

Alvaro N A Monteiro

List of Publications by Year in descending order

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Version: 2024-02-01

218
papers

10,141
citations

34016

52
h-index

40881

93
g-index

225
all docs

225
docs citations

225
times ranked

14086
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. <i>Nature Genetics</i> , 2013, 45, 371-384.	9.4	493
2	Evidence for a transcriptional activation function of BRCA1 C-terminal region. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 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 Cancer Predisposition Genes. <i>American Journal of Human Genetics</i> , 2007, 81, 873-883.	2.6	416
4	Principles for the post-GWAS functional characterization of cancer risk loci. <i>Nature Genetics</i> , 2011, 43, 513-518.	9.4	392
5	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. <i>Nature Genetics</i> , 2017, 49, 680-691.	9.4	356
6	Integrated Evaluation of DNA Sequence Variants of Unknown Clinical Significance: Application to BRCA1 and BRCA2. <i>American Journal of Human Genetics</i> , 2004, 75, 535-544.	2.6	351
7	BRCA1 regulates p53-dependent gene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 2302-2306.	3.3	340
8	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. <i>Nature Genetics</i> , 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. <i>Human Mutation</i> , 2012, 33, 2-7.	1.1	269
10	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. <i>Nature Genetics</i> , 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). <i>Human Mutation</i> , 2012, 33, 8-21.	1.1	190
12	PALB2, CHEK2 and ATM rare variants and cancer risk: data from COGS. <i>Journal of Medical Genetics</i> , 2016, 53, 800-811.	1.5	174
13	A multigene mutation classification of 468 colorectal cancers reveals a prognostic role for APC. <i>Nature Communications</i> , 2016, 7, 11743.	5.8	170
14	BRCA1 and BRCA2 genetic testing pitfalls and recommendations for managing variants of uncertain clinical significance. <i>Annals of Oncology</i> , 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. <i>Cancer Discovery</i> , 2016, 6, 1052-1067.	7.7	157
16	Functional analysis of BRCA1 C-terminal missense mutations identified in breast and ovarian cancer families. <i>Human Molecular Genetics</i> , 2001, 10, 353-360.	1.4	147
17	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. <i>Nature Communications</i> , 2013, 4, 1628.	5.8	144
18	Comprehensive Analysis of Missense Variations in the BRCT Domain of BRCA1 by Structural and Functional Assays. <i>Cancer Research</i> , 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. <i>Human Molecular Genetics</i> , 2015, 24, 5356-5366.	1.4	128
20	Biallelic Deleterious <i>BRCA1</i> Mutations in a Woman with Early-Onset Ovarian Cancer. <i>Cancer Discovery</i> , 2013, 3, 399-405.	7.7	124
21	A guide for functional analysis of <i>BRCA1</i> variants of uncertain significance. <i>Human Mutation</i> , 2012, 33, 1526-1537.	1.1	117
22	p53 Acetylation Is Crucial for Its Transcription-independent Proapoptotic Functions. <i>Journal of Biological Chemistry</i> , 2009, 284, 11171-11183.	1.6	111
23	Determination of Cancer Risk Associated with Germ Line <i>BRCA1</i> Missense Variants by Functional Analysis. <i>Cancer Research</i> , 2007, 67, 1494-1501.	0.4	110
24	Functional Assays for Analysis of Variants of Uncertain Significance in <i>BRCA2</i> . <i>Human Mutation</i> , 2014, 35, 151-164.	1.1	107
25	Structure-Based Assessment of Missense Mutations in Human <i>BRCA1</i> . <i>Cancer Research</i> , 2004, 64, 3790-3797.	0.4	103
26	Large scale multifactorial likelihood quantitative analysis of <i>BRCA1</i> and <i>BRCA2</i> variants: An ENIGMA resource to support clinical variant classification. <i>Human Mutation</i> , 2019, 40, 1557-1578.	1.1	102
27	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. <i>Nature Communications</i> , 2013, 4, 1627.	5.8	98
28	A functional variant in <i>HOXA11-AS</i> , a novel long non-coding RNA, inhibits the oncogenic phenotype of epithelial ovarian cancer. <i>Oncotarget</i> , 2015, 6, 34745-34757.	0.8	98
29	Assessment of functional effects of unclassified genetic variants. <i>Human Mutation</i> , 2008, 29, 1314-1326.	1.1	93
30	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016, 7, 11375.	5.8	93
31	Cancer variation associated with the position of the mutation in the <i>BRCA2</i> gene. <i>Familial Cancer</i> , 2002, 3, 1-10.	0.9	91
32	A high frequency of <i>BRCA</i> mutations in young black women with breast cancer residing in Florida. <i>Cancer</i> , 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. <i>Nature Genetics</i> , 2019, 51, 815-823.	9.4	89
34	Charting the Landscape of Tandem BRCT Domain-Mediated Protein Interactions. <i>Science Signaling</i> , 2012, 5, rs6.	1.6	88
35	<i>BRCA1</i> : exploring the links to transcription. <i>Trends in Biochemical Sciences</i> , 2000, 25, 469-474.	3.7	81
36	Proteome-wide Profiling of Clinical PARP Inhibitors Reveals Compound-Specific Secondary Targets. <i>Cell Chemical Biology</i> , 2016, 23, 1490-1503.	2.5	80

