Alvaro N A Monteiro

List of Publications by Year in Descending Order

170 papers	7,854 citations	47 h-index	84 g-index
225 ext. papers	9,167 ext. citations	7.6 avg, IF	5.35 L-index

#	Paper	IF	Citations
170	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	11	12
169	Effects of long-term norepinephrine treatment on normal immortalized ovarian and fallopian tube cells. *Scientific Reports*, **2021**, 11, 14334	4.9	0
168	The non-canonical target PARP16 contributes to polypharmacology of the PARP inhibitor talazoparib and its synergy with WEE1 inhibitors. *Cell Chemical Biology*, **2021**,	8.2	3
167	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	8.1	5
166	PALB2 Variants: Protein Domains and Cancer Susceptibility. *Trends in Cancer*, **2021**, 7, 188-197	12.5	1
165	Functional evidence (II) protein and enzyme function **2021**, 145-168		
164	Breast and Prostate Cancer Risks for Male BRCA1 and BRCA2 Pathogenic Variant Carriers Using Polygenic Risk Scores. *Journal of the National Cancer Institute*, **2021**,	9.7	3
163	Scratching Below the Ovarian Cancer GWAS Surface. *Cancer Epidemiology Biomarkers and Prevention*, **2021**, 30, 1604-1606	4	
162	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	5.8	14
161	Norepinephrine-Induced DNA Damage in Ovarian Cancer Cells. *International Journal of Molecular Sciences*, **2020**, 21,	6.3	9
160	Network of Interactions between ZIKA Virus Non-Structural Proteins and Human Host Proteins. *Cells*, **2020**, 9,	7.9	10
159	Functional Landscape of Common Variants Associated with Susceptibility to Epithelial Ovarian Cancer. *Current Epidemiology Reports*, **2020**, 7, 49-57	2.9	2
158	Functional characterization of 84 PALB2 variants of uncertain significance. *Genetics in Medicine*, **2020**, 22, 622-632	8.1	20
157	Acceptability and outcomes of multigene panel testing among young Black breast cancer survivors. *Breast Journal*, **2020**, 26, 2112-2114	1.2	
156	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	4.7	52
155	CTDP1 regulates breast cancer survival and DNA repair through BRCT-specific interactions with FANCI. *Cell Death Discovery*, **2019**, 5, 105	6.9	10
154	epiTAD: a web application for visualizing chromosome conformation capture data in the context of genetic epidemiology. *Bioinformatics*, **2019**, 35, 4462-4464	7.2	1

153	Germline Missense Variants in : New Trends and Challenges for Clinical Annotation. *Cancers*, **2019**, 11,	6.6	9
152	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	4.8	4
151	Towards controlled terminology for reporting germline cancer susceptibility variants: an ENIGMA report. *Journal of Medical Genetics*, **2019**, 56, 347-357	5.8	19
150	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	36.3	33
149	An Interactive Resource to Probe Genetic Diversity and Estimated Ancestry in Cancer Cell Lines. *Cancer Research*, **2019**, 79, 1263-1273	10.1	24
148	Genome-wide Analysis of Common Copy Number Variation and Epithelial Ovarian Cancer Risk. *Cancer Epidemiology Biomarkers and Prevention*, **2019**, 28, 1117-1126	4	8
147	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	5.4	19
146	Comprehensive annotation of BRCA1 and BRCA2 missense variants by functionally validated sequence-based computational prediction models. *Genetics in Medicine*, **2019**, 21, 71-80	8.1	36
145	DNA damage response and repair in perspective: Aedes aegypti, Drosophila melanogaster and Homo sapiens. *Parasites and Vectors*, **2019**, 12, 533	4	17
144	A global functional analysis of missense mutations reveals two major hotspots in the PALB2 tumor suppressor. *Nucleic Acids Research*, **2019**, 47, 10662-10677	20.1	22
143	Germline variants in cancer genes in high-risk non-BRCA patients from Puerto Rico. *Scientific Reports*, **2019**, 9, 17769	4.9	7
142	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	8.1	2
141	Functional Analysis and Fine Mapping of the 9p22.2 Ovarian Cancer Susceptibility Locus. *Cancer Research*, **2019**, 79, 467-481	10.1	11
140	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	10.1	28
139	Clinical testing of and : a worldwide snapshot of technological practices. *Npj Genomic Medicine*, **2018**, 3, 7	6.2	29
138	Assessment of the Clinical Relevance of BRCA2 Missense Variants by Functional and Computational Approaches. *American Journal of Human Genetics*, **2018**, 102, 233-248	11	38
137	No Evidence for the Pathogenicity of the BRCA2 c.6937 + 594T>G Deep Intronic Variant: A Case-Control Analysis. *Genetic Testing and Molecular Biomarkers*, **2018**, 22, 85-89	1.6	3
136	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. *PLoS ONE*, **2018**, 13, e0197561	3.7	9

