Honglin Song

List of Publications by Year
in descending order

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52	4,484	147566	174990
papers	citations	31 h-index	52 g-index

52	52	52	7727
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	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
2	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	9.4	356
3	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. Nature Genetics, 2013, 45, 362-370.	9.4	326
4	A genome-wide association study identifies susceptibility loci for ovarian cancer at 2q31 and 8q24. Nature Genetics, 2010, 42, 874-879.	9.4	321
5	Germline Mutations in the BRIP1, BARD1, PALB2, and NBN Genes in Women With Ovarian Cancer. Journal of the National Cancer Institute, 2015, 107, .	3.0	311
6	A genome-wide association study identifies a new ovarian cancer susceptibility locus on 9p22.2. Nature Genetics, 2009, 41, 996-1000.	9.4	276
7	Common variants at 19p13 are associated with susceptibility to ovarian cancer. Nature Genetics, 2010, 42, 880-884.	9.4	235
8	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	9.4	221
9	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. Cancer Discovery, 2016, 6, 1052-1067.	7.7	157
10	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. Nature Communications, 2013, 4, 1628.	5.8	144
11	The contribution of deleterious germline mutations in BRCA1, BRCA2 and the mismatch repair genes to ovarian cancer in the population. Human Molecular Genetics, 2014, 23, 4703-4709.	1.4	112
12	Association of vitamin D levels and risk of ovarian cancer: a Mendelian randomization study. International Journal of Epidemiology, 2016, 45, 1619-1630.	0.9	111
13	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. Nature Communications, 2013, 4, 1627.	5.8	98
14	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	5.8	78
15	LIN28B Polymorphisms Influence Susceptibility to Epithelial Ovarian Cancer. Cancer Research, 2011, 71, 3896-3903.	0.4	75
16	Consortium analysis of 7 candidate SNPs for ovarian cancer. International Journal of Cancer, 2008, 123, 380-388.	2.3	73
17	Adult body mass index and risk of ovarian cancer by subtype: a Mendelian randomization study. International Journal of Epidemiology, 2016, 45, 884-895.	0.9	71
18	Common variants in mismatch repair genes and risk of invasive ovarian cancer. Carcinogenesis, 2006, 27, 2235-2242.	1.3	67

#	Article	IF	Citations
19	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. Nature Communications, 2015, 6, 8234.	5.8	63
20	Tagging Single Nucleotide Polymorphisms in the BRIP1 Gene and Susceptibility to Breast and Ovarian Cancer. PLoS ONE, 2007, 2, e268.	1.1	54
21	A Transcriptome-Wide Association Study Among 97,898 Women to Identify Candidate Susceptibility Genes for Epithelial Ovarian Cancer Risk. Cancer Research, 2018, 78, 5419-5430.	0.4	54
22	A risk prediction algorithm for ovarian cancer incorporatingBRCA1, BRCA2, common alleles and other familial effects. Journal of Medical Genetics, 2015, 52, 465-475.	1.5	52
23	Association between tumour infiltrating lymphocytes, histotype and clinical outcome in epithelial ovarian cancer. BMC Cancer, 2017, 17, 657.	1.1	48
24	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. PLoS ONE, 2015, 10, e0128106.	1.1	44
25	Telomere structure and maintenance gene variants and risk of five cancer types. International Journal of Cancer, 2016, 139, 2655-2670.	2.3	43
26	PPM1DMosaic Truncating Variants in Ovarian Cancer Cases May Be Treatment-Related Somatic Mutations. Journal of the National Cancer Institute, 2016, 108, djv347.	3.0	43
27	Development and Validation of the Gene Expression Predictor of High-grade Serous Ovarian Carcinoma Molecular SubTYPE (PrOTYPE). Clinical Cancer Research, 2020, 26, 5411-5423.	3.2	43
28	Germline whole exome sequencing and large-scale replication identifies FANCM as a likely high grade serous ovarian cancer susceptibility gene. Oncotarget, 2017, 8, 50930-50940.	0.8	43
29	Association between invasive ovarian cancer susceptibility and 11 best candidate SNPs from breast cancer genome-wide association study. Human Molecular Genetics, 2009, 18, 2297-2304.	1.4	42
30	Common Variants in RB1 Gene and Risk of Invasive Ovarian Cancer. Cancer Research, 2006, 66, 10220-10226.	0.4	39
31	Clinical and pathological associations of PTEN expression in ovarian cancer: a multicentre study from the Ovarian Tumour Tissue Analysis Consortium. British Journal of Cancer, 2020, 123, 793-802.	2.9	35
32	Genome-wide Analysis Identifies Novel Loci Associated with Ovarian Cancer Outcomes: Findings from the Ovarian Cancer Association Consortium. Clinical Cancer Research, 2015, 21, 5264-5276.	3.2	33
33	Effects of Common Germ-Line Genetic Variation in Cell Cycle Genes on Ovarian Cancer Survival. Clinical Cancer Research, 2008, 14, 1090-1095.	3.2	29
34	Network-Based Integration of GWAS and Gene Expression Identifies a HOX-Centric Network Associated with Serous Ovarian Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1574-1584.	1.1	28
35	Population-based targeted sequencing of 54 candidate genes identifiesPALB2as a susceptibility gene for high-grade serous ovarian cancer. Journal of Medical Genetics, 2021, 58, 305-313.	1.5	26
36	Cigarette smoking is associated with adverse survival among women with ovarian cancer: Results from a pooled analysis of 19 studies. International Journal of Cancer, 2017, 140, 2422-2435.	2.3	25