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37	Classification of BRCA1 missense variants of unknown clinical significance. <i>Journal of Medical Genetics</i> , 2005, 42, 138-146.	1.5	79
38	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
39	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. <i>Journal of the National Cancer Institute</i> , 2016, 108, djv315.	3.0	77
40	Establishment of a continuous cell line from fibrotic schistosomal granulomas in mice livers. <i>In Vitro Cellular and Developmental Biology - Plant</i> , 1985, 21, 382-390.	0.9	75
41	Phosphatases in the cellular response to DNA damage. <i>Cell Communication and Signaling</i> , 2010, 8, 27.	2.7	75
42	<i>LIN28B</i> Polymorphisms Influence Susceptibility to Epithelial Ovarian Cancer. <i>Cancer Research</i> , 2011, 71, 3896-3903.	0.4	75
43	<i>BRCA2</i> Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. <i>Cancer Research</i> , 2017, 77, 2789-2799.	0.4	75
44	Prevalence of BRCA1 and BRCA2 mutations in breast cancer patients from Brazil. <i>Breast Cancer Research and Treatment</i> , 2007, 103, 349-353.	1.1	71
45	Functional assays provide a robust tool for the clinical annotation of genetic variants of uncertain significance. <i>Npj Genomic Medicine</i> , 2016, 1, .	1.7	70
46	The Role of PALB2 in the DNA Damage Response and Cancer Predisposition. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1886.	1.8	70
47	Assessment of the Clinical Relevance of BRCA2 Missense Variants by Functional and Computational Approaches. <i>American Journal of Human Genetics</i> , 2018, 102, 233-248.	2.6	64
48	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
49	The spectrum of BRCA1 and BRCA2 alleles in Latin America and the Caribbean: a clinical perspective. <i>Breast Cancer Research and Treatment</i> , 2015, 154, 441-453.	1.1	63
50	Functional Impact of Missense Variants in BRCA1 Predicted by Supervised Learning. <i>PLoS Computational Biology</i> , 2007, 3, e26.	1.5	57
51	Circadian pathway genes in relation to glioma risk and outcome. <i>Cancer Causes and Control</i> , 2014, 25, 25-32.	0.8	57
52	Dual Targeting of WEE1 and PLK1 by AZD1775 Elicits Single Agent Cellular Anticancer Activity. <i>ACS Chemical Biology</i> , 2017, 12, 1883-1892.	1.6	57
53	BRCA1: the enigma of tissue-specific tumor development. <i>Trends in Genetics</i> , 2003, 19, 312-315.	2.9	54
54	A Computational Method to Classify Variants of Uncertain Significance Using Functional Assay Data with Application to <i>BRCA1</i> . <i>Cancer Epidemiology Biomarkers and Prevention</i> , 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. <i>Genetics in Medicine</i> , 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. <i>Cancer Research</i> , 2019, 79, 505-517.	0.4	49
57	Functional assays for BRCA1 and BRCA2. <i>International Journal of Biochemistry and Cell Biology</i> , 2007, 39, 298-310.	1.2	48
58	Differences in BRCA counseling and testing practices based on ordering provider type. <i>Genetics in Medicine</i> , 2015, 17, 51-57.	1.1	47
59	BRCT domains: A little more than kin, and less than kind. <i>FEBS Letters</i> , 2012, 586, 2711-2716.	1.3	44
60	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. <i>PLoS ONE</i> , 2015, 10, e0128106.	1.1	44
61	Clinical testing of BRCA1 and BRCA2: a worldwide snapshot of technological practices. <i>Npj Genomic Medicine</i> , 2018, 3, 7.	1.7	44
62	Breast Cancer Susceptibility and the DNA Damage Response. <i>Cancer Control</i> , 2005, 12, 127-136.	0.7	43
