meta-analysis for Detecting Pleiotropic Polymorphisms for Stature, Fatness and Reproduction in Beef Cattle. <i>PLoS Genetics</i> , 2014, 10, e1004198.	1.5	247
24	Selection for complex traits leaves little or no classic signatures of selection. <i>BMC Genomics</i> , 2014, 15, 246.	1.2	124
25	Adaptation of gastrointestinal nematode parasites to host genotype: single locus simulation models. <i>Genetics Selection Evolution</i> , 2013, 45, 14.	1.2	21
26	Comparing linkage and association analyses in sheep points to a better way of doing GWAS. <i>Genetical Research</i> , 2012, 94, 191-203.	0.3	22
27	Genetic architecture of body size in mammals. <i>Genome Biology</i> , 2012, 13, 244.	13.9	68
28	Understanding and predicting complex traits: knowledge from cattle. <i>Human Molecular Genetics</i> , 2012, 21, R45-R51.	1.4	64
29	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.	0.3	67