## Melissa A Brown

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Caution: Plasmid DNA topology affects luciferase assay reproducibility and outcomes. BioTechniques, 2019, 67, 94-96.	0.8	5
2	Towards controlled terminology for reporting germline cancer susceptibility variants: an ENIGMA report. Journal of Medical Genetics, 2019, 56, 347-357.	1.5	32
3	MicroRNA-196a is regulated by ER and is a prognostic biomarker in ER+ breast cancer. British Journal of Cancer, 2019, 120, 621-632.	2.9	29
4	Non-Coding Variants in BRCA1 and BRCA2 Genes: Potential Impact on Breast and Ovarian Cancer Predisposition. Cancers, 2018, 10, 453.	1.7	14
5	MiR-29b-1-5p is altered in BRCA1 mutant tumours and is a biomarker in basal-like breast cancer. Oncotarget, 2018, 9, 33577-33588.	0.8	15
6	<i>BRCA1</i> and <i>BRCA2</i> 5′ noncoding region variants identified in breast cancer patients alter promoter activity and protein binding. Human Mutation, 2018, 39, 2025-2039.	1.1	15
7	TRPC1 is a differential regulator of hypoxia-mediated events and Akt signaling in PTEN-deficient breast cancer cells. Journal of Cell Science, 2017, 130, 2292-2305.	1.2	69
8	Long Noncoding RNAs CUPID1 and CUPID2 Mediate Breast Cancer Risk at 11q13 by Modulating the Response to DNA Damage. American Journal of Human Genetics, 2017, 101, 255-266.	2.6	77
9	Long-range regulators of the lncRNA <i>HOTAIR</i> enhance its prognostic potential in breast cancer. Human Molecular Genetics, 2016, 25, 3269-3283.	1.4	58
10	The calcium pump plasma membrane Ca2+-ATPase 2 (PMCA2) regulates breast cancer cell proliferation and sensitivity to doxorubicin. Scientific Reports, 2016, 6, 25505.	1.6	53
11	The voltage gated Ca2+-channel Cav3.2 and therapeutic responses in breast cancer. Cancer Cell International, 2016, 16, 24.	1.8	34
12	Non-coding RNAs in Mammary Gland Development and Disease. Advances in Experimental Medicine and Biology, 2016, 886, 121-153.	0.8	25
13	No association between HPV positive breast cancer and expression of human papilloma viral transcripts. Scientific Reports, 2015, 5, 18081.	1.6	21
14	Methylome sequencing in triple-negative breast cancer reveals distinct methylation clusters with prognostic value. Nature Communications, 2015, 6, 5899.	5.8	162
15	Fine-Scale Mapping of the 5q11.2 Breast Cancer Locus Reveals at Least Three Independent Risk Variants Regulating MAP3K1. American Journal of Human Genetics, 2015, 96, 5-20.	2.6	76
16	Consequences of germline variation disrupting the constitutional translational initiation codon start sites of <i>MLH1</i> and <i>BRCA2</i> : Use of potential alternative start sites and implications for predicting variant pathogenicity. Molecular Carcinogenesis, 2015, 54, 513-522.	1.3	14
17	Comprehensive annotation of splice junctions supports pervasive alternative splicing at the BRCA1 locus: a report from the ENIGMA consortium. Human Molecular Genetics, 2014, 23, 3666-3680.	1.4	96
18	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	5.8	105