63	An Interactive Resource to Probe Genetic Diversity and Estimated Ancestry in Cancer Cell Lines. <i>Cancer Research</i> , 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. <i>European Journal of Human Genetics</i> , 2008, 16, 820-832.	1.4	42
65	Identification of Filamin A as a BRCA1-interacting protein required for efficient DNA repair. <i>Cell Cycle</i> , 2010, 9, 1421-1433.	1.3	42
66	Rare <i>TP53</i> genetic variant associated with glioma risk and outcome. <i>Journal of Medical Genetics</i> , 2012, 49, 420-421.	1.5	42
67	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
68	Functional characterization of 84 PALB2 variants of uncertain significance. <i>Genetics in Medicine</i> , 2020, 22, 622-632.	1.1	40
69	A global functional analysis of missense mutations reveals two major hotspots in the PALB2 tumor suppressor. <i>Nucleic Acids Research</i> , 2019, 47, 10662-10677.	6.5	39
70	Analysis of a set of missense, frameshift, and in-frame deletion variants of BRCA1. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2009, 660, 1-11.	0.4	38
71	Mutational heterogeneity in non-serous ovarian cancers. <i>Scientific Reports</i> , 2017, 7, 9728.	1.6	35
72	Common BRCA1 Variants and Transcriptional Activation. <i>American Journal of Human Genetics</i> , 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. <i>Cell Cycle</i> , 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. <i>Journal of Medical Genetics</i> , 2020, 57, 509-518.	1.5	33
75	Understanding Germ-Line Mutations in BRCA1. <i>Cancer Biology and Therapy</i> , 2004, 3, 515-520.	1.5	32
76	Early Onset Breast Cancer in a Registry-based Sample of African-American Women: BRCA Mutation Prevalence, and Other Personal and System-level Clinical Characteristics. <i>Breast Journal</i> , 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. <i>Clinical Genetics</i> , 2014, 85, 49-53.	1.0	32
78	BRCA1 Circos: a visualisation resource for functional analysis of missense variants. <i>Journal of Medical Genetics</i> , 2015, 52, 224-230.	1.5	32
79	DNA damage response and repair in perspective: <i>Aedes aegypti</i> , <i>Drosophila melanogaster</i> and <i>Homo sapiens</i> . <i>Parasites and Vectors</i> , 2019, 12, 533.	1.0	32
80	Towards controlled terminology for reporting germline cancer susceptibility variants: an ENIGMA report. <i>Journal of Medical Genetics</i> , 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. <i>Journal of Biological Chemistry</i> , 2019, 294, 5980-5992.	1.6	32
82	Strong functional data for pathogenicity or neutrality classify BRCA2 DNA-binding-domain variants of uncertain significance. <i>American Journal of Human Genetics</i> , 2021, 108, 458-468.	2.6	31
83	BRCA1 Protein and Nucleolin Colocalize in Breast Carcinoma Tissue and Cancer Cell Lines. <i>American Journal of Pathology</i> , 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. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 1574-1584.	1.1	28
85	Functional analysis of the 11q23.3 glioma susceptibility locus implicates PHLDB1 and DDX6 in glioma susceptibility. <i>Scientific Reports</i> , 2015, 5, 17367.	1.6	27
86	Specificity in signaling by c-Yes. <i>Frontiers in Bioscience - Landmark</i> , 2003, 8, s185-205.	3.0	25
87	Characterization of LGALS3 (galectin-3) as a player in DNA damage response. <i>Cancer Biology and Therapy</i> , 2014, 15, 840-850.	1.5	25
88	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
89	Lessons from postgenome-wide association studies: functional analysis of cancer predisposition loci. <i>Journal of Internal Medicine</i> , 2013, 274, 414-424.	2.7	24
90	Common variants at the CHEK2 gene locus and risk of epithelial ovarian cancer. <i>Carcinogenesis</i> , 2015, 36, 1341-1353.	1.3	24

