Alvaro N A Monteiro

List of Publications by Year
in descending order

218	10,141	39113 52	46524 93
papers	citations	h-index	g-index

225	225	225	15444
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	Evidence for a transcriptional activation function of BRCA1 C-terminal region. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 13595-13599.	3.3	430
3	A Systematic Genetic Assessment of 1,433 Sequence Variants of Unknown Clinical Significance in the BRCA1 and BRCA2 Breast Cancerâ€“Predisposition Genes. American Journal of Human Genetics, 2007, 81, 873-883.	2.6	416
4	Principles for the post-GWAS functional characterization of cancer risk loci. Nature Genetics, 2011, 43, 513-518.	9.4	392
5	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	9.4	356
6	Integrated Evaluation of DNA Sequence Variants of Unknown Clinical Significance: Application to BRCA1 and BRCA2. American Journal of Human Genetics, 2004, 75, 535-544.	2.6	351
7	BRCA1 regulates p53-dependent gene expression. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 2302-2306.	3.3	340
8	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. Nature Genetics, 2013, 45, 362-370.	9.4	326
9	ENIGMA-Evidence-based network for the interpretation of germline mutant alleles: An international initiative to evaluate risk and clinical significance associated with sequence variation in BRCA1 and BRCA2 genes. Human Mutation, 2012, 33, 2-7.	1.1	269
10	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	9.4	221
11	A review of a multifactorial probability-based model for classification of BRCA1 and BRCA2 variants of uncertain significance (VUS). Human Mutation, 2012, 33, 8-21.	1.1	190
12	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	1.5	174
13	A multigene mutation classification of 468 colorectal cancers reveals a prognostic role for APC. Nature Communications, 2016, 7, 11743.	5.8	170
14	BRCA1 and BRCA2 genetic testingâ€”pitfalls and recommendations for managing variants of uncertain clinical significance. Annals of Oncology, 2015, 26, 2057-2065.	0.6	163
15	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
16	Functional analysis of BRCA1 C-terminal missense mutations identified in breast and ovarian cancer families. Human Molecular Genetics, 2001, 10, 353-360.	1.4	147
17	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. Nature Communications, 2013, 4, 1628.	5.8	144
18	Comprehensive Analysis of Missense Variations in the BRCT Domain of BRCA1 by Structural and Functional Assays. Cancer Research, 2010, 70, 4880-4890.	0.4	138

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19	Genetic determinants of telomere length and risk of common cancers: a Mendelian randomization study. Human Molecular Genetics, 2015, 24, 5356-5366.	1.4	128
20	Biallelic Deleterious BRCA1 Mutations in a Woman with Early-Onset Ovarian Cancer. Cancer Discovery, 2013, 3, 399-405.	7.7	124
21	A guide for functional analysis ofBRCA1variants of uncertain significance. Human Mutation, 2012, 33, 1526-1537.	1.1	117
22	p53 Acetylation Is Crucial for Its Transcription-independent Proapoptotic Functions. Journal of Biological Chemistry, 2009, 284, 11171-11183.	1.6	111
23	Determination of Cancer Risk Associated with Germ Line BRCA1 Missense Variants by Functional Analysis. Cancer Research, 2007, 67, 1494-1501.	0.4	110
24	Functional Assays for Analysis of Variants of Uncertain Significance inBRCA2. Human Mutation, 2014, 35, 151-164.	1.1	107
25	Structure-Based Assessment of Missense Mutations in Human BRCA1. Cancer Research, 2004, 64, 3790-3797.	0.4	103
26	Large scale multifactorial likelihood quantitative analysis of BRCA1 and BRCA2 variants: An ENIGMA resource to support clinical variant classification. Human Mutation, 2019, 40, 1557-1578.	1.1	102
27	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. Nature Communications, 2013, 4, 1627.	5.8	98
28	A functional variant in HOXA11-AS, a novel long non-coding RNA, inhibits the oncogenic phenotype of epithelial ovarian cancer. Oncotarget, 2015, 6, 34745-34757.	0.8	98
29	Assessment of functional effects of unclassified genetic variants. Human Mutation, 2008, 29, 1314-1326.	1.1	93
30	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	5.8	93
31	Cancer variation associated with the position of the mutation in the BRCA2 gene. Familial Cancer, 2002, 3, 1-10.	0.9	91
32	A high frequency of BRCA mutations in young black women with breast cancer residing in Florida. Cancer, 2015, 121, 4173-4180.	2.0	91
33	A transcriptome-wide association study of high-grade serous epithelial ovarian cancer identifies new susceptibility genes and splice variants. Nature Genetics, 2019, 51, 815-823.	9.4	89
34	Charting the Landscape of Tandem BRCT Domainâ€"Mediated Protein Interactions. Science Signaling, 2012, 5, rs6.	1.6	88
35	BRCA1: exploring the links to transcription. Trends in Biochemical Sciences, 2000, 25, 469-474.	3.7	81
36	Proteome-wide Profiling of Clinical PARP Inhibitors Reveals Compound-Specific Secondary Targets. Cell Chemical Biology, 2016, 23, 1490-1503.	2.5	80

