Kylie L Gorringe

List of Publications by Year
in descending order

100 papers	4,509 citations	117625 34 h-index	114465 63 g-index
103 all docs	103 docs citations	103 times ranked	8002 citing authors

#	Article	IF	Citations
1	CONTRA: copy number analysis for targeted resequencing. Bioinformatics, 2012, 28, 1307-1313.	4.1	308
2	No evidence of clonal somatic genetic alterations in cancer-associated fibroblasts from human breast and ovarian carcinomas. Nature Genetics, 2008, 40, 650-655.	21.4	269
3	IL6-STAT3-HIF Signaling and Therapeutic Response to the Angiogenesis Inhibitor Sunitinib in Ovarian Clear Cell Cancer. Clinical Cancer Research, 2011, 17, 2538-2548.	7.0	217
4	Gender Differences in Publication Output: Towards an Unbiased Metric of Research Performance. PLoS ONE, 2006, 1, e127.	2.5	206
5	An activating Pik3ca mutation coupled with Pten loss is sufficient to initiate ovarian tumorigenesis in mice. Journal of Clinical Investigation, 2012, 122, 553-557.	8.2	174
6	Distinctive patterns of gene expression in premalignant gastric mucosa and gastric cancer. Cancer Research, 2003, 63, 2569-77.	0.9	172
7	High-Resolution Single Nucleotide Polymorphism Array Analysis of Epithelial Ovarian Cancer Reveals Numerous Microdeletions and Amplifications. Clinical Cancer Research, 2007, 13, 4731-4739.	7.0	154
8	Molecular profiling of low grade serous ovarian tumours identifies novel candidate driver genes. Oncotarget, 2015, 6, 37663-37677.	1.8	142
9	Mutational landscape of mucinous ovarian carcinoma and its neoplastic precursors. Genome Medicine, 2015, 7, 87.	8.2	126
10	The molecular origin and taxonomy of mucinous ovarian carcinoma. Nature Communications, 2019, 10, 3935.	12.8	110
11	<i><scp>RNF43</scp></i> is a tumour suppressor gene mutated in mucinous tumours of the ovary. Journal of Pathology, 2013, 229, 469-476.	4.5	102
12	Degenerate Oligonucleotide Primed-Polymerase Chain Reaction-Based Array Comparative Genomic Hybridization for Extensive Amplicon Profiling of Breast Cancers. American Journal of Pathology, 2001, 158, 1623-1631.	3.8	98
13	Identification of Candidate Growth Promoting Genes in Ovarian Cancer through Integrated Copy Number and Expression Analysis. PLoS ONE, 2010, 5, e9983.	2.5	95
14	Amplicon-Dependent CCNE1 Expression Is Critical for Clonogenic Survival after Cisplatin Treatment and Is Correlated with 20q11 Gain in Ovarian Cancer. PLoS ONE, 2010, 5, e15498.	2.5	92
15	Molecular cytogenetic analysis of breast cancer cell lines. British Journal of Cancer, 2000, 83, 1309-1317.	6.4	91
16	Novel regions of chromosomal amplification at 6p21, 5p13, and 12q14 in gastric cancer identified by array comparative genomic hybridization. Genes Chromosomes and Cancer, 2005, 42, 247-259.	2.8	90
17	Ductal Carcinoma In Situ Biology, Biomarkers, and Diagnosis. Frontiers in Oncology, 2017, 7, 248.	2.8	88
18	Loss of heterozygosity: what is it good for?. BMC Medical Genomics, 2015, 8, 45.	1.5	85

