

Natalia Bogdanova

List of Publications by Year in descending order

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42
papers

1,973
citations

304368

22
h-index

264894

42
g-index

42
all docs

42
docs citations

42
times ranked

4396
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. <i>Nature Genetics</i> , 2017, 49, 680-691.	9.4	356
2	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. <i>Nature Genetics</i> , 2015, 47, 164-171.	9.4	221
3	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
4	Nijmegen Breakage Syndrome mutations and risk of breast cancer. <i>International Journal of Cancer</i> , 2008, 122, 802-806.	2.3	120
5	Association of vitamin D levels and risk of ovarian cancer: a Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2016, 45, 1619-1630.	0.9	111
6	Association of two mutations in the CHEK2 gene with breast cancer. <i>International Journal of Cancer</i> , 2005, 116, 263-266.	2.3	82
7	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
8	Adult body mass index and risk of ovarian cancer by subtype: a Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2016, 45, 884-895.	0.9	71
9	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
10	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. <i>Human Molecular Genetics</i> , 2014, 23, 6096-6111.	1.4	53
11	Hereditary breast cancer: ever more pieces to the polygenic puzzle. <i>Hereditary Cancer in Clinical Practice</i> , 2013, 11, 12.	0.6	48
12	PALB2 mutations in German and Russian patients with bilateral breast cancer. <i>Breast Cancer Research and Treatment</i> , 2011, 126, 545-550.	1.1	47
13	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. <i>PLoS ONE</i> , 2015, 10, e0128106.	1.1	44
14	Germline whole exome sequencing and large-scale replication identifies FANCM as a likely high grade serous ovarian cancer susceptibility gene. <i>Oncotarget</i> , 2017, 8, 50930-50940.	0.8	43
15	A nonsense mutation (E1978X) in the ATM gene is associated with breast cancer. <i>Breast Cancer Research and Treatment</i> , 2009, 118, 207-211.	1.1	42
16	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. <i>Human Molecular Genetics</i> , 2015, 24, 2966-2984.	1.4	40
17	Network-Based Integration of GWAS and Gene Expression Identifies a HOX-Centric Network Associated with Serous Ovarian Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 1574-1584.	1.1	28
18	BARD1 is a Low/Moderate Breast Cancer Risk Gene: Evidence Based on an Association Study of the Central European p.Q564X Recurrent Mutation. <i>Cancers</i> , 2019, 11, 740.	1.7	25

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19	Common Genetic Variation in Circadian Rhythm Genes and Risk of Epithelial Ovarian Cancer (EOC). <i>Journal of Genetics and Genome Research</i> , 2015, 2, .	0.3	25
20	NBS1 variant I171V and breast cancer risk. <i>Breast Cancer Research and Treatment</i> , 2008, 112, 75-79.	1.1	24
21	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
22	Fine-Scale Mapping of the 4q24 Locus Identifies Two Independent Loci Associated with Breast Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 1680-1691.	1.1	24
23	Enrichment of putative PAX8 target genes at serous epithelial ovarian cancer susceptibility loci. <i>British Journal of Cancer</i> , 2017, 116, 524-535.	2.9	23
24	Epithelial-Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. <i>Genetic Epidemiology</i> , 2015, 39, 689-697.	0.6	22
25	Population distribution and ancestry of the cancer protective MDM2 SNP285 (rs117039649). <i>Oncotarget</i> , 2014, 5, 8223-8234.	0.8	22
26	Rare ATAD5 missense variants in breast and ovarian cancer patients. <i>Cancer Letters</i> , 2016, 376, 173-177.	3.2	21
27	Analysis of a RECQL splicing mutation, c.1667_1667+3delAGTA, in breast cancer patients and controls from Central Europe. <i>Familial Cancer</i> , 2017, 16, 181-186.	0.9	20
28	Assessing the genetic architecture of epithelial ovarian cancer histological subtypes. <i>Human Genetics</i> , 2016, 135, 741-756.	1.8	19
29	Exome sequencing and case-control analyses identify <i>RCC1</i> as a candidate breast cancer susceptibility gene. <i>International Journal of Cancer</i> , 2018, 142, 2512-2517.	2.3	17
30	Evaluating the ovarian cancer gonadotropin hypothesis: A candidate gene study. <i>Gynecologic Oncology</i> , 2015, 136, 542-548.	0.6	15
31	Adult height is associated with increased risk of ovarian cancer: a Mendelian randomisation study. <i>British Journal of Cancer</i> , 2018, 118, 1123-1129.	2.9	15
32	Inherited variants affecting RNA editing may contribute to ovarian cancer susceptibility: results from a large-scale collaboration. <i>Oncotarget</i> , 2016, 7, 72381-72394.	0.8	13
33	Prevalence of the BLM nonsense mutation, p.Q548X, in ovarian cancer patients from Central and Eastern Europe. <i>Familial Cancer</i> , 2015, 14, 145-149.	0.9	12
34	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. <i>PLoS ONE</i> , 2018, 13, e0197561.	1.1	9
35	Exome sequencing study of Russian breast cancer patients suggests a predisposing role for USP39. <i>Breast Cancer Research and Treatment</i> , 2020, 179, 731-742.	1.1	9
36	Assessment of the role of translationally controlled tumor protein 1 (TPT1/TCTP) in breast cancer susceptibility and ATM signaling. <i>Clinical and Translational Radiation Oncology</i> , 2019, 15, 99-107.	0.9	7

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37	Assessment of an APOBEC3B truncating mutation, c.783delG, in patients with breast cancer. <i>Breast Cancer Research and Treatment</i> , 2017, 162, 31-37.	1.1	5
38	Assessment of γ -H2AX and 53BP1 Foci in Peripheral Blood Lymphocytes to Predict Subclinical Hematotoxicity and Response in Somatostatin Receptor-Targeted Radionuclide Therapy for Advanced Gastroenteropancreatic Neuroendocrine Tumors. <i>Cancers</i> , 2021, 13, 1516.	1.7	5
39	Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with risk of clear cell ovarian cancer. <i>Oncotarget</i> , 2016, 7, 69097-69110.	0.8	5
40	Gene-Environment Interactions Relevant to Estrogen and Risk of Breast Cancer: Can Gene-Environment Interactions Be Detected Only among Candidate SNPs from Genome-Wide Association Studies?. <i>Cancers</i> , 2021, 13, 2370.	1.7	4
41	rs495139 in the TYMS-ENOSF1 Region and Risk of Ovarian Carcinoma of Mucinous Histology. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2473.	1.8	3
42	Assessment of a FBXW8 frameshift mutation, c.1312_1313delGT, in breast cancer patients and controls from Central Europe. <i>Cancer Genetics</i> , 2018, 220, 38-43.	0.2	1