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37	Classification of BRCA1 missense variants of unknown clinical significance. Journal of Medical Genetics, 2005, 42, 138-146.	1.5	79
38	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	5.8	78
39	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. Journal of the National Cancer Institute, 2016, 108, djv315.	3.0	77
40	Establishment of a continuous cell line from fibrotic schistosomal granulomas in mice livers. In Vitro Cellular and Developmental Biology - Plant, 1985, 21, 382-390.	0.9	75
41	Phosphatases in the cellular response to DNA damage. Cell Communication and Signaling, 2010, 8, 27.	2.7	75
42	LIN28B Polymorphisms Influence Susceptibility to Epithelial Ovarian Cancer. Cancer Research, 2011, 71, 3896-3903.	0.4	75
43	BRCA2 Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799.	0.4	75
44	Prevalence of BRCA1 and BRCA2 mutations in breast cancer patients from Brazil. Breast Cancer Research and Treatment, 2007, 103, 349-353.	1.1	71
45	Functional assays provide a robust tool for the clinical annotation of genetic variants of uncertain significance. Npj Genomic Medicine, 2016, 1, .	1.7	70
46	The Role of PALB2 in the DNA Damage Response and Cancer Predisposition. International Journal of Molecular Sciences, 2017, 18, 1886.	1.8	70
47	Assessment of the Clinical Relevance of BRCA2 Missense Variants by Functional and Computational Approaches. American Journal of Human Genetics, 2018, 102, 233-248.	2.6	64
48	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. Nature Communications, 2015, 6, 8234.	5.8	63
49	The spectrum of BRCA1 and BRCA2 alleles in Latin America and the Caribbean: a clinical perspective. Breast Cancer Research and Treatment, 2015, 154, 441-453.	1.1	63
50	Functional Impact of Missense Variants in BRCA1 Predicted by Supervised Learning. PLoS Computational Biology, 2007, 3, e26.	1.5	57
51	Circadian pathway genes in relation to glioma risk and outcome. Cancer Causes and Control, 2014, 25, 25-32.	0.8	57
52	Dual Targeting of WEE1 and PLK1 by AZD1775 Elicits Single Agent Cellular Anticancer Activity. ACS Chemical Biology, 2017, 12, 1883-1892.	1.6	57
53	BRCA1: the enigma of tissue-specific tumor development. Trends in Genetics, 2003, 19, 312-315.	2.9	54
54	A Computational Method to Classify Variants of Uncertain Significance Using Functional Assay Data with Application to BRCA1. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 1078-1088.	1.1	54