135	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	2.2	4
134	Genetic Testing and Clinical Management Practices for Variants in Non-BRCA1/2 Breast (and Breast/Ovarian) Cancer Susceptibility Genes: An International Survey by the Evidence-Based Network for the Interpretation of Germline Mutant Alleles (ENIGMA) Clinical Working Group. *JCO Precision Oncology*, **2018**, 2,	3.6	12
133	Early transcriptional response of human ovarian and fallopian tube surface epithelial cells to norepinephrine. *Scientific Reports*, **2018**, 8, 8291	4.9	6
132	Enrichment of putative PAX8 target genes at serous epithelial ovarian cancer susceptibility loci. *British Journal of Cancer*, **2017**, 116, 524-535	8.7	18
131	BRCA1 recruitment to damaged DNA sites is dependent on CDK9. *Cell Cycle*, **2017**, 16, 665-672	4.7	7
130	Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. *Cancer Research*, **2017**, 77, 2789-2799	10.1	49
129	Dual Targeting of WEE1 and PLK1 by AZD1775 Elicits Single Agent Cellular Anticancer Activity. *ACS Chemical Biology*, **2017**, 12, 1883-1892	4.9	36
128	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. *Nature Genetics*, **2017**, 49, 680-691	36.3	190
127	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	4	5
126	Mutational heterogeneity in non-serous ovarian cancers. *Scientific Reports*, **2017**, 7, 9728	4.9	29
125	What can yeast tell us about breast cancer?. *Cell Cycle*, **2017**, 16, 157-158	4.7	1
124	DNA repair genes PAXIP1 and TP53BP1 expression is associated with breast cancer prognosis. *Cancer Biology and Therapy*, **2017**, 18, 439-449	4.6	12
123	The Role of PALB2 in the DNA Damage Response and Cancer Predisposition. *International Journal of Molecular Sciences*, **2017**, 18,	6.3	45
122	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	2.2	1
121	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, 1052-67	24.4	104
120	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, 5287-5299	5.6	2
119	Proteome-wide Profiling of Clinical PARP Inhibitors Reveals Compound-Specific Secondary Targets. *Cell Chemical Biology*, **2016**, 23, 1490-1503	8.2	58
118	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. *Nature Communications*, **2016**, 7, 11375	17.4	64

