# Honglin Song

## List of Publications by Year
in descending order

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|---|---|---|---|
| 52<br>papers | 4,484<br>citations | 147566<br>31<br>h-index | 174990<br>52<br>g-index |
| 52<br>all docs | 52<br>docs citations | 52<br>times ranked | 7727<br>citing authors |

| # | Article | IF | Citations |
|---|---------|----|-----------| 
| 1 | Population-based targeted sequencing of 54 candidate genes identifies *PALB2* as a susceptibility gene for high-grade serous ovarian cancer. Journal of Medical Genetics, 2021, 58, 305-313. | 1.5 | 26 |
| 2 | 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 |
| 3 | 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 |
| 4 | 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 |
| 5 | A comprehensive gene–environment interaction analysis in Ovarian Cancer using genome‐wide significant common variants. International Journal of Cancer, 2019, 144, 2192-2205. | 2.3 | 12 |
| 6 | 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 |
| 7 | 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 |
| 8 | Enrichment of putative PAX8 target genes at serous epithelial ovarian cancer susceptibility loci. British Journal of Cancer, 2017, 116, 524-535. | 2.9 | 23 |
| 9 | 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 |
| 10 | Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691. | 9.4 | 356 |
| 11 | 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 |
| 12 | Association between tumour infiltrating lymphocytes, histotype and clinical outcome in epithelial ovarian cancer. BMC Cancer, 2017, 17, 657. | 1.1 | 48 |
| 13 | 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 |
| 14 | 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 |
| 15 | 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 |
| 16 | Assessing the genetic architecture of epithelial ovarian cancer histological subtypes. Human Genetics, 2016, 135, 741-756. | 1.8 | 19 |
| 17 | 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 |
| 18 | Telomere structure and maintenance gene variants and risk of five cancer types. International Journal of Cancer, 2016, 139, 2655-2670. | 2.3 | 43 |

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|---|---------|----|-----------| 
| 19 | 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 |
| 20 | Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast–ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675. | 5.8 | 78 |
| 21 | Assessment of Multifactor Gene–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 |
| 22 | *PPM1D* Mosaic Truncating Variants in Ovarian Cancer Cases May Be Treatment-Related Somatic Mutations. Journal of the National Cancer Institute, 2016, 108, djv347. | 3.0 | 43 |
| 23 | 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 |
| 24 | Investigation of Exomic Variants Associated with Overall Survival in Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 446-454. | 1.1 | 9 |
| 25 | 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 |
| 26 | 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 |
| 27 | Epithelial–Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. Genetic Epidemiology, 2015, 39, 689-697. | 0.6 | 22 |
| 28 | Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. PLoS ONE, 2015, 10, e0128106. | 1.1 | 44 |
| 29 | Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171. | 9.4 | 221 |
| 30 | 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 |
| 31 | 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 |
| 32 | Evaluating the ovarian cancer gonadotropin hypothesis: A candidate gene study. Gynecologic Oncology, 2015, 136, 542-548. | 0.6 | 15 |
| 33 | Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. Nature Communications, 2015, 6, 8234. | 5.8 | 63 |
| 34 | Common variants at the *CHEK2* gene locus and risk of epithelial ovarian cancer. Carcinogenesis, 2015, 36, 1341-1353. | 1.3 | 24 |
| 35 | A risk prediction algorithm for ovarian cancer incorporating *BRCA1, BRCA2*, common alleles and other familial effects. Journal of Medical Genetics, 2015, 52, 465-475. | 1.5 | 52 |
| 36 | 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 |

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|---|---------|----|-----------|
| 37 | 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 |
| 38 | GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. Nature Genetics, 2013, 45, 362-370. | 9.4 | 326 |
| 39 | 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 |
| 40 | Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. Nature Communications, 2013, 4, 1628. | 5.8 | 144 |
| 41 | Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. Nature Communications, 2013, 4, 1627. | 5.8 | 98 |
| 42 | *LIN28B* Polymorphisms Influence Susceptibility to Epithelial Ovarian Cancer. Cancer Research, 2011, 71, 3896-3903. | 0.4 | 75 |
| 43 | Common variants at 19p13 are associated with susceptibility to ovarian cancer. Nature Genetics, 2010, 42, 880-884. | 9.4 | 235 |
| 44 | A genome-wide association study identifies susceptibility loci for ovarian cancer at 2q31 and 8q24. Nature Genetics, 2010, 42, 874-879. | 9.4 | 321 |
| 45 | 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 |
| 46 | A genome-wide association study identifies a new ovarian cancer susceptibility locus on 9p22.2. Nature Genetics, 2009, 41, 996-1000. | 9.4 | 276 |
| 47 | Consortium analysis of 7 candidate SNPs for ovarian cancer. International Journal of Cancer, 2008, 123, 380-388. | 2.3 | 73 |
| 48 | 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 |
| 49 | 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 |
| 50 | Tagging Single Nucleotide Polymorphisms in the BRIP1 Gene and Susceptibility to Breast and Ovarian Cancer. PLoS ONE, 2007, 2, e268. | 1.1 | 54 |
| 51 | Common Variants in RB1 Gene and Risk of Invasive Ovarian Cancer. Cancer Research, 2006, 66, 10220-10226. | 0.4 | 39 |
| 52 | Common variants in mismatch repair genes and risk of invasive ovarian cancer. Carcinogenesis, 2006, 27, 2235-2242. | 1.3 | 67 |