Nicola Miller

List of Publications by Year
in descending order

101 papers	12,210 citations	57681 46 h-index	42259 96 g-index
104 all docs	104 docs citations	104 times ranked	19380 citing authors

#	Article	IF	Citations
1	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	13.7	1,099
2	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	9.4	960
3	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	2.6	711
4	Circulating microRNAs as Novel Minimally Invasive Biomarkers for Breast Cancer. Annals of Surgery, 2010, 251, 499-505.	2.1	600
5	Associations of Breast Cancer Risk Factors With Tumor Subtypes: A Pooled Analysis From the Breast Cancer Association Consortium Studies. Journal of the National Cancer Institute, 2011, 103, 250-263.	3.0	596
6	Breast Cancer Risk Genes â€" Association Analysis in More than 113,000 Women. New England Journal of Medicine, 2021, 384, 428-439.	13.9	532
7	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. Nature Genetics, 2015, 47, 373-380.	9.4	513
8	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.	9.4	493
9	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	3.0	428
10	MicroRNA signatures predict oestrogen receptor, progesterone receptor and HER2/neureceptor status in breast cancer. Breast Cancer Research, 2009, 11, R27.	2.2	375
11	Genome-wide association studies identify four ER negativeâ€"specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	9.4	374
12	Systemic miRNA-195 Differentiates Breast Cancer from Other Malignancies and Is a Potential Biomarker for Detecting Noninvasive and Early Stage Disease. Oncologist, 2010, 15, 673-682.	1.9	295
13	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
14	Potential role of mesenchymal stem cells (MSCs) in the breast tumour microenvironment: stimulation of epithelial to mesenchymal transition (EMT). Breast Cancer Research and Treatment, 2010, 124, 317-326.	1.1	270
15	Identification of suitable endogenous control genes for microRNA gene expression analysis in human breast cancer. BMC Molecular Biology, 2008, 9, 76.	3.0	229
16	MiRNAs as biomarkers and therapeutic targets in cancer. Current Opinion in Pharmacology, 2010, 10, 543-550.	1.7	222
17	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
18	MicroRNA expression profiling to identify and validate reference genes for relative quantification in colorectal cancer. BMC Cancer, 2010, 10, 173.	1.1	193

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19	Differential miRNA Expression in Omental Adipose Tissue and in the Circulation of Obese Patients Identifies Novel Metabolic Biomarkers. Journal of Clinical Endocrinology and Metabolism, 2011, 96, E846-E850.	1.8	190
20	Role of microRNAs in obesity and the metabolic syndrome. Obesity Reviews, 2010, 11, 354-361.	3.1	185
21	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	1.5	174
22	MicroRNAs as Prognostic Indicators and Therapeutic Targets: Potential Effect on Breast Cancer Management. Clinical Cancer Research, 2008, 14, 360-365.	3.2	150
23	A 3â€²-untranslated region KRAS variant and triple-negative breast cancer: a case-control and genetic analysis. Lancet Oncology, The, 2011, 12, 377-386.	5.1	130
24	Bilateral breast cancer: analysis of incidence, outcome, survival and disease characteristics. Breast Cancer Research and Treatment, 2011, 126, 131-140.	1.1	130
25	Dysregulated miR-183 inhibits migration in breast cancer cells. BMC Cancer, 2010, 10, 502.	1.1	121
26	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	9.4	120
27	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	5.8	105
28	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	3.0	99
29	Fine-Scale Mapping of the FGFR2 Breast Cancer Risk Locus: Putative Functional Variants Differentially Bind FOXA1 and E2F1. American Journal of Human Genetics, 2013, 93, 1046-1060.	2.6	98
30	MicroRNA signature analysis in colorectal cancer: identification of expression profiles in stage II tumors associated with aggressive disease. International Journal of Colorectal Disease, 2011, 26, 1415-1422.	1.0	96
31	Identification and Validation of miRNAs as Endogenous Controls for RQ-PCR in Blood Specimens for Breast Cancer Studies. PLoS ONE, 2013, 8, e83718.	1.1	94
32	Identification and Validation of Oncologic miRNA Biomarkers for Luminal A-like Breast Cancer. PLoS ONE, 2014, 9, e87032.	1.1	93
33	A Circulating MicroRNA Signature as a Biomarker for Prostate Cancer in a High Risk Group. Journal of Clinical Medicine, 2015, 4, 1369-1379.	1.0	84
34	Evaluation and validation of candidate endogenous control genes for real-time quantitative PCR studies of breast cancer. BMC Molecular Biology, 2007, 8, 107.	3.0	80
35	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
36	Identification of endogenous control genes for normalisation of real-time quantitative PCR data in colorectal cancer. BMC Molecular Biology, 2010, 11, 12.	3.0	73

