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	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.	5.2	19
2	Breast and Prostate Cancer Risks for MaleBRCA1andBRCA2Pathogenic Variant Carriers Using Polygenic Risk Scores. Journal of the National Cancer Institute, 2022, 114, 109-122.	6.3	19
3	Two distinct mechanisms underlie estrogen-receptor-negative breast cancer susceptibility at the 2p23.2 locus. European Journal of Human Genetics, 2022, 30, 465-473.	2.8	3
4	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. European Journal of Human Genetics, 2022, 30, 349-362.	2.8	23
5	An integrative model for the comprehensive classification of BRCA1 and BRCA2 variants of uncertain clinical significance. Npj Genomic Medicine, 2022, 7, .	3.8	4
6	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.	7.0	7
7	Identification of Two Genetic Loci Associated with Leukopenia after Chemotherapy in Patients with Breast Cancer. Clinical Cancer Research, 2022, 28, 3342-3355.	7.0	3
8	Rare germline variants in PALB2 and BRCA2 in familial and sporadic chordoma. Human Mutation, 2022, 43, 1396-1407.	2.5	3
9	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.	2.4	21
10	PALB2 Variants: Protein Domains and Cancer Susceptibility. Trends in Cancer, 2021, 7, 188-197.	7.4	13
11	Functional evidence (II) protein and enzyme function. , 2021, , 145-168.		0
12	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.	6.2	31
13	Effects of long-term norepinephrine treatment on normal immortalized ovarian and fallopian tube cells. Scientific Reports, 2021, 11, 14334.	3.3	1
14	Scratching Below the Ovarian Cancer GWAS Surface. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 1604-1606.	2.5	0
15	Functional characterization of 84 PALB2 variants of uncertain significance. Genetics in Medicine, 2020, 22, 622-632.	2.4	40
16	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.	3.2	33
17	Norepinephrine-Induced DNA Damage in Ovarian Cancer Cells. International Journal of Molecular Sciences, 2020, 21, 2250.	4.1	21
18	Network of Interactions between ZIKA Virus Non-Structural Proteins and Human Host Proteins. Cells, 2020, 9, 153.	4.1	19

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19	Functional Landscape of Common Variants Associated with Susceptibility to Epithelial Ovarian Cancer. Current Epidemiology Reports, 2020, 7, 49-57.	2.4	6
20	Acceptability and outcomes of multigene panel testing among young Black breast cancer survivors. Breast Journal, 2020, 26, 2112-2114.	1.0	1
21	Abstract C093: An interactive resource to probe ancestry in cancer cell lines. , 2020, , .		0
22	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.	0.9	49
23	Comprehensive annotation of BRCA1 and BRCA2 missense variants by functionally validated sequence-based computational prediction models. Genetics in Medicine, 2019, 21, 71-80.	2.4	52
24	DNA damage response and repair in perspective: Aedes aegypti, Drosophila melanogaster and Homo sapiens. Parasites and Vectors, 2019, 12, 533.	2.5	32
25	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.	2.5	102
26	CTDP1 regulates breast cancer survival and DNA repair through BRCT-specific interactions with FANCI. Cell Death Discovery, 2019, 5, 105.	4.7	14
27	epiTAD: a web application for visualizing chromosome conformation capture data in the context of genetic epidemiology. Bioinformatics, 2019, 35, 4462-4464.	4.1	2
28	Germline Missense Variants in BRCA1: New Trends and Challenges for Clinical Annotation. Cancers, 2019, 11, 522.	3.7	16
29	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.	2.8	6
30	Towards controlled terminology for reporting germline cancer susceptibility variants: an ENIGMA report. Journal of Medical Genetics, 2019, 56, 347-357.	3.2	32
31	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.	21.4	89
32	An Interactive Resource to Probe Genetic Diversity and Estimated Ancestry in Cancer Cell Lines. Cancer Research, 2019, 79, 1263-1273.	0.9	43
33	Genome-wide Analysis of Common Copy Number Variation and Epithelial Ovarian Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 1117-1126.	2.5	21
34	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.	3.4	32
35	A global functional analysis of missense mutations reveals two major hotspots in the PALB2 tumor suppressor. Nucleic Acids Research, 2019, 47, 10662-10677.	14.5	39
36	Germline variants in cancer genes in high-risk non-BRCA patients from Puerto Rico. Scientific Reports, 2019, 9, 17769.	3.3	12