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55	Comprehensive annotation of BRCA1 and BRCA2 missense variants by functionally validated sequence-based computational prediction models. Genetics in Medicine, 2019, 21, 71-80.	1.1	52
56	Genetic Data from Nearly 63,000 Women of European Descent Predicts DNA Methylation Biomarkers and Epithelial Ovarian Cancer Risk. Cancer Research, 2019, 79, 505-517.	0.4	49
57	Functional assays for BRCA1 and BRCA2. International Journal of Biochemistry and Cell Biology, 2007, 39, 298-310.	1.2	48
58	Differences in BRCA counseling and testing practices based on ordering provider type. Genetics in Medicine, 2015, 17, 51-57.	1.1	47
59	BRCT domains: A little more than kin, and less than kind. FEBS Letters, 2012, 586, 2711-2716.	1.3	44
60	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. PLoS ONE, 2015, 10, e0128106.	1.1	44
61	Clinical testing of BRCA1 and BRCA2: a worldwide snapshot of technological practices. Npj Genomic Medicine, 2018, 3, 7.	1.7	44
62	Breast Cancer Susceptibility and the DNA Damage Response. Cancer Control, 2005, 12, 127-136.	0.7	43
63	An Interactive Resource to Probe Genetic Diversity and Estimated Ancestry in Cancer Cell Lines. Cancer Research, 2019, 79, 1263-1273.	0.4	43
64	Pathogenicity of the BRCA1 missense variant M1775K is determined by the disruption of the BRCT phosphopeptide-binding pocket: a multi-modal approach. European Journal of Human Genetics, 2008, 16, 820-832.	1.4	42
65	Identification of Filamin A as a BRCA1-interacting protein required for efficient DNA repair. Cell Cycle, 2010, 9, 1421-1433.	1.3	42
66	RareTP53genetic variant associated with glioma risk and outcome. Journal of Medical Genetics, 2012, 49, 420-421.	1.5	42
67	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. Human Molecular Genetics, 2015, 24, 3595-3607.	1.4	40
68	Functional characterization of 84 PALB2 variants of uncertain significance. Genetics in Medicine, 2020, 22, 622-632.	1.1	40
69	A global functional analysis of missense mutations reveals two major hotspots in the PALB2 tumor suppressor. Nucleic Acids Research, 2019, 47, 10662-10677.	6.5	39
70	Analysis of a set of missense, frameshift, and in-frame deletion variants of BRCA1. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2009, 660, 1-11.	0.4	38
71	Mutational heterogeneity in non-serous ovarian cancers. Scientific Reports, 2017, 7, 9728.	1.6	35
72	Common BRCA1 Variants and Transcriptional Activation. American Journal of Human Genetics, 1997, 61, 761-762.	2.6	34

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73	Negative regulation of CHK2 activity by protein phosphatase 2A is modulated by DNA damage. Cell Cycle, 2010, 9, 736-747.	1.3	34
74	Variants of uncertain clinical significance in hereditary breast and ovarian cancer genes: best practices in functional analysis for clinical annotation. Journal of Medical Genetics, 2020, 57, 509-518.	1.5	33
75	Understanding Germ-Line Mutations inBRCA1. Cancer Biology and Therapy, 2004, 3, 515-520.	1.5	32
76	Early Onset Breast Cancer in a Registry-based Sample of African-American Women:BRCAMutation Prevalence, and Other Personal and System-level Clinical Characteristics. Breast Journal, 2013, 19, 189-192.	0.4	32
77	Modes of delivery of genetic testing services and the uptake of cancer risk management strategies in BRCA1 and BRCA2 carriers. Clinical Genetics, 2014, 85, 49-53.	1.0	32
78	BRCA1 Circos: a visualisation resource for functional analysis of missense variants. Journal of Medical Genetics, 2015, 52, 224-230.	1.5	32
79	DNA damage response and repair in perspective: Aedes aegypti, Drosophila melanogaster and Homo sapiens. Parasites and Vectors, 2019, 12, 533.	1.0	32
80	Towards controlled terminology for reporting germline cancer susceptibility variants: an ENIGMA report. Journal of Medical Genetics, 2019, 56, 347-357.	1.5	32
81	Impact of amino acid substitutions at secondary structures in the BRCT domains of the tumor suppressor BRCA1: Implications for clinical annotation. Journal of Biological Chemistry, 2019, 294, 5980-5992.	1.6	32
82	Strong functional data for pathogenicity or neutrality classify BRCA2 DNA-binding-domain variants of uncertain significance. American Journal of Human Genetics, 2021, 108, 458-468.	2.6	31
83	BRCA1 Protein and Nucleolin Colocalize in Breast Carcinoma Tissue and Cancer Cell Lines. American Journal of Pathology, 2010, 176, 1203-1214.	1.9	28
84	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
85	Functional analysis of the 11q23.3 glioma susceptibility locus implicates PHLDB1 and DDX6 in glioma susceptibility. Scientific Reports, 2015, 5, 17367.	1.6	27
86	Specificity in signaling by c-Yes. Frontiers in Bioscience - Landmark, 2003, 8, s185-205.	3.0	25
87	Characterization ofLGALS3(galectin-3) as a player in DNA damage response. Cancer Biology and Therapy, 2014, 15, 840-850.	1.5	25
88	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
89	Lessons from postgenomeâ€wide association studies: functional analysis of cancer predisposition loci. Journal of Internal Medicine, 2013, 274, 414-424.	2.7	24
90	Common variants at theCHEK2gene locus and risk of epithelial ovarian cancer. Carcinogenesis, 2015, 36, 1341-1353.	1.3	24