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19	Copy Number Analysis Identifies Novel Interactions Between Genomic Loci in Ovarian Cancer. PLoS ONE, 2010, 5, e11408.	2.5	83
20	Mutation and Methylation Analysis of the Chromodomain-Helicase-DNA Binding 5 Gene in Ovarian Cancer. Neoplasia, 2008, 10, 1253-IN32.	5.3	66
21	Relationship of the Breast Ductal Carcinoma <i>In Situ</i> Immune Microenvironment with Clinicopathological and Genetic Features. Clinical Cancer Research, 2017, 23, 5210-5217.	7.0	61
22	Identification of copy number alterations associated with the progression of DCIS to invasive ductal carcinoma. Breast Cancer Research and Treatment, 2012, 133, 889-898.	2.5	60
23	Pre-Invasive Ovarian Mucinous Tumors Are Characterized by <i>CDKN2A</i> and <i>RAS</i> Pathway Aberrations. Clinical Cancer Research, 2012, 18, 5267-5277.	7.0	57
24	Are there any more ovarian tumor suppressor genes? A new perspective using ultra highâ€resolution copy number and loss of heterozygosity analysis. Genes Chromosomes and Cancer, 2009, 48, 931-942.	2.8	56
25	A combination of the immunohistochemical markers CK7 and SATB2 is highly sensitive and specific for distinguishing primary ovarian mucinous tumors from colorectal and appendiceal metastases. Modern Pathology, 2019, 32, 1834-1846.	5.5	54
26	Genomic analysis of lowâ€grade serous ovarian carcinoma to identify key drivers and therapeutic vulnerabilities. Journal of Pathology, 2021, 253, 41-54.	4.5	54
27	Functional Analysis of Genes in Regions Commonly Amplified in High-Grade Serous and Endometrioid Ovarian Cancer. Clinical Cancer Research, 2013, 19, 1411-1421.	7.0	52
28	Breast ductal carcinoma in situ carry mutational driver events representative of invasive breast cancer. Modern Pathology, 2017, 30, 952-963.	5.5	50
29	Therapeutic options for mucinous ovarian carcinoma. Gynecologic Oncology, 2020, 156, 552-560.	1.4	49
30	Molecular analysis of <i>PALB2</i>â€associated breast cancers. Journal of Pathology, 2018, 245, 53-60.	4.5	46
31	Copy number analysis of ductal carcinoma in situ with and without recurrence. Modern Pathology, 2015, 28, 1174-1184.	5.5	40
32	Evidence that both genetic instability and selection contribute to the accumulation of chromosome alterations in cancer. Carcinogenesis, 2005, 26, 923-930.	2.8	39
33	Copy number analysis by low coverage whole genome sequencing using ultra low-input DNA from formalin-fixed paraffin embedded tumor tissue. Genome Medicine, 2016, 8, 121.	8.2	39
34	Ductal carcinoma <i>inÂsitu</i> â€" update on risk assessment and management. Histopathology, 2016, 68, 96-109.	2.9	38
35	Atypical ductal hyperplasia: update on diagnosis, management, and molecular landscape. Breast Cancer Research, 2018, 20, 39.	5.0	38
36	Prevalence of PALB2 mutations in Australian familial breast cancer cases and controls. Breast Cancer Research, 2015, 17, 111.	5.0	36

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37	Prolyl-4-hydroxylase α subunit 2 (P4HA2) expression is a predictor of poor outcome in breast ductal carcinoma in situ (DCIS). British Journal of Cancer, 2018, 119, 1518-1526.	6.4	32
38	Large-scale genomic analysis of ovarian carcinomas. Molecular Oncology, 2009, 3, 157-164.	4.6	31
39	Prognostic significance of cathepsin V (CTSV/CTSL2) in breast ductal carcinoma in situ. Journal of Clinical Pathology, 2020, 73, 76-82.	2.0	31
40	Genetic Analysis of Cancer-Implicated MicroRNA in Ovarian Cancer. Clinical Cancer Research, 2008, 14, 7246-7250.	7.0	29
41	When Is "Type I" Ovarian Cancer Not "Type I"? Indications of an Out-Dated Dichotomy. Frontiers in Oncology, 2018, 8, 654.	2.8	29
42	The clinical and biological significance of HER2 over-expression in breast ductal carcinoma in situ: a large study from a single institution. British Journal of Cancer, 2019, 120, 1075-1082.	6.4	27
43	MicroRNA Genes and Their Target 3′-Untranslated Regions Are Infrequently Somatically Mutated in Ovarian Cancers. PLoS ONE, 2012, 7, e35805.	2.5	27
44	A molecular model for sporadic human aneuploidy. Trends in Genetics, 2006, 22, 218-224.	6.7	26
45	Reevaluation of the BRCA2 truncating allele c.9976A>T (p.Lys3326Ter) in a familial breast cancer context. Scientific Reports, 2015, 5, 14800.	3.3	26
46	Enhanced *GAB2* Expression Is Associated with Improved Survival in High-Grade Serous Ovarian Cancer and Sensitivity to PI3K Inhibition. Molecular Cancer Therapeutics, 2015, 14, 1495-1503.	4.1	26
47	Combined Tumor Sequencing and Case-Control Analyses of RAD51C in Breast Cancer. Journal of the National Cancer Institute, 2019, 111, 1332-1338.	6.3	26
48	The prognostic significance of immune microenvironment in breast ductal carcinoma in situ. British Journal of Cancer, 2020, 122, 1496-1506.	6.4	26
49	Invasion in breast lesions: the role of the epithelial–stroma barrier. Histopathology, 2018, 72, 1075-1083.	2.9	25
50	Exome sequencing of familial high-grade serous ovarian carcinoma reveals heterogeneity for rare candidate susceptibility genes. Nature Communications, 2020, 11, 1640.	12.8	24
51	BARD1 variants are not associated with breast cancer risk in Australian familial breast cancer. Breast Cancer Research and Treatment, 2008, 111, 505-509.	2.5	23
52	Copy Number Aberrations in Benign Serous Ovarian Tumors: A Case for Reclassification?. Clinical Cancer Research, 2011, 17, 7273-7282.	7.0	23
53	Functional and genomic characterization of a xenograft model system for the study of metastasis in triple-negative breast cancer. DMM Disease Models and Mechanisms, 2018, 11, .	2.4	23
54	Thioredoxin-interacting protein is an independent risk stratifier for breast ductal carcinoma in situ. Modern Pathology, 2018, 31, 1807-1815.	5.5	23