117	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. *Nature Communications*, **2016**, 7, 12675	17.4	53
116	Enhancer scanning to locate regulatory regions in genomic loci. *Nature Protocols*, **2016**, 11, 46-60	18.8	8
115	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. *Journal of the National Cancer Institute*, **2016**, 108,	9.7	65
114	Inherited variants affecting RNA editing may contribute to ovarian cancer susceptibility: results from a large-scale collaboration. *Oncotarget*, **2016**, 7, 72381-72394	3.3	11
113	A targeted genetic association study of epithelial ovarian cancer susceptibility. *Oncotarget*, **2016**, 7, 7381-9	3.3	7
112	Exome genotyping arrays to identify rare and low frequency variants associated with epithelial ovarian cancer risk. *Human Molecular Genetics*, **2016**, 25, 3600-3612	5.6	9
111	PALB2, CHEK2 and ATM rare variants and cancer risk: data from COGS. *Journal of Medical Genetics*, **2016**, 53, 800-811	5.8	121
110	Functional assays provide a robust tool for the clinical annotation of genetic variants of uncertain significance. *Npj Genomic Medicine*, **2016**, 1,	6.2	55
109	Response. *Journal of the National Cancer Institute*, **2016**, 108,	9.7	2
108	A multigene mutation classification of 468 colorectal cancers reveals a prognostic role for APC. *Nature Communications*, **2016**, 7, 11743	17.4	113
107	PAXIP1 Potentiates the Combination of WEE1 Inhibitor AZD1775 and Platinum Agents in Lung Cancer. *Molecular Cancer Therapeutics*, **2016**, 15, 1669-81	6.1	17
106	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. *Nature Genetics*, **2015**, 47, 164-71	36.3	177
105	Interleukin polymorphisms associated with overall survival, disease-free survival, and recurrence in non-small cell lung cancer patients. *Molecular Carcinogenesis*, **2015**, 54 Suppl 1, E172-84	5	14
104	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, 1574-84	4	24
103	Genetic determinants of telomere length and risk of common cancers: a Mendelian randomization study. *Human Molecular Genetics*, **2015**, 24, 5356-66	5.6	104
102	BRCA1 and BRCA2 genetic testing-pitfalls and recommendations for managing variants of uncertain clinical significance. *Annals of Oncology*, **2015**, 26, 2057-65	10.3	124
101	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. *Nature Communications*, **2015**, 6, 8234	17.4	40
100	Common variants at the CHEK2 gene locus and risk of epithelial ovarian cancer. *Carcinogenesis*, **2015**, 36, 1341-53	4.6	20

99	The spectrum of BRCA1 and BRCA2 alleles in Latin America and the Caribbean: a clinical perspective. *Breast Cancer Research and Treatment*, **2015**, 154, 441-53	4.4	49
98	Brain tumor risk according to germ-line variation in the MLLT10 locus. *European Journal of Human Genetics*, **2015**, 23, 132-4	5.3	12
97	Functional analysis of the 11q23.3 glioma susceptibility locus implicates PHLDB1 and DDX6 in glioma susceptibility. *Scientific Reports*, **2015**, 5, 17367	4.9	21
96	A high frequency of BRCA mutations in young black women with breast cancer residing in Florida. *Cancer*, **2015**, 121, 4173-80	6.4	64
95	Epithelial-Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. *Genetic Epidemiology*, **2015**, 39, 689-97	2.6	18
94	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. *PLoS ONE*, **2015**, 10, e0128106	3.7	15
93	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. *Human Molecular Genetics*, **2015**, 24, 3595-607	5.6	32
92	Incorporating computational resources in a cancer research program. *Human Genetics*, **2015**, 134, 467-78	6.3	1
91	BRCA1 Circos: a visualisation resource for functional analysis of missense variants. *Journal of Medical Genetics*, **2015**, 52, 224-30	5.8	28
90	Differences in BRCA counseling and testing practices based on ordering provider type. *Genetics in Medicine*, **2015**, 17, 51-7	8.1	34
89	A functional variant in HOXA11-AS, a novel long non-coding RNA, inhibits the oncogenic phenotype of epithelial ovarian cancer. *Oncotarget*, **2015**, 6, 34745-57	3.3	92
88	Common Genetic Variation in Circadian Rhythm Genes and Risk of Epithelial Ovarian Cancer (EOC). *Journal of Genetics and Genome Research*, **2015**, 2,		22
87	Functional assays for analysis of variants of uncertain significance in BRCA2. *Human Mutation*, **2014**, 35, 151-64	4.7	75
86	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	4	25
85	Functional annotation signatures of disease susceptibility loci improve SNP association analysis. *BMC Genomics*, **2014**, 15, 398	4.5	10
84	Probing structure-function relationships in missense variants in the carboxy-terminal region of BRCA1. *PLoS ONE*, **2014**, 9, e97766	3.7	5
83	Characterization of LGALS3 (galectin-3) as a player in DNA damage response. *Cancer Biology and Therapy*, **2014**, 15, 840-50	4.6	22
82	Circadian pathway genes in relation to glioma risk and outcome. *Cancer Causes and Control*, **2014**, 25, 25-32	2.8	35