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37	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.	2.4	2
38	Functional Analysis and Fine Mapping of the 9p22.2 Ovarian Cancer Susceptibility Locus. Cancer Research, 2019, 79, 467-481.	0.9	22
39	Abstract 2669: A role forHOXA5in the transcriptional response of ovarian and fallopian tube surface epithelial cells to norepinephrine. , 2019, , .		0
40	Abstract B021: PARP16 is a novel target of talazoparib which contributes to synergy with adavosertib in SCLC. Molecular Cancer Therapeutics, 2019, 18, B021-B021.	4.1	1
41	Abstract B022: PARP1 complex composition as a predictor of response to PARP inhibitors in BRCA-linked ovarian carcinoma. , 2019, , .		0
42	Abstract 1740: Characterization of CDK9 role in the DNA damage response. , 2019, , .		0
43	Clinical testing of BRCA1 and BRCA2: a worldwide snapshot of technological practices. Npj Genomic Medicine, 2018, 3, 7.	3.8	44
44	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
45	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.	0.7	3
46	Genetic Testing and Clinical Management Practices for Variants in Non-BRCA1/2 Breast (and) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 392 for the Interpretation of Germline Mutant Alleles (ENIGMA) Clinical Working Group. JCO Precision Oncology, 2018, 2, 1-42.	3.0	19
47	Early transcriptional response of human ovarian and fallopian tube surface epithelial cells to norepinephrine. Scientific Reports, 2018, 8, 8291.	3.3	11
48	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. PLoS ONE, 2018, 13, e0197561.	2.5	9
49	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.	1.6	5
50	Enrichment of putative PAX8 target genes at serous epithelial ovarian cancer susceptibility loci. British Journal of Cancer, 2017, 116, 524-535.	6.4	23
51	BRCA1 recruitment to damaged DNA sites is dependent on CDK9. Cell Cycle, 2017, 16, 665-672.	2.6	17
52	BRCA2 Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799.	0.9	75
53	Dual Targeting of WEE1 and PLK1 by AZD1775 Elicits Single Agent Cellular Anticancer Activity. ACS Chemical Biology, 2017, 12, 1883-1892.	3.4	57
54	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	21.4	356

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55	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.	2.5	6
56	Mutational heterogeneity in non-serous ovarian cancers. Scientific Reports, 2017, 7, 9728.	3.3	35
57	What can yeast tell us about breast cancer?. Cell Cycle, 2017, 16, 157-158.	2.6	1
58	DNA repair genes PAXIP1 and TP53BP1 expression is associated with breast cancer prognosis. Cancer Biology and Therapy, 2017, 18, 439-449.	3.4	21
59	The Role of PALB2 in the DNA Damage Response and Cancer Predisposition. International Journal of Molecular Sciences, 2017, 18, 1886.	4.1	70
60	Dissecting genetic risk factors in breast cancer. Oncotarget, 2017, 8, 12540-12541.	1.8	2
61	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.	1.6	1
62	Abstract 1282: Analysis of missense variants inBRCA1BRCT domains. , 2017, , .		0
63	Abstract 1306: Two distinct regulatory mechanisms underlie estrogen receptor negative breast cancer susceptibility at the 2p23.2 locus. , 2017, , .		0
64	Exome genotyping arrays to identify rare and low frequency variants associated with epithelial ovarian cancer risk. Human Molecular Genetics, 2016, 25, 3600-3612.	2.9	17
65	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
66	Functional assays provide a robust tool for the clinical annotation of genetic variants of uncertain significance. Npj Genomic Medicine, 2016, 1, .	3.8	70
67	Response: Table 1.. Journal of the National Cancer Institute, 2016, 108, djw173.	6.3	2
68	A multigene mutation classification of 468 colorectal cancers reveals a prognostic role for APC. Nature Communications, 2016, 7, 11743.	12.8	170
69	PAXIP1 Potentiates the Combination of WEE1 Inhibitor AZD1775 and Platinum Agents in Lung Cancer. Molecular Cancer Therapeutics, 2016, 15, 1669-1681.	4.1	23
70	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.	9.4	157
71	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.	2.9	4
72	Proteome-wide Profiling of Clinical PARP Inhibitors Reveals Compound-Specific Secondary Targets. Cell Chemical Biology, 2016, 23, 1490-1503.	5.2	80

