Stacey L Edwards

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1162490/publications.pdf

Version: 2024-02-01

34 papers	4,190 citations	279487 23 h-index	377514 34 g-index
40 all docs	40 docs citations	40 times ranked	9009 citing authors

#	Article	IF	Citations
1	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	13.7	1,099
2	Beyond GWASs: Illuminating the Dark Road from Association to Function. American Journal of Human Genetics, 2013, 93, 779-797.	2.6	688
3	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. Nature Genetics, 2013, 45, 371-384.	9.4	493
4	Functional Variants at the 11q13 Risk Locus for Breast Cancer Regulate Cyclin D1 Expression through Long-Range Enhancers. American Journal of Human Genetics, 2013, 92, 489-503.	2.6	201
5	Point Mutations in Exon 1B of APC Reveal Gastric Adenocarcinoma and Proximal Polyposis of the Stomach as a Familial Adenomatous Polyposis Variant. American Journal of Human Genetics, 2016, 98, 830-842.	2.6	201
6	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. Nature Genetics, 2018, 50, 968-978.	9.4	184
7	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. Nature Genetics, 2016, 48, 374-386.	9.4	125
8	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	9.4	120
9	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	5.8	105
10	Fine-Scale Mapping of the FGFR2 Breast Cancer Risk Locus: Putative Functional Variants Differentially Bind FOXA1 and E2F1. American Journal of Human Genetics, 2013, 93, 1046-1060.	2.6	98
11	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	5.8	78
12	Five endometrial cancer risk loci identified through genome-wide association analysis. Nature Genetics, 2016, 48, 667-674.	9.4	77
13	Long Noncoding RNAs CUPID1 and CUPID2 Mediate Breast Cancer Risk at 11q13 by Modulating the Response to DNA Damage. American Journal of Human Genetics, 2017, 101, 255-266.	2.6	77
14	Fine-Scale Mapping of the 5q11.2 Breast Cancer Locus Reveals at Least Three Independent Risk Variants Regulating MAP3K1. American Journal of Human Genetics, 2015, 96, 5-20.	2.6	76
15	Evidence that the 5p12 Variant rs10941679 Confers Susceptibility to Estrogen-Receptor-Positive Breast Cancer through FGF10 and MRPS30 Regulation. American Journal of Human Genetics, 2016, 99, 903-911.	2.6	59
16	Long-range regulators of the lncRNAHOTAIRenhance its prognostic potential in breast cancer. Human Molecular Genetics, 2016, 25, 3269-3283.	1.4	58
17	Endometriosis risk alleles at 1p36.12 act through inverse regulation ofCDC42andLINC00339. Human Molecular Genetics, 2016, 25, ddw320.	1.4	56
18	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. Human Molecular Genetics, 2015, 24, 1478-1492.	1.4	50

#	Article	IF	Citations
19	Targeting VEGF with LNA-stabilized G-rich oligonucleotide for efficient breast cancer inhibition. Chemical Communications, 2015, 51, 9499-9502.	2.2	48
20	Polymorphisms in a Putative Enhancer at the 10q21.2 Breast Cancer Risk Locus Regulate NRBF2 Expression. American Journal of Human Genetics, 2015, 97, 22-34.	2.6	37
21	A Common Variant at the 14q32 Endometrial Cancer Risk Locus Activates AKT1 through YY1 Binding. American Journal of Human Genetics, 2016, 98, 1159-1169.	2.6	32
22	eQTL Colocalization Analyses Identify NTN4 as a Candidate Breast Cancer Risk Gene. American Journal of Human Genetics, 2020, 107, 778-787.	2.6	29
23	Germline polymorphisms in an enhancer of PSIP1 are associated with progression-free survival in epithelial ovarian cancer. Oncotarget, 2016, 7, 6353-6368.	0.8	29
24	Chromatin interactome mapping at 139 independent breast cancer risk signals. Genome Biology, 2020, 21, 8.	3.8	27
25	Functional dissection of breast cancer risk-associated TERT promoter variants. Oncotarget, 2017, 8, 67203-67217.	0.8	21
26	Non-coding RNAs underlie genetic predisposition to breast cancer. Genome Biology, 2020, 21, 7.	3.8	21
27	Long-Range Modulation of PAG1 Expression by 8q21 Allergy Risk Variants. American Journal of Human Genetics, 2015, 97, 329-336.	2.6	19
28	Fine scale mapping of the 17q22 breast cancer locus using dense SNPs, genotyped within the Collaborative Oncological Gene-Environment Study (COGs). Scientific Reports, 2016, 6, 32512.	1.6	19
29	MiR-29b-1-5p is altered in BRCA1 mutant tumours and is a biomarker in basal-like breast cancer. Oncotarget, 2018, 9, 33577-33588.	0.8	15
30	BRCA1 and BRCA2 5â€² noncoding region variants identified in breast cancer patients alter promoter activity and protein binding. Human Mutation, 2018, 39, 2025-2039.	1.1	15
31	Genetic and Clinical Predictive Factors of Sulfonylurea Failure in Patients with Type 2 Diabetes. Diabetes Technology and Therapeutics, 2016, 18, 586-593.	2.4	8
32	Identification of a Locus Near ULK1 Associated With Progression-Free Survival in Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 1669-1680.	1.1	5
33	Allelic imbalance in human breast cancer. Oncotarget, 2017, 8, 10763-10764.	0.8	2
34	Genetic determinants of breast cancer risk. Current Opinion in Endocrine and Metabolic Research, 2020, 15, 1-7.	0.6	1