81	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. *Nature Genetics*, **2013**, 45, 362-70, 370e1-2	36.3	267
80	Localization of BRCA1 protein in breast cancer tissue and cell lines with mutations. *Cancer Cell International*, **2013**, 13, 70	6.4	10
79	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. *Nature Genetics*, **2013**, 45, 371-84, 384e1-2	36.3	422
78	Early onset breast cancer in a registry-based sample of African-american women: BRCA mutation prevalence, and other personal and system-level clinical characteristics. *Breast Journal*, **2013**, 19, 189-92	1.2	27
77	Biallelic deleterious BRCA1 mutations in a woman with early-onset ovarian cancer. *Cancer Discovery* , **2013**, 3, 399-405	24.4	106
76	Lessons from postgenome-wide association studies: functional analysis of cancer predisposition loci. *Journal of Internal Medicine*, **2013**, 274, 414-24	10.8	19
75	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. *Nature Communications*, **2013**, 4, 1628	17.4	124
74	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. *Nature Communications*, **2013**, 4, 1627	17.4	85
73	Functional and structural analysis of C-terminal BRCA1 missense variants. *PLoS ONE*, **2013**, 8, e61302	3.7	14
72	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	4.7	143
71	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	4.7	211
70	Charting the landscape of tandem BRCT domain-mediated protein interactions. *Science Signaling*, **2012**, 5, rs6	8.8	74
69	BRCT domains: A little more than kin, and less than kind. *FEBS Letters*, **2012**, 586, 2711-6	3.8	33
68	A guide for functional analysis of BRCA1 variants of uncertain significance. *Human Mutation*, **2012**, 33, 1526-37	4.7	94
67	Rare TP53 genetic variant associated with glioma risk and outcome. *Journal of Medical Genetics*, **2012**, 49, 420-1	5.8	33
66	CHEKing out of mitosis. *Cell Cycle*, **2012**, 11, 1756	4.7	
65	Principles for the post-GWAS functional characterization of cancer risk loci. *Nature Genetics*, **2011**, 43, 513-8	36.3	326
64	Yeast two-hybrid junk sequences contain selected linear motifs. *Nucleic Acids Research*, **2011**, 39, e128	20.1	9

63	A computational method to classify variants of uncertain significance using functional assay data with application to BRCA1. *Cancer Epidemiology Biomarkers and Prevention*, **2011**, 20, 1078-88	4	42
62	LIN28B polymorphisms influence susceptibility to epithelial ovarian cancer. *Cancer Research*, **2011**, 71, 3896-903	10.1	70
61	Principles for the post-GWAS functional characterisation of risk loci. *Nature Precedings*, **2010**,		1
60	Comprehensive analysis of missense variations in the BRCT domain of BRCA1 by structural and functional assays. *Cancer Research*, **2010**, 70, 4880-90	10.1	113
59	Three-color intranuclear staining for measuring mitosis and apoptosis in cells transfected with a GFP-tagged histone. *Biotechnic and Histochemistry*, **2010**, 85, 127-131	1.8	1
58	Identification of Filamin A as a BRCA1-interacting protein required for efficient DNA repair. *Cell Cycle*, **2010**, 9, 1421-33	4.7	34
57	Tandem BRCT Domains: DNA© Praetorian Guard. *Genes and Cancer*, **2010**, 1, 1140-6	2.9	13
56	Negative regulation of CHK2 activity by protein phosphatase 2A is modulated by DNA damage. *Cell Cycle*, **2010**, 9, 736-47	4.7	23
55	BRCA1 protein and nucleolin colocalize in breast carcinoma tissue and cancer cell lines. *American Journal of Pathology*, **2010**, 176, 1203-14	5.8	22
54	In situ protein expression of RRM1, ERCC1, and BRCA1 in metastatic breast cancer patients treated with gemcitabine-based chemotherapy. *Cancer Investigation*, **2010**, 28, 172-80	2.1	22
53	Fine tuning chemotherapy to match BRCA1 status. *Biochemical Pharmacology*, **2010**, 80, 647-53	6	11
52	Phosphatases in the cellular response to DNA damage. *Cell Communication and Signaling*, **2010**, 8, 27	7.5	62
51	p53 acetylation is crucial for its transcription-independent proapoptotic functions. *Journal of Biological Chemistry*, **2009**, 284, 11171-83	5.4	99
50	Ectopic expression of histone H2AX mutants reveals a role for its post-translational modifications. *Cancer Biology and Therapy*, **2009**, 8, 422-34	4.6	13
49	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, 543-9	2.2	11
48	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	3.3	31
47	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, 820-32	5.3	36
46	Somatic alterations in brain tumors. *Oncology Reports*, **2008**,	3.5	1

