

# Identification of six new susceptibility loci for invasive

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Associations of common breast cancer susceptibility alleles with risk of breast cancer subtypes in BRCA1 and BRCA2 mutation carriers. <i>Breast Cancer Research</i> , 2014, 16, 3416.	2.2	57
2	The Impact of Age and Sex in DLBCL: Systems Biology Analyses Identify Distinct Molecular Changes and Signaling Networks. <i>Cancer Informatics</i> , 2015, 14, CIN.S34144.	0.9	18
3	The Cancer Cell Map Initiative: Defining the Hallmark Networks of Cancer. <i>Molecular Cell</i> , 2015, 58, 690-698.	4.5	117
4	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. <i>Human Molecular Genetics</i> , 2015, 24, 3595-3607.	1.4	40
5	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. <i>Nature Genetics</i> , 2015, 47, 373-380.	9.4	513
6	Genome-wide significant risk associations for mucinous ovarian carcinoma. <i>Nature Genetics</i> , 2015, 47, 888-897.	9.4	78
7	Network-Based Integration of GWAS and Gene Expression Identifies a <i>HOX</i> -Centric Network Associated with Serous Ovarian Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 1574-1584.	1.1	28
8	Why have ovarian cancer mortality rates declined? Part III. Prospects for the future. <i>Gynecologic Oncology</i> , 2015, 138, 757-761.	0.6	32
9	Monoallelic Loss of the Imprinted Gene <i>Grb10</i> Promotes Tumor Formation in Irradiated <i>Nf1</i> <sup>+/-</sup> Mice. <i>PLoS Genetics</i> , 2015, 11, e1005235.	1.5	12
10	Genetics of Diabetic Nephropathy: a Long Road of Discovery. <i>Current Diabetes Reports</i> , 2015, 15, 41.	1.7	30
11	Genomic approaches for understanding the genetics of complex disease. <i>Genome Research</i> , 2015, 25, 1432-1441.	2.4	75
12	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. <i>Nature Communications</i> , 2015, 6, 8234.	5.8	63
13	Common variants at the <i>CHEK2</i> gene locus and risk of epithelial ovarian cancer. <i>Carcinogenesis</i> , 2015, 36, 1341-1353.	1.3	24
14	A risk prediction algorithm for ovarian cancer incorporating <i>BRCA1</i> , <i>BRCA2</i> , common alleles and other familial effects. <i>Journal of Medical Genetics</i> , 2015, 52, 465-475.	1.5	52
15	A model for estimating ovarian cancer risk: Application for preventive oophorectomy. <i>Gynecologic Oncology</i> , 2015, 139, 242-247.	0.6	12
16	Ovarian development and disease: The known and the unexpected. <i>Seminars in Cell and Developmental Biology</i> , 2015, 45, 59-67.	2.3	49
17	Genetik des familiären Brust- und Eierstockkrebses: Paneldiagnostik – Möglichkeiten und Grenzen. <i>Medizinische Genetik</i> , 2015, 27, 202-210.	0.1	5
18	Rethinking ovarian cancer II: reducing mortality from high-grade serous ovarian cancer. <i>Nature Reviews Cancer</i> , 2015, 15, 668-679.	12.8	839