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73	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	12.8	93
74	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	12.8	78
75	Enhancer scanning to locate regulatory regions in genomic loci. Nature Protocols, 2016, 11, 46-60.	12.0	14
76	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
77	Inherited variants affecting RNA editing may contribute to ovarian cancer susceptibility: results from a large-scale collaboration. Oncotarget, 2016, 7, 72381-72394.	1.8	13
78	A targeted genetic association study of epithelial ovarian cancer susceptibility. Oncotarget, 2016, 7, 7381-7389.	1.8	7
79	Abstract B11: Mutational heterogeneity in non-serous ovarian cancers.. , 2016, , .		0
80	Abstract PR15: MYC distal enhancers underlie ovarian cancer susceptibility in the 8q24.21 locus.. , 2016, , .		0
81	Abstract B27: Investigation of small GTPase genes in epithelial ovarian cancer.. , 2016, , .		0
82	Abstract 5232: Using an integrated gene-based sequence kernel association test (intSKAT) to identify subtype specific single nucleotide variants in glioma. , 2016, , .		0
83	Functional analysis of the 11q23.3 glioma susceptibility locus implicates PHLDB1 and DDX6 in glioma susceptibility. Scientific Reports, 2015, 5, 17367.	3.3	27
84	A high frequency of BRCA mutations in young black women with breast cancer residing in Florida. Cancer, 2015, 121, 4173-4180.	4.1	91
85	Epithelialâ€Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. Genetic Epidemiology, 2015, 39, 689-697.	1.3	22
86	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. PLoS ONE, 2015, 10, e0128106.	2.5	44
87	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. Human Molecular Genetics, 2015, 24, 3595-3607.	2.9	40
88	Incorporating computational resources in a cancer research program. Human Genetics, 2015, 134, 467-478.	3.8	2
89	BRCA1 Circos: a visualisation resource for functional analysis of missense variants. Journal of Medical Genetics, 2015, 52, 224-230.	3.2	32
90	Differences in BRCA counseling and testing practices based on ordering provider type. Genetics in Medicine, 2015, 17, 51-57.	2.4	47

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91	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	21.4	221
92	Interleukin polymorphisms associated with overall survival, diseaseâ€free survival, and recurrence in nonâ€small cell lung cancer patients. Molecular Carcinogenesis, 2015, 54, E172-84.	2.7	18
93	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.	2.5	28
94	Genetic determinants of telomere length and risk of common cancers: a Mendelian randomization study. Human Molecular Genetics, 2015, 24, 5356-5366.	2.9	128
95	BRCA1 and BRCA2 genetic testingâ€"pitfalls and recommendations for managing variants of uncertain clinical significance. Annals of Oncology, 2015, 26, 2057-2065.	1.2	163
96	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. Nature Communications, 2015, 6, 8234.	12.8	63
97	Common variants at theCHEK2gene locus and risk of epithelial ovarian cancer. Carcinogenesis, 2015, 36, 1341-1353.	2.8	24
98	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
99	Brain tumor risk according to germ-line variation in the MLLT10 locus. European Journal of Human Genetics, 2015, 23, 132-134.	2.8	22
100	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.	1.8	98
101	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
102	Abstract 4633: Evidence that long non-coding RNA variants associate with epithelial ovarian cancer risk. , 2015, , .		0
103	Abstract 4634: Variants within super-enhancer regulatory elements associate with epithelial ovarian cancer risk. , 2015, , .		0
104	Abstract 4635: Inherited variants affecting RNA editing may contribute to ovarian cancer susceptibility. Cancer Research, 2015, 75, 4635-4635.	0.9	1
105	Abstract 841: SNP-FEMS: a method to identify DNA binding proteins interacting with enhancer elements. , 2015, , .		0
106	Abstract 3779: Mutational analysis of MCPH1 C-terminal tandem BRCT domain reveals residues essential for cell cycle arrest. , 2015, , .		0
107	Abstract 3951: Functional analysis of the 11q23.3 glioma susceptibility locus. , 2015, , .		0
108	Abstract 3025: Characterization of CDK9/BRCA1 complex in DNA damage response. , 2015, , .		0