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91	In SituProtein Expression of RRM1, ERCC1, and BRCA1 in Metastatic Breast Cancer Patients Treated with Gemcitabine-Based Chemotherapy. Cancer Investigation, 2009, 28, 172-180.	0.6	23
92	PAXIP1 Potentiates the Combination of WEE1 Inhibitor AZD1775 and Platinum Agents in Lung Cancer. Molecular Cancer Therapeutics, 2016, 15, 1669-1681.	1.9	23
93	Enrichment of putative PAX8 target genes at serous epithelial ovarian cancer susceptibility loci. British Journal of Cancer, 2017, 116, 524-535.	2.9	23
94	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. European Journal of Human Genetics, 2022, 30, 349-362.	1.4	23
95	BRCA1 can stimulate gene transcription by a unique mechanism. EMBO Reports, 2000, 1, 260-265.	2.0	22
96	BRCA1 in breast and ovarian cancer predisposition. Cancer Letters, 2005, 227, 1-7.	3.2	22
97	Epithelialâ€Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. Genetic Epidemiology, 2015, 39, 689-697.	0.6	22
98	Brain tumor risk according to germ-line variation in the MLLT10 locus. European Journal of Human Genetics, 2015, 23, 132-134.	1.4	22
99	Functional Analysis and Fine Mapping of the 9p22.2 Ovarian Cancer Susceptibility Locus. Cancer Research, 2019, 79, 467-481.	0.4	22
100	DNA repair genes PAXIP1 and TP53BP1 expression is associated with breast cancer prognosis. Cancer Biology and Therapy, 2017, 18, 439-449.	1.5	21
101	Genome-wide Analysis of Common Copy Number Variation and Epithelial Ovarian Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 1117-1126.	1.1	21
102	Norepinephrine-Induced DNA Damage in Ovarian Cancer Cells. International Journal of Molecular Sciences, 2020, 21, 2250.	1.8	21
103	Integration of functional assay data results provides strong evidence for classification of hundreds of BRCA1 variants of uncertain significance. Genetics in Medicine, 2021, 23, 306-315.	1.1	21
104	A Naturally Occurring Allele of BRCA1 Coding for a Temperature-Sensitive Mutant Protein. Cancer Biology and Therapy, 2002, 1, 497-501.	1.5	20
105	Cancer risks in first degree relatives of BRCA1 mutation carriers: effects of mutation and proband disease status. Journal of Medical Genetics, 2005, 43, 424-428.	1.5	19
106	Genetic Testing and Clinical Management Practices for Variants in Non-BRCA1/2 Breast (and) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 152 for the Interpretation of Germline Mutant Alleles (ENIGMA) Clinical Working Group. JCO Precision Oncology, 2018, 2, 1-42.	1.5	19
107	Network of Interactions between ZIKA Virus Non-Structural Proteins and Human Host Proteins. Cells, 2020, 9, 153.	1.8	19
108	The non-canonical target PARP16 contributes to polypharmacology of the PARP inhibitor talazoparib and its synergy with WEE1 inhibitors. Cell Chemical Biology, 2022, 29, 202-214.e7.	2.5	19

