

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

34105

52
h-index

40979

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.	21.4	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.	7.1	430
3	A Systematic Genetic Assessment of 1,433 Sequence Variants of Unknown Clinical Significance in the BRCA1 and BRCA2 Breast Cancerâ€Predisposition Genes. <i>American Journal of Human Genetics</i> , 2007, 81, 873-883.	6.2	416
4	Principles for the post-GWAS functional characterization of cancer risk loci. <i>Nature Genetics</i> , 2011, 43, 513-518.	21.4	392
5	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. <i>Nature Genetics</i> , 2017, 49, 680-691.	21.4	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.	6.2	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.	7.1	340
8	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. <i>Nature Genetics</i> , 2013, 45, 362-370.	21.4	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.	2.5	269
10	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. <i>Nature Genetics</i> , 2015, 47, 164-171.	21.4	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.	2.5	190
12	<i>PALB2</i>,<i>CHEK2</i>and<i>ATM</i>rare variants and cancer risk: data from COGS. <i>Journal of Medical Genetics</i> , 2016, 53, 800-811.	3.2	174
13	A multigene mutation classification of 468 colorectal cancers reveals a prognostic role for APC. <i>Nature Communications</i> , 2016, 7, 11743.	12.8	170
14	BRCA1 and BRCA2 genetic testingâ€Ppitfalls and recommendations for managing variants of uncertain clinical significance. <i>Annals of Oncology</i> , 2015, 26, 2057-2065.	1.2	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.	9.4	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.	2.9	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.	12.8	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.	0.9	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.	2.9	128
20	Biallelic Deleterious <i>BRCA1</i> Mutations in a Woman with Early-Onset Ovarian Cancer. <i>Cancer Discovery</i> , 2013, 3, 399-405.	9.4	124
21	A guide for functional analysis of <i>BRCA1</i> variants of uncertain significance. <i>Human Mutation</i> , 2012, 33, 1526-1537.	2.5	117
22	p53 Acetylation Is Crucial for Its Transcription-independent Proapoptotic Functions. <i>Journal of Biological Chemistry</i> , 2009, 284, 11171-11183.	3.4	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.	0.9	110
24	Functional Assays for Analysis of Variants of Uncertain Significance in <i>BRCA2</i> . <i>Human Mutation</i> , 2014, 35, 151-164.	2.5	107
25	Structure-Based Assessment of Missense Mutations in Human <i>BRCA1</i> . <i>Cancer Research</i> , 2004, 64, 3790-3797.	0.9	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.	2.5	102
27	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. <i>Nature Communications</i> , 2013, 4, 1627.	12.8	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.	1.8	98
29	Assessment of functional effects of unclassified genetic variants. <i>Human Mutation</i> , 2008, 29, 1314-1326.	2.5	93
30	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016, 7, 11375.	12.8	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.	1.9	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.	4.1	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.	21.4	89
34	Charting the Landscape of Tandem BRCT Domain-Mediated Protein Interactions. <i>Science Signaling</i> , 2012, 5, rs6.	3.6	88
35	<i>BRCA1</i> : exploring the links to transcription. <i>Trends in Biochemical Sciences</i> , 2000, 25, 469-474.	7.5	81
36	Proteome-wide Profiling of Clinical PARP Inhibitors Reveals Compound-Specific Secondary Targets. <i>Cell Chemical Biology</i> , 2016, 23, 1490-1503.	5.2	80