45	Assessment of functional effects of unclassified genetic variants. *Human Mutation*, **2008**, 29, 1314-26	4.7	85
44	Somatic alterations in brain tumors. *Oncology Reports*, **2008**, 20, 203-10	3.5	3
43	Prevalence of BRCA1 and BRCA2 mutations in breast cancer patients from Brazil. *Breast Cancer Research and Treatment*, **2007**, 103, 349-53	4.4	59
42	Correction: functional analysis of BRCA1 M1628V variant. *Journal of Medical Genetics*, **2007**, 44, e78	5.8	1
41	Functional impact of missense variants in BRCA1 predicted by supervised learning. *PLoS Computational Biology*, **2007**, 3, e26	5	47
40	The accidental cancer geneticist: hilário de gouvã and hereditary retinoblastoma. *Cancer Biology and Therapy*, **2007**, 6, 811-3	4.6	2
39	Determination of cancer risk associated with germ line BRCA1 missense variants by functional analysis. *Cancer Research*, **2007**, 67, 1494-501	10.1	98
38	Functional assays for BRCA1 and BRCA2. *International Journal of Biochemistry and Cell Biology*, **2007**, 39, 298-310	5.6	44
37	A systematic genetic assessment of 1,433 sequence variants of unknown clinical significance in the BRCA1 and BRCA2 breast cancer-predisposition genes. *American Journal of Human Genetics*, **2007**, 81, 873-83	11	360
36	DNA damage response: determining the fate of phosphorylated histone H2AX. *Cancer Biology and Therapy*, **2006**, 5, 142-4	4.6	12
35	Cancer risk assessment at the atomic level. *Cancer Research*, **2006**, 66, 1897-9	10.1	14
34	The P1812A and P25T BRCA1 and the 5164del4 BRCA2 mutations: occurrence in high-risk non-Ashkenazi Jews. *Genetic Testing and Molecular Biomarkers*, **2006**, 10, 200-7		6
33	Involvement of the SH3 domain in Ca2+-mediated regulation of Src family kinases. *Biochimie*, **2006**, 88, 905-11	4.6	4
32	Long-term culture of cholangiocytes from liver fibro-granulomatous lesions. *BMC Gastroenterology*, **2006**, 6, 13	3	7
31	Cancer risks in first degree relatives of BRCA1 mutation carriers: effects of mutation and proband disease status. *Journal of Medical Genetics*, **2006**, 43, 424-8	5.8	16
30	Functional implications of BRCA1 for early detection, prevention, and treatment of breast cancer. *Critical Reviews in Eukaryotic Gene Expression*, **2006**, 16, 233-52	1.3	6
29	BRCA1 in breast and ovarian cancer predisposition. *Cancer Letters*, **2005**, 227, 1-7	9.9	20
28	Breast cancer susceptibility and the DNA damage response. *Cancer Control*, **2005**, 12, 127-36	2.2	36