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19	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. <i>Human Molecular Genetics</i> , 2015, 24, 5955-5964.	1.4	68
20	Defining the risk threshold for risk reducing salpingo-oophorectomy for ovarian cancer prevention in low risk postmenopausal women. <i>Gynecologic Oncology</i> , 2015, 139, 487-494.	0.6	39
21	DNA methylation changes in epithelial ovarian cancer histotypes. <i>Genomics</i> , 2015, 106, 311-321.	1.3	48
22	Germline Mutations in the BRIP1, BARD1, PALB2, and NBN Genes in Women With Ovarian Cancer. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	3.0	311
23	WVVOX CNV-67048 Functions as a Risk Factor for Epithelial Ovarian Cancer in Chinese Women by Negatively Interacting with Oral Contraceptive Use. <i>BioMed Research International</i> , 2016, 2016, 1-7.	0.9	6
24	Fine-Scale Mapping at 9p22.2 Identifies Candidate Causal Variants That Modify Ovarian Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. <i>PLoS ONE</i> , 2016, 11, e0158801.	1.1	10
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26	Specifying the ovarian cancer risk threshold of "premenopausal risk-reducing salpingo-oophorectomy" for ovarian cancer prevention: a cost-effectiveness analysis. <i>Journal of Medical Genetics</i> , 2016, 53, 591-599.	1.5	57
27	<i>MYC</i> and <i>PVT1</i> synergize to regulate <i>RSPO1</i> levels in breast cancer. <i>Cell Cycle</i> , 2016, 15, 881-885.	1.3	27
28	Rare <i>ATAD5</i> missense variants in breast and ovarian cancer patients. <i>Cancer Letters</i> , 2016, 376, 173-177.	3.2	21
29	Genomic approach to understand association between single nucleotide polymorphisms and risk of Korean serous ovarian cancer at stage IIIc. <i>Molecular and Cellular Toxicology</i> , 2016, 12, 21-28.	0.8	0
30	Endometriosis risk alleles at 1p36.12 act through inverse regulation of <i>CDC42</i> and <i>LINC00339</i> . <i>Human Molecular Genetics</i> , 2016, 25, ddw320.	1.4	56
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33	Modifiers of breast and ovarian cancer risks for BRCA1 and BRCA2 mutation carriers. <i>Endocrine-Related Cancer</i> , 2016, 23, T69-T84.	1.6	63
34	A splicing variant of <i>TERT</i> identified by GWAS interacts with menopausal estrogen therapy in risk of ovarian cancer. <i>International Journal of Cancer</i> , 2016, 139, 2646-2654.	2.3	7
35	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. <i>Cancer Discovery</i> , 2016, 6, 1052-1067.	7.7	157
36	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. <i>Nature Communications</i> , 2016, 7, 12675.	5.8	78