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55	Collagen (XI) alpha-1 chain is an independent prognostic factor in breast ductal carcinoma in situ. Modern Pathology, 2019, 32, 1460-1472.	5.5	23
56	Phenotypic characterisation of breast cancer: the role of CDC42. Breast Cancer Research and Treatment, 2017, 164, 317-325.	2.5	22
57	Atypical ductal hyperplasia is a multipotent precursor of breast carcinoma. Journal of Pathology, 2019, 248, 326-338.	4.5	21
58	Refined cut-off for TP53 immunohistochemistry improves prediction of TP53 mutation status in ovarian mucinous tumors: implications for outcome analyses. Modern Pathology, 2021, 34, 194-206.	5.5	21
59	Evaluating the breast cancer predisposition role of rare variants in genes associated with low-penetrance breast cancer risk SNPs. Breast Cancer Research, 2018, 20, 3.	5.0	19
60	Mutations in RECQL are not associated with breast cancer risk in an Australian population. Nature Genetics, 2018, 50, 1346-1348.	21.4	19
61	Legumain is an independent predictor for invasive recurrence in breast ductal carcinoma in situ. Modern Pathology, 2019, 32, 639-649.	5.5	19
62	The genetic architecture of breast papillary lesions as a predictor of progression to carcinoma. Npj Breast Cancer, 2020, 6, 9.	5.2	19
63	Analysis of the Mitogen-activated protein kinase kinase 4 (MAP2K4) tumor suppressor gene in ovarian cancer. BMC Cancer, 2011, 11, 173.	2.6	17
64	Reevaluation of RINT1 as a breast cancer predisposition gene. Breast Cancer Research and Treatment, 2016, 159, 385-392.	2.5	16
65	The prognostic significance of lysosomal protective protein (cathepsin A) in breast ductal carcinoma <i>in situ</i>. Histopathology, 2019, 74, 1025-1035.	2.9	16
66	Molecular comparison of interval and screen-detected breast cancers. Journal of Pathology, 2019, 248, 243-252.	4.5	15
67	Validated biomarker assays confirm that ARID1A loss is confounded with MMR deficiency, CD8+ TIL infiltration, and provides no independent prognostic value in endometriosis-associated ovarian carcinomas. Journal of Pathology, 2022, 256, 388-401.	4.5	15
68	LRH-1 expression patterns in breast cancer tissues are associated with tumour aggressiveness. Oncotarget, 2017, 8, 83626-83636.	1.8	13
69	Clinical and biological roles of Kelch-like family member 7 in breast cancer: a marker of poor prognosis. Breast Cancer Research and Treatment, 2018, 170, 525-533.	2.5	12
70	Investigation of monogenic causes of familial breast cancer: data from the BEACCON case-control study. Npj Breast Cancer, 2021, 7, 76.	5.2	12
71	Geometric characteristics of collagen have independent prognostic significance in breast ductal carcinoma in situ: an image analysis study. Modern Pathology, 2019, 32, 1473-1485.	5.5	11
72	Loss of SMAD4 Is Sufficient to Promote Tumorigenesis in a Model of Dysplastic Barrett's Esophagus. Cellular and Molecular Gastroenterology and Hepatology, 2021, 12, 689-713.	4.5	11