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109	Breast and Prostate Cancer Risks for MaleBRCA1andBRCA2Pathogenic Variant Carriers Using Polygenic Risk Scores. Journal of the National Cancer Institute, 2022, 114, 109-122.	3.0	19
110	Interleukin polymorphisms associated with overall survival, diseaseâ€free survival, and recurrence in nonâ€small cell lung cancer patients. Molecular Carcinogenesis, 2015, 54, E172-84.	1.3	18
111	Ectopic expression of Histone H2AX mutants reveal a role for its post-translational modifications. Cancer Biology and Therapy, 2009, 8, 422-434.	1.5	17
112	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
113	BRCA1 recruitment to damaged DNA sites is dependent on CDK9. Cell Cycle, 2017, 16, 665-672.	1.3	17
114	Functional and Structural Analysis of C-Terminal BRCA1 Missense Variants. PLoS ONE, 2013, 8, e61302.	1.1	16
115	Functional annotation signatures of disease susceptibility loci improve SNP association analysis. BMC Genomics, 2014, 15, 398.	1.2	16
116	Germline Missense Variants in BRCA1: New Trends and Challenges for Clinical Annotation. Cancers, 2019, 11, 522.	1.7	16
117	Yeast-based Assays for Detection and Characterization of Mutations in BRCA1. Breast Disease, 1998, 10, 61-70.	0.4	15
118	Cancer Risk Assessment at the Atomic Level. Cancer Research, 2006, 66, 1897-1899.	0.4	15
119	Tandem BRCT Domains: DNA's Praetorian Guard. Genes and Cancer, 2010, 1, 1140-1146.	0.6	15
120	Fine tuning chemotherapy to match BRCA1 status. Biochemical Pharmacology, 2010, 80, 647-653.	2.0	14
121	Enhancer scanning to locate regulatory regions in genomic loci. Nature Protocols, 2016, 11, 46-60.	5.5	14
122	CTDP1 regulates breast cancer survival and DNA repair through BRCT-specific interactions with FANCI. Cell Death Discovery, 2019, 5, 105.	2.0	14
123	Liver connective tissue cells isolated from human schistosomal fibrosis or alcoholic cirrhosis represent a modified phenotype of smooth muscle cells. Biology of the Cell, 1985, 53, 231-238.	0.7	14
124	Mutations in the BRCT Domain Confer Temperature Sensitivity to BRCA1 in Transcription Activation. Cancer Biology and Therapy, 2002, 1, 502-508.	1.5	13
125	Methods to Classify BRCA1 Variants of Uncertain Clinical Significance: The More the Merrier. Cancer Biology and Therapy, 2004, 3, 458-459.	1.5	13
126	DNA damage response: Determining the fate of phosphorylated histone H2AX. Cancer Biology and Therapy, 2006, 5, 142-144.	1.5	13

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127	Can the Status of the Breast and Ovarian Cancer Susceptibility Gene 1 Product (BRCA1) Predict Response to Taxane-Based Cancer Therapy?. Anti-Cancer Agents in Medicinal Chemistry, 2009, 9, 543-549.	0.9	13
128	Localization of BRCA1 protein in breast cancer tissue and cell lines with mutations. Cancer Cell International, 2013, 13, 70.	1.8	13
129	PALB2 Variants: Protein Domains and Cancer Susceptibility. Trends in Cancer, 2021, 7, 188-197.	3.8	13
130	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
131	Yeast two-hybrid junk sequences contain selected linear motifs. Nucleic Acids Research, 2011, 39, e128-e128.	6.5	12
132	Germline variants in cancer genes in high-risk non-BRCA patients from Puerto Rico. Scientific Reports, 2019, 9, 17769.	1.6	12
133	Absence of constitutional H2AX gene mutations in 101 hereditary breast cancer families. Journal of Medical Genetics, 2003, 40, 51e-51.	1.5	11
134	Early transcriptional response of human ovarian and fallopian tube surface epithelial cells to norepinephrine. Scientific Reports, 2018, 8, 8291.	1.6	11
135	Participation of BRCA1 in DNA Repair Response...Via Transcription. Cancer Biology and Therapy, 2002, 1, 187-188.	1.5	10
136	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. PLoS ONE, 2018, 13, e0197561.	1.1	9
137	In vitro formation of fibrous septa by liver connective tissue cells. In Vitro Cellular & Developmental Biology, 1987, 23, 10-14.	1.0	8
138	TGF Î²1 and PDGF AA override Collagen type I inhibition of proliferation in human liver connective tissue cells. BMC Gastroenterology, 2004, 4, 30.	0.8	8
139	Long-term culture of cholangiocytes from liver fibro-granulomatous lesions. BMC Gastroenterology, 2006, 6, 13.	0.8	8
140	Probing Structure-Function Relationships in Missense Variants in the Carboxy-Terminal Region of BRCA1. PLoS ONE, 2014, 9, e97766.	1.1	8
141	The P1812A and P25TBRCA1and the 5164del4BRCA2Mutations: Occurrence in High-Risk Non-Ashkenazi Jews. Genetic Testing and Molecular Biomarkers, 2006, 10, 200-207.	1.7	7
142	Somatic alterations in brain tumors. Oncology Reports, 2008, , .	1.2	7
143	Functional Implications of BRCA1 for Early Detection, Prevention, and Treatment of Breast Cancer. Critical Reviews in Eukaryotic Gene Expression, 2006, 16, 233-252.	0.4	7
144	A targeted genetic association study of epithelial ovarian cancer susceptibility. Oncotarget, 2016, 7, 7381-7389.	0.8	7