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38	Assessment of Multifactor Gene-Environment Interactions and Ovarian Cancer Risk: Candidate Genes, Obesity, and Hormone-Related Risk Factors. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 780-790.	1.1	10
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46	Moving towards population-based genetic risk prediction for ovarian cancer. <i>BJOG: an International Journal of Obstetrics and Gynaecology</i> , 2017, 124, 855-858.	1.1	5
47	Genetic risk factors for ovarian cancer and their role for endometriosis risk. <i>Gynecologic Oncology</i> , 2017, 145, 142-147.	0.6	24
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50	The lipid metabolism gene FTO influences breast cancer cell energy metabolism via the PI3K/AKT signaling pathway. <i>Oncology Letters</i> , 2017, 13, 4685-4690.	0.8	63
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59	Rethinking ovarian cancer genomics: where genome-wide association studies stand?. <i>Pharmacogenomics</i> , 2017, 18, 1611-1625.	0.6	8
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70	Evaluation of Polygenic Risk Scores for Breast and Ovarian Cancer Risk Prediction in BRCA1 and BRCA2 Mutation Carriers. <i>Journal of the National Cancer Institute</i> , 2017, 109, .	3.0	242
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74	Epidemiology of ovarian cancer: a review. <i>Cancer Biology and Medicine</i> , 2017, 14, 9-32.	1.4	981
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78	Genomic Analysis Using Regularized Regression in High-Grade Serous Ovarian Cancer. <i>Cancer Informatics</i> , 2018, 17, 117693511875534.	0.9	5
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80	Setting the Threshold for Surgical Prevention in Women at Increased Risk of Ovarian Cancer. <i>International Journal of Gynecological Cancer</i> , 2018, 28, 34-42.	1.2	23
81	An Osteoporosis Risk SNP at 1p36.12 Acts as an Allele-Specific Enhancer to Modulate LINC00339 Expression via Long-Range Loop Formation. <i>American Journal of Human Genetics</i> , 2018, 102, 776-793.	2.6	78
82	Robust Tests for Additive Gene-Environment Interaction in Case-Control Studies Using Gene-Environment Independence. <i>American Journal of Epidemiology</i> , 2018, 187, 366-377.	1.6	8
83	Common Genetic Variation and Susceptibility to Ovarian Cancer: Current Insights and Future Directions. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2018, 27, 395-404.	1.1	33
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95	Evaluation of polygenic risk scores for ovarian cancer risk prediction in a prospective cohort study. <i>Journal of Medical Genetics</i> , 2018, 55, 546-554.	1.5	38
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114	Genome-wide association studies identify susceptibility loci for epithelial ovarian cancer in east Asian women. <i>Gynecologic Oncology</i> , 2019, 153, 343-355.	0.6	28
115	Influence of obesity on surgical complications of patients with ovarian tumors. <i>Oncology Letters</i> , 2019, 17, 4590-4594.	0.8	3
116	Systematic evaluation of cancer-specific genetic risk score for 11 types of cancer in The Cancer Genome Atlas and Electronic Medical Records and Genomics cohorts. <i>Cancer Medicine</i> , 2019, 8, 3196-3205.	1.3	22
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126	Evaluation of associations between genetically predicted circulating protein biomarkers and breast cancer risk. <i>International Journal of Cancer</i> , 2020, 146, 2130-2138.	2.3	13
127	Whole-exome sequencing of ovarian cancer families uncovers putative predisposition genes. <i>International Journal of Cancer</i> , 2020, 146, 2147-2155.	2.3	12
128	Ovarian Cancer Risk Variants Are Enriched in Histotype-Specific Enhancers and Disrupt Transcription Factor Binding Sites. <i>American Journal of Human Genetics</i> , 2020, 107, 622-635.	2.6	14
129	Estrogen Regulation of mTOR Signaling and Mitochondrial Function in Invasive Lobular Carcinoma Cell Lines Requires WNT4. <i>Cancers</i> , 2020, 12, 2931.	1.7	20

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135	Mechanisms of Long Non-Coding RNAs in Cancers and Their Dynamic Regulations. <i>Cancers</i> , 2020, 12, 1245.	1.7	95
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137	Fallopian tube initiation of high grade serous ovarian cancer and ovarian metastasis: Mechanisms and therapeutic implications. <i>Cancer Letters</i> , 2020, 476, 152-160.	3.2	18
138	Stable expansion of high-grade serous ovarian cancer organoids requires a low Wnt environment. <i>EMBO Journal</i> , 2020, 39, e104013.	3.5	70
139	Applications of Next Generation Sequencing to the Analysis of Familial Breast/Ovarian Cancer. <i>High-Throughput</i> , 2020, 9, 1.	4.4	22
140	Functional Landscape of Common Variants Associated with Susceptibility to Epithelial Ovarian Cancer. <i>Current Epidemiology Reports</i> , 2020, 7, 49-57.	1.1	6
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142	Genetically Defined, Syngeneic Organoid Platform for Developing Combination Therapies for Ovarian Cancer. <i>Cancer Discovery</i> , 2021, 11, 362-383.	7.7	50
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144	Recent Advances and Future Directions of Diagnostic and Prognostic Prediction Models in Ovarian Cancer. <i>Journal of Shanghai Jiaotong University (Science)</i> , 2021, 26, 10-16.	0.5	0
145	Role of Infections and Tissue Inflammation in the Pathology of the Fallopian Tube and High-Grade Serous Ovarian Cancer. <i>Physiology in Health and Disease</i> , 2021, , 271-312.	0.2	0
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152	Changes in Stem Cell Regulation and Epithelial Organisation during Carcinogenesis and Disease Progression in Gynaecological Malignancies. <i>Cancers</i> , 2021, 13, 3349.	1.7	2
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156	Genetic polymorphisms in gynecologic cancers. , 2021, , 169-193.		0
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