Celia Mt Greenwood

List of Publications by Year
in descending order

21
papers

2,189
citations

623734

14
h-index

752698

20
g-index

23
all docs

23
docs citations

23
times ranked

5694
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide association scan identifies a colorectal cancer susceptibility locus on chromosome 8q24. Nature Genetics, 2007, 39, 989-994.	21.4	676
2	Functional normalization of 450k methylation array data improves replication in large cancer studies. Genome Biology, 2014, 15, 503.	8.8	665
3	Control Genes and Variability: Absence of Ubiquitous Reference Transcripts in Diverse Mammalian Expression Studies. Genome Research, 2002, 12, 292-297.	5.5	315
4	An evaluation of methods correcting for cell-type heterogeneity in DNA methylation studies. Genome Biology, 2016, 17, 84.	8.8	137
5	Analysis of Affected Sib Pairs, with Covariatesâ€"With and Without Constraints. American Journal of Human Genetics, 1999, 64, 871-885.	6.2	57
6	Effect Sizes of Deletions and Duplications on Autism Risk Across the Genome. American Journal of Psychiatry, 2021, 178, 87-98.	7.2	50
7	General psychopathology, internalising and externalising in children and functional outcomes in late adolescence. Journal of Child Psychology and Psychiatry and Allied Disciplines, 2019, 60, 1183-1190.	5.2	45
8	Maternal Prenatal Mood, Pregnancy-Specific Worries, and Early Child Psychopathology: Findings From the DREAM BIG Consortium. Journal of the American Academy of Child and Adolescent Psychiatry, 2021, 60, 186-197.	0.5	40
9	Agreement in DNA methylation levels from the Illumina 450K array across batches, tissues, and time. Epigenetics, 2018, 13, 19-32.	2.7	39
10	Gene networks show associations with seed region connectivity. Human Brain Mapping, 2017, 38, 3126-3140.	3.6	32
11	Incorporation of covariates into genome scanning using sib-pair analysis in bipolar affective disorder. Genetic Epidemiology, 1997, 14, 635-640.	1.3	28
12	funtooNorm: an R package for normalization of DNA methylation data when there are multiple cell or tissue types. Bioinformatics, 2016, 32, 593-595.	4.1	22
13	Down-Weighting of Multiple Affected Sib Pairs Leads to Biased Likelihood-Ratio Tests, under the Assumption of No Linkage. American Journal of Human Genetics, 1999, 64, 1248-1252.	6.2	20
14	Optimal selection of markers for validation or replication from genome-wide association studies. Genetic Epidemiology, 2007, 31, 396-407.	1.3	15
15	Combined polygenic risk scores of different psychiatric traits predict general and specific psychopathology in childhood. Journal of Child Psychology and Psychiatry and Allied Disciplines, 2022, 63, 636-645.	5.2	14
16	Regression models for allele sharing: analysis of accumulating data in affected sib pair studies. Statistics in Medicine, 2002, 21, 431-444.	1.6	8
17	Principal component of explained variance: An efficient and optimal data dimension reduction framework for association studies. Statistical Methods in Medical Research, 2018, 27, 1331-1350.	1.5	7
18	Pedigree Selection and Tests of Linkage in a Hutterite Asthma Pedigree. Genetic Epidemiology, 2001, 21, S244-51.	1.3	6

#	Article	IF	Citations
19	Evidence of linkage to chromosome 1 for early age of onset of rheumatoid arthritis and HLA marker DRB1 genotype in NARAC data. BMC Proceedings, 2007, 1, S78.	1.6	2
20	Corrections to the Parameterization of Constraints on Allele Sharing in Sibling Pairs Alter Covariate-Parameter Estimates but Not Sharing-Probability Estimates or Power of Tests for Linkage. American Journal of Human Genetics, 2005, 76, 187-189.	6.2	1
21	Validation of linkage by sampling based on environmental exposures. Genetic Epidemiology, 1999, 17, S593-S598.	1.3	0