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91	<i>In Situ</i> Protein Expression of RRM1, ERCC1, and BRCA1 in Metastatic Breast Cancer Patients Treated with Gemcitabine-Based Chemotherapy. <i>Cancer Investigation</i> , 2009, 28, 172-180.	0.6	23
92	PAXIP1 Potentiates the Combination of WEE1 Inhibitor AZD1775 and Platinum Agents in Lung Cancer. <i>Molecular Cancer Therapeutics</i> , 2016, 15, 1669-1681.	1.9	23
93	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
94	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. <i>European Journal of Human Genetics</i> , 2022, 30, 349-362.	1.4	23
95	BRCA1 can stimulate gene transcription by a unique mechanism. <i>EMBO Reports</i> , 2000, 1, 260-265.	2.0	22
96	BRCA1 in breast and ovarian cancer predisposition. <i>Cancer Letters</i> , 2005, 227, 1-7.	3.2	22
97	Epithelial-Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. <i>Genetic Epidemiology</i> , 2015, 39, 689-697.	0.6	22
98	Brain tumor risk according to germ-line variation in the MLLT10 locus. <i>European Journal of Human Genetics</i> , 2015, 23, 132-134.	1.4	22
99	Functional Analysis and Fine Mapping of the 9p22.2 Ovarian Cancer Susceptibility Locus. <i>Cancer Research</i> , 2019, 79, 467-481.	0.4	22
100	DNA repair genes PAXIP1 and TP53BP1 expression is associated with breast cancer prognosis. <i>Cancer Biology and Therapy</i> , 2017, 18, 439-449.	1.5	21
101	Genome-wide Analysis of Common Copy Number Variation and Epithelial Ovarian Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 28, 1117-1126.	1.1	21
102	Norepinephrine-Induced DNA Damage in Ovarian Cancer Cells. <i>International Journal of Molecular Sciences</i> , 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. <i>Genetics in Medicine</i> , 2021, 23, 306-315.	1.1	21
104	A Naturally Occurring Allele of BRCA1 Coding for a Temperature-Sensitive Mutant Protein. <i>Cancer Biology and Therapy</i> , 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. <i>Journal of Medical Genetics</i> , 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. <i>JCO Precision Oncology</i> , 2018, 2, 1-42.	1.5	19
107	Network of Interactions between ZIKA Virus Non-Structural Proteins and Human Host Proteins. <i>Cells</i> , 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. <i>Cell Chemical Biology</i> , 2022, 29, 202-214.e7.	2.5	19