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37	Classification of BRCA1 missense variants of unknown clinical significance. Journal of Medical Genetics, 2005, 42, 138-146.	3.2	79
38	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	12.8	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.	6.3	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.	2.1	75
41	Phosphatases in the cellular response to DNA damage. Cell Communication and Signaling, 2010, 8, 27.	6.5	75
42	<i>LIN28B</i> Polymorphisms Influence Susceptibility to Epithelial Ovarian Cancer. Cancer Research, 2011, 71, 3896-3903.	0.9	75
43	<i>BRCA2</i> Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799.	0.9	75
44	Prevalence of BRCA1 and BRCA2 mutations in breast cancer patients from Brazil. Breast Cancer Research and Treatment, 2007, 103, 349-353.	2.5	71
45	Functional assays provide a robust tool for the clinical annotation of genetic variants of uncertain significance. Npj Genomic Medicine, 2016, 1, .	3.8	70
46	The Role of PALB2 in the DNA Damage Response and Cancer Predisposition. International Journal of Molecular Sciences, 2017, 18, 1886.	4.1	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.	6.2	64
48	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. Nature Communications, 2015, 6, 8234.	12.8	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.	2.5	63
50	Functional Impact of Missense Variants in BRCA1 Predicted by Supervised Learning. PLoS Computational Biology, 2007, 3, e26.	3.2	57
51	Circadian pathway genes in relation to glioma risk and outcome. Cancer Causes and Control, 2014, 25, 25-32.	1.8	57
52	Dual Targeting of WEE1 and PLK1 by AZD1775 Elicits Single Agent Cellular Anticancer Activity. ACS Chemical Biology, 2017, 12, 1883-1892.	3.4	57
53	BRCA1: the enigma of tissue-specific tumor development. Trends in Genetics, 2003, 19, 312-315.	6.7	54
54	A Computational Method to Classify Variants of Uncertain Significance Using Functional Assay Data with Application to <i>BRCA1</i> . Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 1078-1088.	2.5	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.	2.4	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.	0.9	49
57	Functional assays for BRCA1 and BRCA2. <i>International Journal of Biochemistry and Cell Biology</i> , 2007, 39, 298-310.	2.8	48
58	Differences in BRCA counseling and testing practices based on ordering provider type. <i>Genetics in Medicine</i> , 2015, 17, 51-57.	2.4	47
59	BRCT domains: A little more than kin, and less than kind. <i>FEBS Letters</i> , 2012, 586, 2711-2716.	2.8	44
60	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. <i>PLoS ONE</i> , 2015, 10, e0128106.	2.5	44
61	Clinical testing of BRCA1 and BRCA2: a worldwide snapshot of technological practices. <i>Npj Genomic Medicine</i> , 2018, 3, 7.	3.8	44
62	Breast Cancer Susceptibility and the DNA Damage Response. <i>Cancer Control</i> , 2005, 12, 127-136.	1.8	43
63	An Interactive Resource to Probe Genetic Diversity and Estimated Ancestry in Cancer Cell Lines. <i>Cancer Research</i> , 2019, 79, 1263-1273.	0.9	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.	2.8	42
65	Identification of Filamin A as a BRCA1-interacting protein required for efficient DNA repair. <i>Cell Cycle</i> , 2010, 9, 1421-1433.	2.6	42
66	Rare <i>TP53</i> genetic variant associated with glioma risk and outcome. <i>Journal of Medical Genetics</i> , 2012, 49, 420-421.	3.2	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.	2.9	40
68	Functional characterization of 84 PALB2 variants of uncertain significance. <i>Genetics in Medicine</i> , 2020, 22, 622-632.	2.4	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.	14.5	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.	1.0	38
71	Mutational heterogeneity in non-serous ovarian cancers. <i>Scientific Reports</i> , 2017, 7, 9728.	3.3	35
72	Common BRCA1 Variants and Transcriptional Activation. <i>American Journal of Human Genetics</i> , 1997, 61, 761-762.	6.2	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.	2.6	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.	3.2	33
75	Understanding Germ-Line Mutations in BRCA1. <i>Cancer Biology and Therapy</i> , 2004, 3, 515-520.	3.4	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.	1.0	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.	2.0	32
78	BRCA1 Circos: a visualisation resource for functional analysis of missense variants. <i>Journal of Medical Genetics</i> , 2015, 52, 224-230.	3.2	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.	2.5	32
80	Towards controlled terminology for reporting germline cancer susceptibility variants: an ENIGMA report. <i>Journal of Medical Genetics</i> , 2019, 56, 347-357.	3.2	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.	3.4	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.	6.2	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.	3.8	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.	2.5	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.	3.3	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.	3.4	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.	6.0	24
90	Common variants at the CHEK2 gene locus and risk of epithelial ovarian cancer. <i>Carcinogenesis</i> , 2015, 36, 1341-1353.	2.8	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.	1.3	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.	4.1	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.	6.4	23
94	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. <i>European Journal of Human Genetics</i> , 2022, 30, 349-362.	2.8	23
95	BRCA1 can stimulate gene transcription by a unique mechanism. <i>EMBO Reports</i> , 2000, 1, 260-265.	4.5	22
96	BRCA1 in breast and ovarian cancer predisposition. <i>Cancer Letters</i> , 2005, 227, 1-7.	7.2	22
97	Epithelial-Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. <i>Genetic Epidemiology</i> , 2015, 39, 689-697.	1.3	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.	2.8	22
99	Functional Analysis and Fine Mapping of the 9p22.2 Ovarian Cancer Susceptibility Locus. <i>Cancer Research</i> , 2019, 79, 467-481.	0.9	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.	3.4	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.	2.5	21
102	Norepinephrine-Induced DNA Damage in Ovarian Cancer Cells. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2250.	4.1	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.	2.4	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.	3.4	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.	3.2	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.	3.0	19
107	Network of Interactions between ZIKA Virus Non-Structural Proteins and Human Host Proteins. <i>Cells</i> , 2020, 9, 153.	4.1	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.	5.2	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.	6.3	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.	2.7	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.	3.4	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.	2.9	17
113	<i>BRCA1</i> recruitment to damaged DNA sites is dependent on CDK9. <i>Cell Cycle</i> , 2017, 16, 665-672.	2.6	17
114	Functional and Structural Analysis of C-Terminal <i>BRCA1</i> Missense Variants. <i>PLoS ONE</i> , 2013, 8, e61302.	2.5	16
115	Functional annotation signatures of disease susceptibility loci improve SNP association analysis. <i>BMC Genomics</i> , 2014, 15, 398.	2.8	16
116	Germline Missense Variants in <i>BRCA1</i> : New Trends and Challenges for Clinical Annotation. <i>Cancers</i> , 2019, 11, 522.	3.7	16
117	Yeast-based Assays for Detection and Characterization of Mutations in <i>BRCA1</i> . <i>Breast Disease</i> , 1998, 10, 61-70.	0.8	15
118	Cancer Risk Assessment at the Atomic Level. <i>Cancer Research</i> , 2006, 66, 1897-1899.	0.9	15
119	Tandem BRCT Domains: DNA's Praetorian Guard. <i>Genes and Cancer</i> , 2010, 1, 1140-1146.	1.9	15
120	Fine tuning chemotherapy to match <i>BRCA1</i> status. <i>Biochemical Pharmacology</i> , 2010, 80, 647-653.	4.4	14
121	Enhancer scanning to locate regulatory regions in genomic loci. <i>Nature Protocols</i> , 2016, 11, 46-60.	12.0	14
122	CTDP1 regulates breast cancer survival and DNA repair through BRCT-specific interactions with FANCI. <i>Cell Death Discovery</i> , 2019, 5, 105.	4.7	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.	2.0	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.	3.4	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.	3.4	13
126	DNA damage response: Determining the fate of phosphorylated histone H2AX. <i>Cancer Biology and Therapy</i> , 2006, 5, 142-144.	3.4	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.	1.7	13
128	Localization of BRCA1 protein in breast cancer tissue and cell lines with mutations. <i>Cancer Cell International</i> , 2013, 13, 70.	4.1	13
129	PALB2 Variants: Protein Domains and Cancer Susceptibility. <i>Trends in Cancer</i> , 2021, 7, 188-197.	7.4	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.	1.8	13
131	Yeast two-hybrid junk sequences contain selected linear motifs. <i>Nucleic Acids Research</i> , 2011, 39, e128-e128.	14.5	12
132	Germline variants in cancer genes in high-risk non-BRCA patients from Puerto Rico. <i>Scientific Reports</i> , 2019, 9, 17769.	3.3	12
133	Absence of constitutional H2AX gene mutations in 101 hereditary breast cancer families. <i>Journal of Medical Genetics</i> , 2003, 40, 51e-51.	3.2	11
134	Early transcriptional response of human ovarian and fallopian tube surface epithelial cells to norepinephrine. <i>Scientific Reports</i> , 2018, 8, 8291.	3.3	11
135	Participation of BRCA1 in DNA Repair Response...Via Transcription. <i>Cancer Biology and Therapy</i> , 2002, 1, 187-188.	3.4	10
136	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. <i>PLoS ONE</i> , 2018, 13, e0197561.	2.5	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.	2.0	8
139	Long-term culture of cholangiocytes from liver fibro-granulomatous lesions. <i>BMC Gastroenterology</i> , 2006, 6, 13.	2.0	8
140	Probing Structure-Function Relationships in Missense Variants in the Carboxy-Terminal Region of BRCA1. <i>PLoS ONE</i> , 2014, 9, e97766.	2.5	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, , .	2.6	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.	0.9	7
144	A targeted genetic association study of epithelial ovarian cancer susceptibility. <i>Oncotarget</i> , 2016, 7, 7381-7389.	1.8	7