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145	A nuclear function for the tumor suppressor BRCA1. Histology and Histopathology, 2000, 15, 299-307.	0.5	7
146	Classification of BRCA2 Variants of Uncertain Significance (VUS) Using an ACMG/AMP Model Incorporating a Homology-Directed Repair (HDR) Functional Assay. Clinical Cancer Research, 2022, 28, 3742-3751.	3.2	7
147	Integration of Population-Level Genotype Data with Functional Annotation Reveals Over-Representation of Long Noncoding RNAs at Ovarian Cancer Susceptibility Loci. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 116-125.	1.1	6
148	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
149	Functional Landscape of Common Variants Associated with Susceptibility to Epithelial Ovarian Cancer. Current Epidemiology Reports, 2020, 7, 49-57.	1.1	6
150	Interaction of human liver connective tissue cells, skin fibroblasts and smooth muscle cells with collagen gels. Hepatology, 1987, 7, 665-671.	3.6	5
151	Genetic testing and clinical management practices for variants in non-BRCA1/2 breast (and/or ovarian) cancer susceptibility genes: An international survey by the Enigma Clinical Working Group.. Journal of Clinical Oncology, 2018, 36, 1539-1539.	0.8	5
152	Functional Restoration of BRCA1 Nonsense Mutations by Aminoglycoside-Induced Readthrough. Frontiers in Pharmacology, 0, 13, .	1.6	5
153	Involvement ofÂtheÂSH3 domain inÂCa2+-mediated regulation ofÂSrc family kinases. Biochimie, 2006, 88, 905-911.	1.3	4
154	Germline missense pathogenic variants in the BRCA1 BRCT domain, p.Gly1706Glu and p.Ala1708Glu, increase cellular sensitivity to PARP inhibitor olaparib by a dominant negative effect. Human Molecular Genetics, 2016, 25, ddw343.	1.4	4
155	Somatic alterations in brain tumors. Oncology Reports, 2008, 20, 203-10.	1.2	4
156	An integrative model for the comprehensive classification of BRCA1 and BRCA2 variants of uncertain clinical significance. Npj Genomic Medicine, 2022, 7, .	1.7	4
157	The accidental cancer geneticist: HilÃ¡rio de GouvÃªa and hereditary retinoblastoma. Cancer Biology and Therapy, 2007, 6, 811-813.	1.5	3
158	Epigenetic tumor suppression by BRCA1. Nature Medicine, 2011, 17, 1183-1185.	15.2	3
159	No Evidence for the Pathogenicity of the BRCA2 c.6937â€‰+â€‰594T>G Deep Intronic Variant: A Caseâ€“Control Analysis. Genetic Testing and Molecular Biomarkers, 2018, 22, 85-89.	0.3	3
160	Two distinct mechanisms underlie estrogen-receptor-negative breast cancer susceptibility at the 2p23.2 locus. European Journal of Human Genetics, 2022, 30, 465-473.	1.4	3
161	Identification of Two Genetic Loci Associated with Leukopenia after Chemotherapy in Patients with Breast Cancer. Clinical Cancer Research, 2022, 28, 3342-3355.	3.2	3
162	Rare germline variants in PALB2 and BRCA2 in familial and sporadic chordoma. Human Mutation, 2022, 43, 1396-1407.	1.1	3