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109	Breast and Prostate Cancer Risks for Male <i>BRCA1</i> and <i>BRCA2</i> Pathogenic Variant Carriers Using Polygenic Risk Scores. <i>Journal of the National Cancer Institute</i> , 2022, 114, 109-122.	3.0	19
110	Interleukin polymorphisms associated with overall survival, disease-free survival, and recurrence in non-small cell lung cancer patients. <i>Molecular Carcinogenesis</i> , 2015, 54, E172-84.	1.3	18
111	Ectopic expression of Histone H2AX mutants reveal a role for its post-translational modifications. <i>Cancer Biology and Therapy</i> , 2009, 8, 422-434.	1.5	17
112	Exome genotyping arrays to identify rare and low frequency variants associated with epithelial ovarian cancer risk. <i>Human Molecular Genetics</i> , 2016, 25, 3600-3612.	1.4	17
113	<i>BRCA1</i> recruitment to damaged DNA sites is dependent on CDK9. <i>Cell Cycle</i> , 2017, 16, 665-672.	1.3	17
114	Functional and Structural Analysis of C-Terminal <i>BRCA1</i> Missense Variants. <i>PLoS ONE</i> , 2013, 8, e61302.	1.1	16
115	Functional annotation signatures of disease susceptibility loci improve SNP association analysis. <i>BMC Genomics</i> , 2014, 15, 398.	1.2	16
116	Germline Missense Variants in <i>BRCA1</i> : New Trends and Challenges for Clinical Annotation. <i>Cancers</i> , 2019, 11, 522.	1.7	16
117	Yeast-based Assays for Detection and Characterization of Mutations in <i>BRCA1</i> . <i>Breast Disease</i> , 1998, 10, 61-70.	0.4	15
118	Cancer Risk Assessment at the Atomic Level. <i>Cancer Research</i> , 2006, 66, 1897-1899.	0.4	15
119	Tandem BRCT Domains: DNA's Praetorian Guard. <i>Genes and Cancer</i> , 2010, 1, 1140-1146.	0.6	15
120	Fine tuning chemotherapy to match <i>BRCA1</i> status. <i>Biochemical Pharmacology</i> , 2010, 80, 647-653.	2.0	14
121	Enhancer scanning to locate regulatory regions in genomic loci. <i>Nature Protocols</i> , 2016, 11, 46-60.	5.5	14
122	CTDP1 regulates breast cancer survival and DNA repair through BRCT-specific interactions with FANCI. <i>Cell Death Discovery</i> , 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. <i>Biology of the Cell</i> , 1985, 53, 231-238.	0.7	14
124	Mutations in the BRCT Domain Confer Temperature Sensitivity to <i>BRCA1</i> in Transcription Activation. <i>Cancer Biology and Therapy</i> , 2002, 1, 502-508.	1.5	13
125	Methods to Classify <i>BRCA1</i> Variants of Uncertain Clinical Significance: The More the Merrier. <i>Cancer Biology and Therapy</i> , 2004, 3, 458-459.	1.5	13
126	DNA damage response: Determining the fate of phosphorylated histone H2AX. <i>Cancer Biology and Therapy</i> , 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?. <i>Anti-Cancer Agents in Medicinal Chemistry</i> , 2009, 9, 543-549.	0.9	13
128	Localization of BRCA1 protein in breast cancer tissue and cell lines with mutations. <i>Cancer Cell International</i> , 2013, 13, 70.	1.8	13
129	PALB2 Variants: Protein Domains and Cancer Susceptibility. <i>Trends in Cancer</i> , 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. <i>Oncotarget</i> , 2016, 7, 72381-72394.	0.8	13
131	Yeast two-hybrid junk sequences contain selected linear motifs. <i>Nucleic Acids Research</i> , 2011, 39, e128-e128.	6.5	12
132	Germline variants in cancer genes in high-risk non-BRCA patients from Puerto Rico. <i>Scientific Reports</i> , 2019, 9, 17769.	1.6	12
133	Absence of constitutional H2AX gene mutations in 101 hereditary breast cancer families. <i>Journal of Medical Genetics</i> , 2003, 40, 51e-51.	1.5	11
134	Early transcriptional response of human ovarian and fallopian tube surface epithelial cells to norepinephrine. <i>Scientific Reports</i> , 2018, 8, 8291.	1.6	11
135	Participation of BRCA1 in DNA Repair Response...Via Transcription. <i>Cancer Biology and Therapy</i> , 2002, 1, 187-188.	1.5	10
136	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. <i>PLoS ONE</i> , 2018, 13, e0197561.	1.1	9
137	In vitro formation of fibrous septa by liver connective tissue cells. <i>In Vitro Cellular & Developmental Biology</i> , 1987, 23, 10-14.	1.0	8
138	TGF β 1 and PDGF AA override Collagen type I inhibition of proliferation in human liver connective tissue cells. <i>BMC Gastroenterology</i> , 2004, 4, 30.	0.8	8
139	Long-term culture of cholangiocytes from liver fibro-granulomatous lesions. <i>BMC Gastroenterology</i> , 2006, 6, 13.	0.8	8
140	Probing Structure-Function Relationships in Missense Variants in the Carboxy-Terminal Region of BRCA1. <i>PLoS ONE</i> , 2014, 9, e97766.	1.1	8
141	The P1812A and P25TBRCA1 and the 5164del4BRCA2 Mutations: Occurrence in High-Risk Non-Ashkenazi Jews. <i>Genetic Testing and Molecular Biomarkers</i> , 2006, 10, 200-207.	1.7	7
142	Somatic alterations in brain tumors. <i>Oncology Reports</i> , 2008, , .	1.2	7
143	Functional Implications of BRCA1 for Early Detection, Prevention, and Treatment of Breast Cancer. <i>Critical Reviews in Eukaryotic Gene Expression</i> , 2006, 16, 233-252.	0.4	7
144	A targeted genetic association study of epithelial ovarian cancer susceptibility. <i>Oncotarget</i> , 2016, 7, 7381-7389.	0.8	7

