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	Assessment of Î³-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. Cancers, 2021, 13, 1516.	1.7	5
2	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?. Cancers, 2021, 13, 2370.	1.7	4
3	Exome sequencing study of Russian breast cancer patients suggests a predisposing role for USP39. Breast Cancer Research and Treatment, 2020, 179, 731-742.	1.1	9
4	BARD1 is a Low/Moderate Breast Cancer Risk Gene: Evidence Based on an Association Study of the Central European p.Q564X Recurrent Mutation. Cancers, 2019, 11, 740.	1.7	25
5	Assessment of the role of translationally controlled tumor protein 1 (TPT1/TCTP) in breast cancer susceptibility and ATM signaling. Clinical and Translational Radiation Oncology, 2019, 15, 99-107.	0.9	7
6	Adult height is associated with increased risk of ovarian cancer: a Mendelian randomisation study. British Journal of Cancer, 2018, 118, 1123-1129.	2.9	15
7	Exome sequencing and caseâ€“control analyses identify RCC1 as a candidate breast cancer susceptibility gene. International Journal of Cancer, 2018, 142, 2512-2517.	2.3	17
8	Assessment of a FBXW8 frameshift mutation, c.1312_1313delGT, in breast cancer patients and controls from Central Europe. Cancer Genetics, 2018, 220, 38-43.	0.2	1
9	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. PLoS ONE, 2018, 13, e0197561.	1.1	9
10	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
11	Enrichment of putative PAX8 target genes at serous epithelial ovarian cancer susceptibility loci. British Journal of Cancer, 2017, 116, 524-535.	2.9	23
12	Assessment of an APOBEC3B truncating mutation, c.783delG, in patients with breast cancer. Breast Cancer Research and Treatment, 2017, 162, 31-37.	1.1	5
13	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	9.4	356
14	Analysis of a RECQL splicing mutation, c.1667_1667+3delAGTA, in breast cancer patients and controls from Central Europe. Familial Cancer, 2017, 16, 181-186.	0.9	20
15	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
16	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
17	Rare ATAD5 missense variants in breast and ovarian cancer patients. Cancer Letters, 2016, 376, 173-177.	3.2	21
18	Assessing the genetic architecture of epithelial ovarian cancer histological subtypes. Human Genetics, 2016, 135, 741-756.	1.8	19

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19	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
20	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
21	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	5.8	78
22	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
23	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
24	Epithelialâ€Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. Genetic Epidemiology, 2015, 39, 689-697.	0.6	22
25	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. PLoS ONE, 2015, 10, e0128106.	1.1	44
26	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	1.4	40
27	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	9.4	221
28	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
29	Evaluating the ovarian cancer gonadotropin hypothesis: A candidate gene study. Gynecologic Oncology, 2015, 136, 542-548.	0.6	15
30	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. Nature Communications, 2015, 6, 8234.	5.8	63
31	Common variants at theCHEK2gene locus and risk of epithelial ovarian cancer. Carcinogenesis, 2015, 36, 1341-1353.	1.3	24
32	Fine-Scale Mapping of the 4q24 Locus Identifies Two Independent Loci Associated with Breast Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1680-1691.	1.1	24
33	Prevalence of the BLM nonsense mutation, p.Q548X, in ovarian cancer patients from Central and Eastern Europe. Familial Cancer, 2015, 14, 145-149.	0.9	12
34	Common Genetic Variation in Circadian Rhythm Genes and Risk of Epithelial Ovarian Cancer (EOC). Journal of Genetics and Genome Research, 2015, 2, .	0.3	25
35	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. Human Molecular Genetics, 2014, 23, 6096-6111.	1.4	53
36	Population distribution and ancestry of the cancer protective MDM2 SNP285 (rs117039649). Oncotarget, 2014, 5, 8223-8234.	0.8	22

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37	Hereditary breast cancer: ever more pieces to the polygenic puzzle. Hereditary Cancer in Clinical Practice, 2013, 11, 12.	0.6	48
38	PALB2 mutations in German and Russian patients with bilateral breast cancer. Breast Cancer Research and Treatment, 2011, 126, 545-550.	1.1	47
39	A nonsense mutation (E1978X) in the ATM gene is associated with breast cancer. Breast Cancer Research and Treatment, 2009, 118, 207-211.	1.1	42
40	NBS1 variant I171V and breast cancer risk. Breast Cancer Research and Treatment, 2008, 112, 75-79.	1.1	24
41	Nijmegen Breakage Syndrome mutations and risk of breast cancer. International Journal of Cancer, 2008, 122, 802-806.	2.3	120
42	Association of two mutations in theCHEK2 gene with breast cancer. International Journal of Cancer, 2005, 116, 263-266.	2.3	82