27	Classification of BRCA1 missense variants of unknown clinical significance. *Journal of Medical Genetics*, **2005**, 42, 138-46	5.8	73
26	Structure-based assessment of missense mutations in human BRCA1: implications for breast and ovarian cancer predisposition. *Cancer Research*, **2004**, 64, 3790-7	10.1	92
25	Understanding germ-line mutations in BRCA1. *Cancer Biology and Therapy*, **2004**, 3, 515-20	4.6	30
24	TGF beta1 and PDGF AA override collagen type I inhibition of proliferation in human liver connective tissue cells. *BMC Gastroenterology*, **2004**, 4, 30	3	7
23	Cancer variation associated with the position of the mutation in the BRCA2 gene. *Familial Cancer*, **2004**, 3, 1-10	3	77
22	Integrated evaluation of DNA sequence variants of unknown clinical significance: application to BRCA1 and BRCA2. *American Journal of Human Genetics*, **2004**, 75, 535-44	11	312
21	Specificity in signaling by c-Yes. *Frontiers in Bioscience - Landmark*, **2003**, 8, s185-205	2.8	23
20	BRCA1: the enigma of tissue-specific tumor development. *Trends in Genetics*, **2003**, 19, 312-5	8.5	50
19	Absence of constitutional H2AX gene mutations in 101 hereditary breast cancer families. *Journal of Medical Genetics*, **2003**, 40, e51	5.8	10
18	Participation of BRCA1 in the DNA repair response...via transcription. *Cancer Biology and Therapy*, **2002**, 1, 187-8	4.6	10
17	Mutations in the BRCT domain confer temperature sensitivity to BRCA1 in transcription activation. *Cancer Biology and Therapy*, **2002**, 1, 502-8	4.6	11
16	A naturally occurring allele of BRCA1 coding for a temperature-sensitive mutant protein. *Cancer Biology and Therapy*, **2002**, 1, 497-501	4.6	15
15	Functional analysis of BRCA1 C-terminal missense mutations identified in breast and ovarian cancer families. *Human Molecular Genetics*, **2001**, 10, 353-60	5.6	123
14	BRCA1: exploring the links to transcription. *Trends in Biochemical Sciences*, **2000**, 25, 469-74	10.3	75
13	BRCA1 can stimulate gene transcription by a unique mechanism. *EMBO Reports*, **2000**, 1, 260-5	6.5	16
12	A nuclear function for the tumor suppressor BRCA1. *Histology and Histopathology*, **2000**, 15, 299-307	1.4	6
11	BRCA1 regulates p53-dependent gene expression. *Proceedings of the National Academy of Sciences of the United States of America*, **1998**, 95, 2302-6	11.5	317
10	Yeast-based assays for detection and characterization of mutations in BRCA1. *Breast Disease*, **1998**, 10, 61-70	1.6	15

9	Common BRCA1 variants and transcriptional activation. *American Journal of Human Genetics*, **1997**, 61, 761-2	11	32
8	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, 13595-9	11.5	391
7	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, 149-55	2.6	2
6	Interaction of human liver connective tissue cells, skin fibroblasts and smooth muscle cells with collagen gels. *Hepatology*, **1987**, 7, 665-71	11.2	5
5	In vitro formation of fibrous septa by liver connective tissue cells. *In Vitro Cellular & Developmental Biology*, **1987**, 23, 10-4		8
4	Establishment of a continuous cell line from fibrotic schistosomal granulomas in mice livers. *In Vitro Cellular and Developmental Biology - Plant*, **1985**, 21, 382-90	2.3	61
3	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, 231-8	3.5	14
2	Polygenic Risk Modelling for Prediction of Epithelial Ovarian Cancer Risk		1
1	Combining genome-wide studies of breast, prostate, ovarian and endometrial cancers maps cross-cancer susceptibility loci and identifies new genetic associations		2