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145	A nuclear function for the tumor suppressor BRCA1. <i>Histology and Histopathology</i> , 2000, 15, 299-307.	0.5	7
146	Classification of <i>BRCA2</i> Variants of Uncertain Significance (VUS) Using an ACMG/AMP Model Incorporating a Homology-Directed Repair (HDR) Functional Assay. <i>Clinical Cancer Research</i> , 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. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017, 26, 116-125.	1.1	6
148	Evaluation of vitamin D biosynthesis and pathway target genes reveals <i>UGT2A1/2</i> and <i>EGFR</i> polymorphisms associated with epithelial ovarian cancer in African American Women. <i>Cancer Medicine</i> , 2019, 8, 2503-2513.	1.3	6
149	Functional Landscape of Common Variants Associated with Susceptibility to Epithelial Ovarian Cancer. <i>Current Epidemiology Reports</i> , 2020, 7, 49-57.	1.1	6
150	Interaction of human liver connective tissue cells, skin fibroblasts and smooth muscle cells with collagen gels. <i>Hepatology</i> , 1987, 7, 665-671.	3.6	5
151	Genetic testing and clinical management practices for variants in non- <i>BRCA1/2</i> breast (and/or ovarian) cancer susceptibility genes: An international survey by the Enigma Clinical Working Group.. <i>Journal of Clinical Oncology</i> , 2018, 36, 1539-1539.	0.8	5
152	Functional Restoration of <i>BRCA1</i> Nonsense Mutations by Aminoglycoside-Induced Readthrough. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	5
153	Involvement of the SH3 domain in Ca ²⁺ -mediated regulation of Src family kinases. <i>Biochimie</i> , 2006, 88, 905-911.	1.3	4
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