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163	Complement-dependent induction of DNA synthesis and cell proliferation in human liver connective tissue cells in vitro. In Vitro Cellular and Developmental Biology - Animal, 1995, 31, 149-155.	0.7	2
164	Incorporating computational resources in a cancer research program. Human Genetics, 2015, 134, 467-478.	1.8	2
165	Response: Table 1.. Journal of the National Cancer Institute, 2016, 108, djw173.	3.0	2
166	epiTAD: a web application for visualizing chromosome conformation capture data in the context of genetic epidemiology. Bioinformatics, 2019, 35, 4462-4464.	1.8	2
167	Lessons learned from two decades of BRCA1 and BRCA2 genetic testing: the evolution of data sharing and variant classification. Genetics in Medicine, 2019, 21, 1476-1480.	1.1	2
168	Dissecting genetic risk factors in breast cancer. Oncotarget, 2017, 8, 12540-12541.	0.8	2
169	Abstract 4850: Variation in circadian rhythm genes influence epithelial ovarian cancer risk and invasiveness.. , 2013, , .		2
170	Correction: Functional analysis of BRCA1 M1628V variant. Journal of Medical Genetics, 2007, 44, e78-e78.	1.5	1
171	Principles for the post-GWAS functional characterisation of risk loci. Nature Precedings, 2010, , .	0.1	1
172	Three-color intranuclear staining for measuring mitosis and apoptosis in cells transfected with a GFP-tagged histone. Biotechnic and Histochemistry, 2010, 85, 127-131.	0.7	1
173	What can yeast tell us about breast cancer?. Cell Cycle, 2017, 16, 157-158.	1.3	1
174	Acceptability and outcomes of multigene panel testing among young Black breast cancer survivors. Breast Journal, 2020, 26, 2112-2114.	0.4	1
175	Effects of long-term norepinephrine treatment on normal immortalized ovarian and fallopian tube cells. Scientific Reports, 2021, 11, 14334.	1.6	1
176	Abstract 1649: Genome-wide association study of copy number variations in serous epithelial ovarian cancer susceptibility. , 2012, , .		1
177	Abstract 4635: Inherited variants affecting RNA editing may contribute to ovarian cancer susceptibility. Cancer Research, 2015, 75, 4635-4635.	0.4	1
178	Abstract 2783: Common functional mechanisms underlying pleiotropy at the 19p13.1 breast and ovarian cancer cusceptibility locus. , 2015, , .		1
179	Phase II trial of AZD1775 in combination with carboplatin and paclitaxel in stage IV squamous cell lung cancer (sqNSCLC): Preliminary results.. Journal of Clinical Oncology, 2017, 35, e20672-e20672.	0.8	1
180	Abstract B021: PARP16 is a novel target of talazoparib which contributes to synergy with adavosertib in SCLC. Molecular Cancer Therapeutics, 2019, 18, B021-B021.	1.9	1