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37	Common variants at theCHEK2gene locus and risk of epithelial ovarian cancer. Carcinogenesis, 2015, 36, 1341-1353.	1.3	24
38	Enrichment of putative PAX8 target genes at serous epithelial ovarian cancer susceptibility loci. British Journal of Cancer, 2017, 116, 524-535.	2.9	23
39	Epithelialâ€Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. Genetic Epidemiology, 2015, 39, 689-697.	0.6	22
40	The association between socioeconomic status and tumour stage at diagnosis of ovarian cancer: A pooled analysis of 18 case-control studies. Cancer Epidemiology, 2016, 41, 71-79.	0.8	20
41	Assessing the genetic architecture of epithelial ovarian cancer histological subtypes. Human Genetics, 2016, 135, 741-756.	1.8	19
42	Exome genotyping arrays to identify rare and low frequency variants associated with epithelial ovarian cancer risk. Human Molecular Genetics, 2016, 25, 3600-3612.	1.4	17
43	Evaluating the ovarian cancer gonadotropin hypothesis: A candidate gene study. Gynecologic Oncology, 2015, 136, 542-548.	0.6	15
44	Association Study of Prostate Cancer Susceptibility Variants with Risks of Invasive Ovarian, Breast, and Colorectal Cancer. Cancer Research, 2008, 68, 8837-8842.	0.4	14
45	Inherited variants affecting RNA editing may contribute to ovarian cancer susceptibility: results from a large-scale collaboration. Oncotarget, 2016, 7, 72381-72394.	0.8	13
46	A comprehensive geneâ€“environment interaction analysis in Ovarian Cancer using genomeâ€wide significant common variants. International Journal of Cancer, 2019, 144, 2192-2205.	2.3	12
47	Assessment of Multifactor Geneâ€“Environment Interactions and Ovarian Cancer Risk: Candidate Genes, Obesity, and Hormone-Related Risk Factors. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 780-790.	1.1	10
48	Investigation of Exomic Variants Associated with Overall Survival in Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 446-454.	1.1	9
49	Evaluation of vitamin D biosynthesis and pathway target genes reveals UGT2A1/2 and EGFR polymorphisms associated with epithelial ovarian cancer in African American Women. Cancer Medicine, 2019, 8, 2503-2513.	1.3	6
50	Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with risk of clear cell ovarian cancer. Oncotarget, 2016, 7, 69097-69110.	0.8	5
51	No Evidence That Genetic Variation in the Myeloid-Derived Suppressor Cell Pathway Influences Ovarian Cancer Survival. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 420-424.	1.1	3
52	rs495139 in the TYMS-ENOSF1 Region and Risk of Ovarian Carcinoma of Mucinous Histology. International Journal of Molecular Sciences, 2018, 19, 2473.	1.8	3