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37	Ki-67 as a Prognostic Biomarker in Invasive Breast Cancer. Cancers, 2021, 13, 4455.	1.7	73
38	Gene Expression Analysis of Diagnostic Biopsies Predicts Pathological Response to Neoadjuvant Chemoradiotherapy of Esophageal Cancer. Annals of Surgery, 2009, 250, 729-737.	2.1	71
39	The impact of Oncotype DX testing on breast cancer management and chemotherapy prescribing patterns in a tertiary referral centre. European Journal of Cancer, 2014, 50, 2763-2770.	1.3	71
40	The Therapeutic Potential of MicroRNAs: Disease Modulators and Drug Targets. Pharmaceutical Research, 2011, 28, 3016-3029.	1.7	67
41	miRNA expressions in rectal cancer as predictors of response to neoadjuvant chemoradiation therapy. International Journal of Colorectal Disease, 2013, 28, 247-260.	1.0	65
42	Circulating miRNA Signatures: Promising Prognostic Tools for Cancer. Journal of Clinical Oncology, 2010, 28, e573-e574.	0.8	62
43	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	3.0	56
44	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. Human Molecular Genetics, 2014, 23, 6096-6111.	1.4	53
45	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	2.9	52
46	Comparison of 6q25 Breast Cancer Hits from Asian and European Genome Wide Association Studies in the Breast Cancer Association Consortium (BCAC). PLoS ONE, 2012, 7, e42380.	1.1	51
47	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	1.1	49
48	Relationship between Circulating and Tissue microRNAs in a Murine Model of Breast Cancer. PLoS ONE, 2012, 7, e50459.	1.1	44
49	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	2.2	43
50	Mismatch repair protein expression in colorectal cancer. Journal of Gastrointestinal Oncology, 2013, 4, 397-408.	0.6	42
51	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	1.4	40
52	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. Human Molecular Genetics, 2015, 24, 285-298.	1.4	38
53	NCOA3 coactivator is a transcriptional target of XBP1 and regulates PERKâ€“eIF2Î±â€“ATF4 signalling in breast cancer. Oncogene, 2016, 35, 5860-5871.	2.6	38
54	Low penetrance breast cancer predisposition SNPs are site specific. Breast Cancer Research and Treatment, 2009, 117, 151-159.	1.1	37

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55	Systemic mirnas as potential biomarkers for malignancy. International Journal of Cancer, 2012, 131, 2215-2222.	2.3	37
56	Circulating microRNAs: promising breast cancer Biomarkers. Breast Cancer Research, 2011, 13, 402; author reply 403.	2.2	35
57	11q13 is a susceptibility locus for hormone receptor positive breast cancer. Human Mutation, 2012, 33, 1123-1132.	1.1	35
58	Evaluation of variants in the CHEK2, BRIP1 and PALB2 genes in an Irish breast cancer cohort. Breast Cancer Research and Treatment, 2010, 121, 203-210.	1.1	32
59	A large-scale assessment of two-way SNP interactions in breast cancer susceptibility using 46 450 cases and 42 461 controls from the breast cancer association consortium. Human Molecular Genetics, 2014, 23, 1934-1946.	1.4	32
60	Prospective Assessment of Systemic MicroRNAs as Markers of Response to Neoadjuvant Chemotherapy in Breast Cancer. Cancers, 2020, 12, 1820.	1.7	31
61	The KRAS-Variant Is Associated with Risk of Developing Double Primary Breast and Ovarian Cancer. PLoS ONE, 2012, 7, e37891.	1.1	30
62	MicroRNA Expression Profiles and Breast Cancer Chemotherapy. International Journal of Molecular Sciences, 2021, 22, 10812.	1.8	30
63	A review of expression profiling of circulating microRNAs in men with prostate cancer. BJU International, 2013, 111, 17-21.	1.3	29
64	The Role of MicroRNA as Clinical Biomarkers for Breast Cancer Surgery and Treatment. International Journal of Molecular Sciences, 2021, 22, 8290.	1.8	29
65	Clinical applications of gene expression in colorectal cancer. Journal of Gastrointestinal Oncology, 2013, 4, 144-57.	0.6	28
66	Confirmation of 5p12 As a Susceptibility Locus for Progesterone-Receptorâ€“Positive, Lower Grade Breast Cancer. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 2222-2231.	1.1	27
67	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	2.2	26
68	17q12-21 â€“ The pursuit of targeted therapy in breast cancer. Cancer Treatment Reviews, 2010, 36, 224-229.	3.4	25
69	TheMASProto-oncogene Is Imprinted in Human Breast Tissue. Genomics, 1997, 46, 509-512.	1.3	24
70	Targeted resequencing of the microRNAome and 3â€²UTRome reveals functional germline DNA variants with altered prevalence in epithelial ovarian cancer. Oncogene, 2015, 34, 2125-2137.	2.6	24
71	MicroRNAs in Molecular Classification and Pathogenesis of Breast Tumors. Cancers, 2021, 13, 5332.	1.7	24
72	Estrogen Induces Repression of the Breast Cancer and Salivary Gland Expression Gene in an Estrogen Receptor Î±â€“Dependent Manner. Cancer Research, 2008, 68, 106-114.	0.4	23