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181	CHEKing out of mitosis. Cell Cycle, 2012, 11, 1756-1756.	1.3	0
182	Functional evidence (II) protein and enzyme function. , 2021, , 145-168.		0
183	Scratching Below the Ovarian Cancer GWAS Surface. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 1604-1606.	1.1	0
184	Functional impact of missense variants in BRCA1 predicted by supervised learning. PLoS Computational Biology, 2005, preprint, e26.	1.5	0
185	Abstract 1117: Characterization of BAT1 (UAP56) interaction with BARD1. , 2010, , .		0
186	Abstract 3927: Characterization of galectin 3 as a putative BRCA1/BARD1 ubiquitin E3 ligase substrate. , 2011, , .		0
187	Abstract 3892: Discovery and analysis of COMMD1 in the DNA damage response network. , 2011, , .		0
188	Abstract 4729: Pathway and gene set analyses for epithelial ovarian cancer (EOC) genome-wide association study (GWAS). , 2011, , .		0
189	Abstract A71: BRCA mutations and surgical decision making in a sample of young black women with invasive breast cancer. , 2011, , .		0
190	Abstract 4444: BRCA1 Circos: A visualization tool for BRCA1 missense variants. , 2012, , .		0
191	Abstract 2927: MicroRNA binding site polymorphisms influence ovarian cancer risk in the collaborative oncological gene-environment study. , 2012, , .		0
192	Abstract 3095: The host cell reactivation (HCR) assay for measuring DNA repair capacity (DRC) in cancer research after 20 years; re-evaluation and lessons learned. , 2012, , .		0
193	Abstract 2132: Characterization of galectin 3 as a novel BARD1 interaction partner. , 2012, , .		0
194	Abstract 4579: Variants in long non-coding RNAs are associated with epithelial ovarian cancer risk in a pooled analysis of three genome-wide association studies.. , 2013, , .		0
195	Abstract 1352: Epithelial-mesenchymal transition (EMT) gene variants influence epithelial ovarian cancer risk in women of European, African and Asian ancestry.. , 2013, , .		0
196	Abstract 3644: Variation in transmembrane transport genes influence epithelial ovarian cancer risk and histopathologic subtype.. , 2013, , .		0
197	Abstract 946: Exome genotyping array identifies rare and low-frequency variants that may be associated with ovarian cancer risk. , 2014, , .		0
198	Abstract 480: CDK9 (a novel BRCA1/BARD1 interaction partner) downregulates BRCA1-mediated transcription. , 2014, , .		0

#	Article	IF	Citations
199	Abstract 3285: Functional analysis of the 9p22 locus implicates the transcriptional regulation ofBNC2as a mechanism in ovarian cancer predisposition. , 2014, , .		0
200	Abstract 5483: Implications of the type ofBRCA1germline mutation in the treatment of patients with hereditary breast cancer. , 2014, , .		0
201	Abstract 3283: GWAS identifies risk variants for mucinous ovarian carcinoma. , 2014, , .		0
202	Abstract 2414: Overexpression of PAXIP1 potentiates WEE1 inhibitor action in lung cancer cells. , 2014, , .		0
203	Abstract 4633: Evidence that long non-coding RNA variants associate with epithelial ovarian cancer risk. , 2015, , .		0
204	Abstract 4634: Variants within super-enhancer regulatory elements associate with epithelial ovarian cancer risk. , 2015, , .		0
205	Abstract 841: SNP-FEMS: a method to identify DNA binding proteins interacting with enhancer elements. , 2015, , .		0
206	Abstract 3779: Mutational analysis of MCPH1 C-terminal tandem BRCT domain reveals residues essential for cell cycle arrest. , 2015, , .		0
207	Abstract 3951: Functional analysis of the 11q23.3 glioma susceptibility locus. , 2015, , .		0
208	Abstract 3025: Characterization of CDK9/BRCA1 complex in DNA damage response. , 2015, , .		0
209	Abstract B11: Mutational heterogeneity in non-serous ovarian cancers.. , 2016, , .		0
210	Abstract PR15: MYC distal enhancers underlie ovarian cancer susceptibility in the 8q24.21 locus.. , 2016, , .		0
211	Abstract B27: Investigation of small GTPase genes in epithelial ovarian cancer.. , 2016, , .		0
212	Abstract 5232: Using an integrated gene-based sequence kernel association test (intSKAT) to identify subtype specific single nucleotide variants in glioma. , 2016, , .		0
213	Abstract 1282: Analysis of missense variants inBRCA1BRCT domains. , 2017, , .		0
214	Abstract 1306: Two distinct regulatory mechanisms underlie estrogen receptor negative breast cancer susceptibility at the 2p23.2 locus. , 2017, , .		0
215	Abstract 2669: A role forHOXA5in the transcriptional response of ovarian and fallopian tube surface epithelial cells to norepinephrine. , 2019, , .		0
216	Abstract B022: PARP1 complex composition as a predictor of response to PARP inhibitors in BRCA-linked ovarian carcinoma. , 2019, , .		0

#	Article	IF	Citations
217	Abstract C093: An interactive resource to probe ancestry in cancer cell lines. , 2020, , .		0
218	Abstract 1740: Characterization of CDK9 role in the DNA damage response. , 2019, , .		0