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73	BRCA2 carriers with male breast cancer show elevated tumour methylation. BMC Cancer, 2017, 17, 641.	2.6	10
74	Chemokine (Câ€C motif) receptor 7 (CCR7) associates with the tumour immune microenvironment but not progression in invasive breast carcinoma. Journal of Pathology: Clinical Research, 2017, 3, 105-114.	3.0	9
75	Options for the Treatment of Mucinous Ovarian Carcinoma. Current Treatment Options in Oncology, 2021, 22, 114.	3.0	9
76	Molecular characterization of low-grade serous ovarian carcinoma identifies genomic aberrations according to hormone receptor expression. Npj Precision Oncology, 2022, 6, .	5.4	9
77	Molecular comparison of pure ovarian fibroma with serous benign ovarian tumours. BMC Research Notes, 2020, 13, 349.	1.4	8
78	Highâ€resolution copy number arrays in cancer and the problem of normal genome copy number variation. Genes Chromosomes and Cancer, 2008, 47, 933-938.	2.8	7
79	Evaluation of the association of heterozygous germline variants in NTHL1 with breast cancer predisposition: an international multi-center study of 47,180 subjects. Npj Breast Cancer, 2021, 7, 52.	5.2	7
80	Analysis of KLLN as a high-penetrance breast cancer predisposition gene. Breast Cancer Research and Treatment, 2012, 134, 543-547.	2.5	6
81	Primary mucinous ovarian neoplasms rarely show germ cell histogenesis. Histopathology, 2021, 78, 640-642.	2.9	6
82	The Protein Landscape of Mucinous Ovarian Cancer: Towards a Theranostic. Cancers, 2021, 13, 5596.	3.7	6
83	Evaluating statistical approaches to define clonal origin of tumours using bulk DNA sequencing: context is everything. Genome Biology, 2022, 23, 43.	8.8	6
84	Appraisal of the technologies and review of the genomic landscape of ductal carcinoma in situ of the breast. Breast Cancer Research, 2015, 17, 80.	5.0	5
85	Germline whole exome sequencing of a family with appendiceal mucinous tumours presenting with pseudomyxoma peritonei. BMC Cancer, 2020, 20, 369.	2.6	5
86	The TP53 mutation rate differs in breast cancers that arise in women with high or low mammographic density. Npj Breast Cancer, 2020, 6, 34.	5.2	4
87	Breast cancer risk and the BRCA1 interacting protein CTIP. Breast Cancer Research and Treatment, 2008, 112, 351-352.	2.5	3
88	Genomic Aberrations of BRCA1-Mutated Fallopian Tube Carcinomas. American Journal of Pathology, 2014, 184, 1871-1876.	3.8	2
89	Exploiting sequence similarity to validate the sensitivity of SNP arrays in detecting fine-scaled copy number variations. Bioinformatics, 2010, 26, 1007-1014.	4.1	1
90	Reply to the Baaderâ€"Meinhof phenomenon in ductal carcinoma *in situ* of the breast. Histopathology, 2016, 69, 523-524.	2.9	1

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91	Benign serous ovarian tumour: a redefining moment?. Hereditary Cancer in Clinical Practice, 2012, 10, A83.	1.5	0
92	Abstract LB-348: Identifying novel oncogenes in ovarian cancer using integrative genomics and gene-knock downs. , 2010, , .		0
93	Abstract LB-271: Benign ovarian serous tumors: A redefining moment. , 2011, , .		0
94	Identifying Associations Between Genomic Alterations in Tumors. Methods in Molecular Biology, 2013, 1049, 9-19.	0.9	0
95	Abstract A3: Mucinous ovarian tumors: Are they all the same?. , 2013, , .		0
96	Abstract B22: Genomic and functional analysis of gene amplification in high-grade serous and endometrioid ovarian cancer. , 2013, , .		0
97	Abstract A13: Molecular profiling of low grade serous ovarian tumors. , 2013, , .		0
98	Abstract B08: Genomics analyses of less common epithelial ovarian cancer subtypes.. , 2016, , .		0
99	Genomic Analysis. , 2016, , 83-106.		0
100	Glucagonoma Masquerading as a Mucinous Cancer of the Ovary: Lessons from Cell Biology. , 0, , .		0