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145	A nuclear function for the tumor suppressor BRCA1. <i>Histology and Histopathology</i> , 2000, 15, 299-307.	0.7	7
146	Classification of BRCA2 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.	7.0	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.	2.5	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. <i>Cancer Medicine</i> , 2019, 8, 2503-2513.	2.8	6
149	Functional Landscape of Common Variants Associated with Susceptibility to Epithelial Ovarian Cancer. <i>Current Epidemiology Reports</i> , 2020, 7, 49-57.	2.4	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.	7.3	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.. <i>Journal of Clinical Oncology</i> , 2018, 36, 1539-1539.	1.6	5
152	Functional Restoration of BRCA1 Nonsense Mutations by Aminoglycoside-Induced Readthrough. <i>Frontiers in Pharmacology</i> , 0, 13, .	3.5	5
153	Involvement of the SH3 domain in Ca ²⁺ -mediated regulation of Src family kinases. <i>Biochimie</i> , 2006, 88, 905-911.	2.6	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. <i>Human Molecular Genetics</i> , 2016, 25, ddw343.	2.9	4
155	Somatic alterations in brain tumors. <i>Oncology Reports</i> , 2008, 20, 203-10.	2.6	4
156	An integrative model for the comprehensive classification of BRCA1 and BRCA2 variants of uncertain clinical significance. <i>Npj Genomic Medicine</i> , 2022, 7, .	3.8	4
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