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73	Interactions between the estrogen receptor, its cofactors and microRNAs in breast cancer. Breast Cancer Research and Treatment, 2009, 116, 425-432.	1.1	23
74	Clinicopathological response to neoadjuvant therapies and pathological complete response as a biomarker of survival in human epidermal growth factor receptor-2 enriched breast cancer â€“ A retrospective cohort study. Breast, 2021, 59, 67-75.	0.9	22
75	FGF receptor genes and breast cancer susceptibility: results from the Breast Cancer Association Consortium. British Journal of Cancer, 2014, 110, 1088-1100.	2.9	21
76	The TGFBR1*6A/9A polymorphism is not associated with differential risk of breast cancer. Breast Cancer Research and Treatment, 2010, 119, 437-442.	1.1	18
77	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	0.6	18
78	A germline mutation in the BRCA13â€™UTR predicts Stage IV breast cancer. BMC Cancer, 2014, 14, 421.	1.1	14
79	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. Breast Cancer Research, 2014, 16, R51.	2.2	14
80	Inherited variants in the inner centromere protein (INCENP) gene of the chromosomal passenger complex contribute to the susceptibility of ER-negative breast cancer. Carcinogenesis, 2015, 36, 256-271.	1.3	14
81	Topoisomerase 2 Alpha and the Case for Individualized Breast Cancer Therapy. Annals of Surgical Oncology, 2010, 17, 1392-1397.	0.7	12
82	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. Human Molecular Genetics, 2014, 23, 6034-6046.	1.4	12
83	Lobular Breast Cancer in a CDH1 Splice Site Mutation Carrier: Case Report and Review of the Literature. Clinical Breast Cancer, 2014, 14, e47-e51.	1.1	11
84	Estrogen withdrawal, increased breast cancer risk and the KRAS-variant. Cell Cycle, 2015, 14, 2091-2099.	1.3	11
85	The double agents in liquid biopsy: promoter and informant biomarkers of early metastases in breast cancer. Molecular Cancer, 2022, 21, 95.	7.9	11
86	MicroRNA Expression Profiling Predicts Nodal Status and Disease Recurrence in Patients Treated with Curative Intent for Colorectal Cancer. Cancers, 2022, 14, 2109.	1.7	11
87	TOP2A Amplification in the Absence of That of HER-2/neu: Toward Individualization of Chemotherapeutic Practice in Breast Cancer. Oncologist, 2011, 16, 949-955.	1.9	10
88	Systemic microRNAs: novel biomarkers for colorectal and other cancers?. Gut, 2010, 59, 1002-1004.	6.1	9
89	Expression levels of HER2/neu and those of collocated genes at 17q12-21, in breast cancer. Oncology Reports, 2012, 28, 365-9.	1.2	8
90	Investigating the association of rs2910164 with cancer predisposition in an Irish cohort. Endocrine Connections, 2017, 6, 614-624.	0.8	5

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91	mRNA/miRNA correlations in colorectal cancer: novel mechanisms in cancer initiation and progression. International Journal of Colorectal Disease, 2013, 28, 1031-1034.	1.0	4
92	Familial breast cancer genetic testing in the West of Ireland. Irish Journal of Medical Science, 2014, 183, 199-206.	0.8	3
93	Overview of MicroRNA Expression in Predicting Response to Neoadjuvant Therapies in Human Epidermal Growth Receptor-2 Enriched Breast Cancer â€“ A Systematic Review. Breast Cancer: Basic and Clinical Research, 2022, 16, 117822342210866.	0.6	3
94	Association between KRAS rs61764370 and triple-negative breast cancerâ€”a false positive? â€“ Authors' reply. Lancet Oncology, The, 2011, 12, 724.	5.1	1
95	A genetic variant at 12p11 significantly modifies breast cancer risk in a genetically homogenous island population. Breast Cancer Research and Treatment, 2015, 149, 41-47.	1.1	1
96	Diagnostic yield of a custom-designed multi-gene cancer panel in Irish patients with breast cancer. Irish Journal of Medical Science, 2020, 189, 849-864.	0.8	1
97	FOXE1 polymorphism rs965513 predisposes to thyroid cancer in a European cohort. Endocrine Oncology, 2021, 1, 1-8.	0.1	0
98	Harmonising the human biobanking consent process: an Irish experience. HRB Open Research, 0, 4, 96.	0.3	0
99	Harmonising the human biobanking consent process: an Irish experience. HRB Open Research, 2021, 4, 96.	0.3	0
100	Harmonising the human biobanking consent process: an Irish experience. HRB Open Research, 0, 4, 96.	0.3	0
101	A Novel Surrogate Nomogram Capable of Predicting OncotypeDX Recurrence ScoreÂ©. Journal of Personalized Medicine, 2022, 12, 1117.	1.1	0