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19	Comparison of mRNA Splicing Assay Protocols across Multiple Laboratories: Recommendations for Best Practice in Standardized Clinical Testing. Clinical Chemistry, 2014, 60, 341-352.	1.5	95
20	Multifactorial Likelihood Assessment of BRCA1 and BRCA2 Missense Variants Confirms That BRCA1:c.122A>G(p.His41Arg) Is a Pathogenic Mutation. PLoS ONE, 2014, 9, e86836.	1.1	17
21	Longâ€range transcriptional regulation of breast cancer genes. Genes Chromosomes and Cancer, 2013, 52, 113-125.	1.5	7
22	Functional Variants at the 11q13 Risk Locus for Breast Cancer Regulate Cyclin D1 Expression through Long-Range Enhancers. American Journal of Human Genetics, 2013, 92, 489-503.	2.6	201
23	BRCA1 R1699Q variant displaying ambiguous functional abrogation confers intermediate breast and ovarian cancer risk. Journal of Medical Genetics, 2012, 49, 525-532.	1.5	97
24	Protein arginine methyltransferase 6-dependent gene expression and splicing: association with breast cancer outcomes. Endocrine-Related Cancer, 2012, 19, 509-526.	1.6	37
25	eLCR: electrochemical detection of single DNA base changes via Ligase Chain Reaction. Chemical Communications, 2012, 48, 12014.	2.2	38
26	Androgen receptor expression predicts breast cancer survival: the role of genetic and epigenetic events. BMC Cancer, 2012, 12, 132.	1.1	51
27	A guide for functional analysis of <i>BRCA1</i> variants of uncertain significance. Human Mutation, 2012, 33, 1526-1537.	1.1	117
28	Identification of fifteen novel germline variants in the <i>BRCA1</i> 3′UTR reveals a variant in a breast cancer case that introduces a functional <i>miR-103</i> target site. Human Mutation, 2012, 33, 1665-1675.	1.1	49
29	Expression and Function of the Protein Tyrosine Phosphatase Receptor J (PTPRJ) in Normal Mammary Epithelial Cells and Breast Tumors. PLoS ONE, 2012, 7, e40742.	1.1	22
30	Analysis of Brca1-deficient mouse mammary glands reveals reciprocal regulation of Brca1 and c-kit. Oncogene, 2011, 30, 1597-1607.	2.6	26
31	SNORD-host RNA <i>Zfas1</i> is a regulator of mammary development and a potential marker for breast cancer. Rna, 2011, 17, 878-891.	1.6	321
32	Splicing and multifactorial analysis of intronic BRCA1 and BRCA2 sequence variants identifies clinically significant splicing aberrations up to 12 nucleotides from the intron/exon boundary. Human Mutation, 2011, 32, 678-687.	1.1	74
33	ORAI1-Mediated Calcium Influx in Lactation and in Breast Cancer. Molecular Cancer Therapeutics, 2011, 10, 448-460.	1.9	188
34	p53-Dependent BRCA1 Nuclear Export Controls Cellular Susceptibility to DNA Damage. Cancer Research, 2011, 71, 5546-5557.	0.4	72
35	Constitutional Methylation of the <i>BRCA1</i> Promoter Is Specifically Associated with <i>BRCA1</i> Mutation-Associated Pathology in Early-Onset Breast Cancer. Cancer Prevention Research, 2011, 4, 23-33.	0.7	147
36	Identification and functional analysis of novel BRCA1 transcripts, including mouse Brca1-Iris and human pseudo-BRCA1. Breast Cancer Research and Treatment, 2010, 119, 239-247.	1.1	15

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37	Detection of splicing aberrations caused by BRCA1 and BRCA2 sequence variants encoding missense substitutions: implications for prediction of pathogenicity. Human Mutation, 2010, 31, E1484-E1505.	1.1	86
38	Effect of BRCA2 sequence variants predicted to disrupt exonic splice enhancers on BRCA2transcripts. BMC Medical Genetics, 2010, 11, 80.	2.1	25
39	Identification and Characterization of a Novel Melanoma Tumor Suppressor Gene on Human Chromosome 6q21. Clinical Cancer Research, 2009, 15, 797-803.	3.2	19
40	Classifying <i>MLH1</i> and <i>MSH2</i> variants using bioinformatic prediction, splicing assays, segregation, and tumor characteristics. Human Mutation, 2009, 30, 757-770.	1.1	60
41	A novel synthetic adjuvant enhances dendritic cell function. Immunology, 2009, 128, e582-8.	2.0	31
42	Aberrant luminal progenitors as the candidate target population for basal tumor development in BRCA1 mutation carriers. Nature Medicine, 2009, 15, 907-913.	15.2	1,261
43	Colocalisation of predicted exonic splicing enhancers in BRCA2 with reported sequence variants. Breast Cancer Research and Treatment, 2008, 110, 227-234.	1.1	15
44	Targeted disruption of Brca1 in restricted compartments of the mouse mammary epithelia. Breast Cancer Research and Treatment, 2008, 112, 237-241.	1.1	8
45	Localization of plasma membrane and secretory calcium pumps in the mammary gland. Biochemical and Biophysical Research Communications, 2008, 369, 977-981.	1.0	74
46	Dynamic interactions between the promoter and terminator regions of the mammalian <i>BRCA1</i> gene. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 5160-5165.	3.3	127
47	Posttranscriptional Regulation of the Breast Cancer Susceptibility Gene BRCA1 by the RNA Binding Protein HuR. Cancer Research, 2008, 68, 9469-9478.	0.4	49
48	BRCA1 and BRCA2 Missense Variants of High and Low Clinical Significance Influence Lymphoblastoid Cell Line Post-Irradiation Gene Expression. PLoS Genetics, 2008, 4, e1000080.	1.5	12
49	Clinical Classification of <i>BRCA1 </i> and <i>BRCA2 </i> DNA Sequence Variants: The Value of Cytokeratin Profiles and Evolutionary Analysis—A Report From the kConFab Investigators. Journal of Clinical Oncology, 2008, 26, 1657-1663.	0.8	72
50	Pre-mRNA splicing aberrations and cancer. Frontiers in Bioscience - Landmark, 2008, 13, 1090.	3.0	31
51	Identification of BRCA1 missense substitutions that confer partial functional activity: potential moderate risk variants?. Breast Cancer Research, 2007, 9, R82.	2.2	58
52	Regulation ofBRCA1messenger RNA stability in human epithelial cell lines and during cell cycle progression. FEBS Letters, 2007, 581, 3435-3442.	1.3	9
53	Prediction of BRCA1 and BRCA2 mutation status using post-irradiation assays of lymphoblastoid cell lines is compromised by inter-cell-line phenotypic variability. Breast Cancer Research and Treatment, 2007, 104, 257-266.	1.1	8
54	Disruption of BRCA1 function results in telomere lengthening and increased anaphase bridge formation in immortalized cell lines. Genes Chromosomes and Cancer, 2006, 45, 277-289.	1.5	37

