Leanne M Wallace

List of Publications by Year
in descending order

35 papers	2,030 citations	394286 19 h-index	377752 34 g-index
37 all docs	37 docs citations	37 times ranked	4466 citing authors

#	Article	IF	Citations
1	Genome-wide association study identifies a locus at 7p15.2 associated with endometriosis. Nature Genetics, 2011, 43, 51-54.	9.4	261
2	Meta-analysis identifies five novel loci associated with endometriosis highlighting key genes involved in hormone metabolism. Nature Communications, 2017, 8, 15539.	5.8	230
3	Common variants in TMPRSS6 are associated with iron status and erythrocyte volume. Nature Genetics, 2009, 41, 1173-1175.	9.4	226
4	Common and rare variant association analyses in amyotrophic lateral sclerosis identify 15 risk loci with distinct genetic architectures and neuron-specific biology. Nature Genetics, 2021, 53, 1636-1648.	9.4	223
5	Autism-related dietary preferences mediate autism-gut microbiome associations. Cell, 2021, 184, 5916-5931.e17.	13.5	172
6	Analysis of DNA methylation associates the cystineâ€“glutamate antiporter SLC7A11 with risk of Parkinsonâ€™s disease. Nature Communications, 2020, 11, 1238.	5.8	85
7	Sequence Variants in Three Loci Influence Monocyte Counts and Erythrocyte Volume. American Journal of Human Genetics, 2009, 85, 745-749.	2.6	73
8	Association ofOPRD1polymorphisms with heroin dependence in a large case-control series. Addiction Biology, 2014, 19, 111-121.	1.4	70
9	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. Human Molecular Genetics, 2015, 24, 5955-5964.	1.4	68
10	ANKK1, TTC12, and NCAM1 Polymorphisms and Heroin Dependence. JAMA Psychiatry, 2013, 70, 325.	6.0	66
11	Meta-analysis of genome-wide DNA methylation identifies shared associations across neurodegenerative disorders. Genome Biology, 2021, 22, 90.	3.8	49
12	Genome-Wide Association Shows thatÂPigmentation Genes Play a Role in SkinÂAging. Journal of Investigative Dermatology, 2017, 137, 1887-1894.	0.3	48
13	Rapid inexpensive genome-wide association using pooled whole blood. Genome Research, 2009, 19, 2075-2080.	2.4	45
14	Genome-wide study of DNA methylation shows alterations in metabolic, inflammatory, and cholesterol pathways in ALS. Science Translational Medicine, 2022, 14, eabj0264.	5.8	38
15	High-density fine-mapping of a chromosome 10q26 linkage peak suggests association between endometriosis and variants close to CYP2C19. Fertility and Sterility, 2011, 95, 2236-2240.	0.5	36
16	Genetic analysis of endometriosis and depression identifies shared loci and implicates causal links with gastric mucosa abnormality. Human Genetics, 2021, 140, 529-552.	1.8	36
17	The genetic regulation of transcription in human endometrial tissue. Human Reproduction, 2017, 32, 893-904.	0.4	32
18	A genome wide linkage scan for dizygotic twinning in 525 families of mothers of dizygotic twins. Human Reproduction, 2010, 25, 1569-1580.	0.4	31

#	Article	IF	Citations
19	Endometrial vezatin and its association with endometriosis risk. Human Reproduction, 2016, 31, 999-1013.	0.4	25
20	Significant out-of-sample classification from methylation profile scoring for amyotrophic lateral sclerosis. Npj Genomic Medicine, 2020, 5, 10.	1.7	25
21	LPAR1andITGA4regulate peripheral blood monocyte counts. Human Mutation, 2011, 32, 873-876.	1.1	20
22	Study protocol for the Australian autism biobank: an international resource to advance autism discovery research. BMC Pediatrics, 2018, 18, 284.	0.7	20
23	Genetic overlap analysis of endometriosis and asthma identifies shared loci implicating sex hormones and thyroid signalling pathways. Human Reproduction, 2022, 37, 366-383.	0.4	19
24	Genetic analyses of gynecological disease identify genetic relationships between uterine fibroids and endometrial cancer, and a novel endometrial cancer genetic risk region at the WNT4 1p36.12 locus. Human Genetics, 2021, 140, 1353-1365.	1.8	18
25	Analysis of potential protein-modifying variants in 9000 endometriosis patients and 150000 controls of European ancestry. Scientific Reports, 2017, 7, 11380.	1.6	16
26	Polygenic risk score analysis for amyotrophic lateral sclerosis leveraging cognitive performance, educational attainment and schizophrenia. European Journal of Human Genetics, 2022, 30, 532-539.	1.4	16
27	Microsatellite Stable Colorectal Cancers Stratified by the BRAF V600E Mutation Show Distinct Patterns of Chromosomal Instability. PLoS ONE, 2014, 9, e91739.	1.1	15
28	Examining the association of NRXN3 SNPs with borderline personality disorder phenotypes in heroin dependent cases and socio-economically disadvantaged controls. Drug and Alcohol Dependence, 2013, 128, 187-193.	1.6	12
29	Functional characterisation of the amyotrophic lateral sclerosis risk locus GPX3/TNIP1. Genome Medicine, 2022, 14, 7.	3.6	12
30	Analysis of common genetic variation and rare CNVs in the Australian Autism Biobank. Molecular Autism, 2021, 12, 12.	2.6	11
31	Accuracy of Inferred APOE Genotypes for a Range of Genotyping Arrays and Imputation Reference Panels. Journal of Alzheimer's Disease, 2018, 64, 49-54.	1.2	9
32	Cumulative influence of parity-related genomic changes in multiple sclerosis. Journal of Neuroimmunology, 2019, 328, 38-49.	1.1	9
33	Two Corpora Lutea Seen at 6â€“13 Weeks' Gestation Infers Dizygosity Among Spontaneous Same-Sexed Dichorionic Twins. Twin Research and Human Genetics, 2009, 12, 180-182.	0.3	3
34	Association between DNA methylation variability and self-reported exposure to heavy metals. Scientific Reports, 2022, 12, .	1.6	2
35	Genome-Wide Association Study Identifies a Locus at 7p15.2 Associated With Endometriosis. Obstetrical and Gynecological Survey, 2011, 66, 214-216.	0.2	0