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109	Abstract 2783: Common functional mechanisms underlying pleiotropy at the 19p13.1 breast and ovarian cancer cusceptibility locus. , 2015, , .		1
110	Probing Structure-Function Relationships in Missense Variants in the Carboxy-Terminal Region of BRCA1. PLoS ONE, 2014, 9, e97766.	2.5	8
111	Characterization ofLGALS3(galectin-3) as a player in DNA damage response. Cancer Biology and Therapy, 2014, 15, 840-850.	3.4	25
112	Circadian pathway genes in relation to glioma risk and outcome. Cancer Causes and Control, 2014, 25, 25-32.	1.8	57
113	Functional Assays for Analysis of Variants of Uncertain Significance inBRCA2. Human Mutation, 2014, 35, 151-164.	2.5	107
114	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.	2.0	32
115	Functional annotation signatures of disease susceptibility loci improve SNP association analysis. BMC Genomics, 2014, 15, 398.	2.8	16
116	Abstract 946: Exome genotyping array identifies rare and low-frequency variants that may be associated with ovarian cancer risk. , 2014, , .		0
117	Abstract 480: CDK9 (a novel BRCA1/BARD1 interaction partner) downregulates BRCA1-mediated transcription. , 2014, , .		0
118	Abstract 3285: Functional analysis of the 9p22 locus implicates the transcriptional regulation ofBNC2as a mechanism in ovarian cancer predisposition. , 2014, , .		0
119	Abstract 5483: Implications of the type ofBRCA1germline mutation in the treatment of patients with hereditary breast cancer. , 2014, , .		0
120	Abstract 3283: GWAS identifies risk variants for mucinous ovarian carcinoma. , 2014, , .		0
121	Abstract 2414: Overexpression of PAXIP1 potentiates WEE1 inhibitor action in lung cancer cells. , 2014, , .		0
122	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. Nature Genetics, 2013, 45, 362-370.	21.4	326
123	Localization of BRCA1 protein in breast cancer tissue and cell lines with mutations. Cancer Cell International, 2013, 13, 70.	4.1	13
124	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.	21.4	493
125	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.	1.0	32
126	Biallelic Deleterious BRCA1 Mutations in a Woman with Early-Onset Ovarian Cancer. Cancer Discovery, 2013, 3, 399-405.	9.4	124

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127	Lessons from postgenomeâ€wide association studies: functional analysis of cancer predisposition loci. Journal of Internal Medicine, 2013, 274, 414-424.	6.0	24
128	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. Nature Communications, 2013, 4, 1628.	12.8	144
129	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. Nature Communications, 2013, 4, 1627.	12.8	98
130	Functional and Structural Analysis of C-Terminal BRCA1 Missense Variants. PLoS ONE, 2013, 8, e61302.	2.5	16
131	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
132	Abstract 1352: Epithelial-mesenchymal transition (EMT) gene variants influence epithelial ovarian cancer risk in women of European, African and Asian ancestry.. , 2013, , .		0
133	Abstract 3644: Variation in transmembrane transport genes influence epithelial ovarian cancer risk and histopathologic subtype.. , 2013, , .		0
134	Abstract 4850: Variation in circadian rhythm genes influence epithelial ovarian cancer risk and invasiveness.. , 2013, , .		2
135	RareTP53genetic variant associated with glioma risk and outcome. Journal of Medical Genetics, 2012, 49, 420-421.	3.2	42
136	CHEKing out of mitosis. Cell Cycle, 2012, 11, 1756-1756.	2.6	0
137	Charting the Landscape of Tandem BRCT Domainâ€“Mediated Protein Interactions. Science Signaling, 2012, 5, rs6.	3.6	88
138	BRCT domains: A little more than kin, and less than kind. FEBS Letters, 2012, 586, 2711-2716.	2.8	44
139	A guide for functional analysis ofBRCA1variants of uncertain significance. Human Mutation, 2012, 33, 1526-1537.	2.5	117
140	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.	2.5	190
141	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.	2.5	269
142	Abstract 4444: BRCA1 Circos: A visualization tool for BRCA1 missense variants. , 2012, , .		0
143	Abstract 2927: MicroRNA binding site polymorphisms influence ovarian cancer risk in the collaborative oncological gene-environment study. , 2012, , .		0
144	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