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55	Genetic and Histopathologic Evaluation of BRCA1 and BRCA2 DNA Sequence Variants of Unknown Clinical Significance. Cancer Research, 2006, 66, 2019-2027.	0.4	153
56	Method for the generation and cultivation of functional three-dimensional mammary constructs without exogenous extracellular matrix. Cell and Tissue Research, 2005, 320, 207-210.	1.5	32
57	Roles of heterogeneous nuclear ribonucleoproteins A and B in cell proliferation. Journal of Cell Science, 2005, 118, 3173-3183.	1.2	102
58	Identification of two evolutionarily conserved and functional regulatory elements in intron 2 of the human BRCA1 gene. Genomics, 2005, 86, 316-328.	1.3	31
59	Evolutionary conservation analysis increases the colocalization of predicted exonic splicing enhancers in the BRCA1gene with missense sequence changes and in-frame deletions, but not polymorphisms. Breast Cancer Research, 2005, 7, R929-39.	2.2	24
60	Brca1 inactivation induces p27Kip1-dependent cell cycle arrest and delayed development in the mouse mammary gland. Oncogene, 2004, 23, 6136-6145.	2.6	18
61	MMTV-trBrca1 mice display strain-dependent abnormalities in vaginal development. International Journal of Developmental Biology, 2004, 48, 675-678.	0.3	5
62	GermlineBRCA1 promoter deletions in UK and Australian familial breast cancer patients: Identification of a novel deletion consistent withBRCA1:?BRCA1 recombination. Human Mutation, 2002, 19, 435-442.	1.1	32
63	Expression of a truncated Brca1 protein delays lactational mammary development in transgenic mice. Transgenic Research, 2002, 11, 467-478.	1.3	26
64	Gene replacement with the human BRCA1 locus: tissue specific expression and rescue of embryonic lethality in mice. Oncogene, 2000, 19, 4085-4090.	2.6	23
65	Identification of a C/G polymorphism in the promoter region of the BRCA1 gene and its use as a marker for rapid detection of promoter deletions. British Journal of Cancer, 1999, 79, 759-763.	2.9	8
66	Tumor Suppressor Genes and Human Cancer. Advances in Genetics, 1997, 36, 45-135.	0.8	30
67	Studies on inherited cancers: Outcomes and challenges of 25 years. Trends in Genetics, 1997, 13, 202-206.	2.9	18
68	Mutations and alternative splicing of theBRCA1 gene in UK breast/ovarian cancer families. , 1997, 18, 102-110.		43
69	Distinct transcription start sites generate two forms of BRCA1 mRNA. Human Molecular Genetics, 1995, 4, 2259-2264.	1.4	99
70	Leukemia inhibitory factor (LIF) infusion stimulates skeletal muscle regeneration after injury: Injured muscle expresses lif mRNA. Journal of the Neurological Sciences, 1994, 123, 108-113.	0.3	124
71	Towards cloning the familial breast-ovarian cancer gene on chromosome 17. Current Opinion in Genetics and Development, 1994, 4, 439-445.	1.5	6
72	Alternatively spliced RNAs encode several isoforms of CD46 (MCP), a regulator of complement activation. Immunogenetics, 1991, 33, 335-344.	1.2	78

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73	Deletion mapping and expression in Escherichia coli of the large genomic segment of a birnavirus. Virology, 1987, 161, 145-152.	1.1	207
74	Opacity genes in Neisseria gonorrhoeae: Control of phase and antigenic variation. Cell, 1986, 47, 61-71.	13.5	470