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145	Abstract 2132: Characterization of galectin 3 as a novel BARD1 interaction partner. , 2012, , .		0
146	Abstract 1649: Genome-wide association study of copy number variations in serous epithelial ovarian cancer susceptibility. , 2012, , .		1
147	Principles for the post-GWAS functional characterization of cancer risk loci. Nature Genetics, 2011, 43, 513-518.	21.4	392
148	Yeast two-hybrid junk sequences contain selected linear motifs. Nucleic Acids Research, 2011, 39, e128-e128.	14.5	12
149	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.	2.5	54
150	LIN28B Polymorphisms Influence Susceptibility to Epithelial Ovarian Cancer. Cancer Research, 2011, 71, 3896-3903.	0.9	75
151	Epigenetic tumor suppression by BRCA1. Nature Medicine, 2011, 17, 1183-1185.	30.7	3
152	Abstract 3927: Characterization of galectin 3 as a putative BRCA1/BARD1 ubiquitin E3 ligase substrate. , 2011, , .		0
153	Abstract 3892: Discovery and analysis of COMMD1 in the DNA damage response network. , 2011, , .		0
154	Abstract 4729: Pathway and gene set analyses for epithelial ovarian cancer (EOC) genome-wide association study (GWAS). , 2011, , .		0
155	Abstract A71: BRCA mutations and surgical decision making in a sample of young black women with invasive breast cancer. , 2011, , .		0
156	Fine tuning chemotherapy to match BRCA1 status. Biochemical Pharmacology, 2010, 80, 647-653.	4.4	14
157	Phosphatases in the cellular response to DNA damage. Cell Communication and Signaling, 2010, 8, 27.	6.5	75
158	Principles for the post-GWAS functional characterisation of risk loci. Nature Precedings, 2010, , .	0.1	1
159	Comprehensive Analysis of Missense Variations in the BRCT Domain of BRCA1 by Structural and Functional Assays. Cancer Research, 2010, 70, 4880-4890.	0.9	138
160	Three-color intranuclear staining for measuring mitosis and apoptosis in cells transfected with a GFP-tagged histone. Biotechnic and Histochemistry, 2010, 85, 127-131.	1.3	1
161	Identification of Filamin A as a BRCA1-interacting protein required for efficient DNA repair. Cell Cycle, 2010, 9, 1421-1433.	2.6	42
162	Tandem BRCT Domains: DNA's Praetorian Guard. Genes and Cancer, 2010, 1, 1140-1146.	1.9	15

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163	Negative regulation of CHK2 activity by protein phosphatase 2A is modulated by DNA damage. Cell Cycle, 2010, 9, 736-747.	2.6	34
164	BRCA1 Protein and Nucleolin Colocalize in Breast Carcinoma Tissue and Cancer Cell Lines. American Journal of Pathology, 2010, 176, 1203-1214.	3.8	28
165	Abstract 1117: Characterization of BAT1 (UAP56) interaction with BARD1. , 2010, , .		0
166	p53 Acetylation Is Crucial for Its Transcription-independent Proapoptotic Functions. Journal of Biological Chemistry, 2009, 284, 11171-11183.	3.4	111
167	Ectopic expression of Histone H2AX mutants reveal a role for its post-translational modifications. Cancer Biology and Therapy, 2009, 8, 422-434.	3.4	17
168	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.	1.7	13
169	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.	1.0	38
170	In SituProtein Expression of RRM1, ERCC1, and BRCA1 in Metastatic Breast Cancer Patients Treated with Gemcitabine-Based Chemotherapy. Cancer Investigation, 2009, 28, 172-180.	1.3	23
171	Assessment of functional effects of unclassified genetic variants. Human Mutation, 2008, 29, 1314-1326.	2.5	93
172	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.	2.8	42
173	Somatic alterations in brain tumors. Oncology Reports, 2008, , .	2.6	7
174	Somatic alterations in brain tumors. Oncology Reports, 2008, 20, 203-10.	2.6	4
175	Correction: Functional analysis of BRCA1 M1628V variant. Journal of Medical Genetics, 2007, 44, e78-e78.	3.2	1
176	Functional Impact of Missense Variants in BRCA1 Predicted by Supervised Learning. PLoS Computational Biology, 2007, 3, e26.	3.2	57
177	The accidental cancer geneticist: HilÃ¡rio de GouvÃªa and hereditary retinoblastoma. Cancer Biology and Therapy, 2007, 6, 811-813.	3.4	3
178	Determination of Cancer Risk Associated with Germ Line BRCA1 Missense Variants by Functional Analysis. Cancer Research, 2007, 67, 1494-1501.	0.9	110
179	Functional assays for BRCA1 and BRCA2. International Journal of Biochemistry and Cell Biology, 2007, 39, 298-310.	2.8	48
180	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.	6.2	416

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181	Prevalence of BRCA1 and BRCA2 mutations in breast cancer patients from Brazil. Breast Cancer Research and Treatment, 2007, 103, 349-353.	2.5	71
182	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
183	Involvement ofÂtheÂSH3 domain inÂCa2+-mediated regulation ofÂSrc family kinases. Biochimie, 2006, 88, 905-911.	2.6	4
184	Long-term culture of cholangiocytes from liver fibro-granulomatous lesions. BMC Gastroenterology, 2006, 6, 13.	2.0	8
185	DNA damage response: Determining the fate of phosphorylated histone H2AX. Cancer Biology and Therapy, 2006, 5, 142-144.	3.4	13
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