Georgina L Ryland

List of Publications by Year in descending order

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48 papers

2,056 citations

430874 18 h-index 254184 43 g-index

52 all docs 52 docs citations

52 times ranked 5227 citing authors

#	Article	IF	CITATIONS
1	CONTRA: copy number analysis for targeted resequencing. Bioinformatics, 2012, 28, 1307-1313.	4.1	308
2	Exome Sequencing Identifies Rare Deleterious Mutations in DNA Repair Genes FANCC and BLM as Potential Breast Cancer Susceptibility Alleles. PLoS Genetics, 2012, 8, e1002894.	3.5	186
3	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
4	Molecular profiling of low grade serous ovarian tumours identifies novel candidate driver genes. Oncotarget, 2015, 6, 37663-37677.	1.8	142
5	Mutational landscape of mucinous ovarian carcinoma and its neoplastic precursors. Genome Medicine, 2015, 7, 87.	8.2	126
6	The molecular origin and taxonomy of mucinous ovarian carcinoma. Nature Communications, 2019, 10, 3935.	12.8	110
7	<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
8	Inferring copy number and genotype in tumour exome data. BMC Genomics, 2014, 15, 732.	2.8	102
9	Loss of heterozygosity: what is it good for?. BMC Medical Genomics, 2015, 8, 45.	1.5	85
10	Analysis of RAD51C germline mutations in high-risk breast and ovarian cancer families and ovarian cancer patients. Human Mutation, 2012, 33, 95-99.	2.5	64
11	Frequent activating STAT3 mutations and novel recurrent genomic abnormalities detected in breast implant-associated anaplastic large cell lymphoma. Oncotarget, 2018, 9, 36126-36136.	1.8	62
12	Multiplexed transcriptome analysis to detect ALK, ROS1 and RET rearrangements in lung cancer. Scientific Reports, 2017, 7, 42259.	3.3	49
13	Therapeutic options for mucinous ovarian carcinoma. Gynecologic Oncology, 2020, 156, 552-560.	1.4	49
14	High dose-rate brachytherapy of localized prostate cancer converts tumors from cold to hot., 2020, 8, e000792.		45
15	A simple consensus approach improves somatic mutation prediction accuracy. Genome Medicine, 2013, 5, 90.	8.2	33
16	Novel genomic findings in multiple myeloma identified through routine diagnostic sequencing. Journal of Clinical Pathology, 2018, 71, 895-899.	2.0	28
17	MicroRNA Genes and Their Target 3′-Untranslated Regions Are Infrequently Somatically Mutated in Ovarian Cancers. PLoS ONE, 2012, 7, e35805.	2.5	27
18	ALLSorts: an RNA-Seq subtype classifier for B-cell acute lymphoblastic leukemia. Blood Advances, 2022, 6, 4093-4097.	5.2	25

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19	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
20	JAFFAL: detecting fusion genes with long-read transcriptome sequencing. Genome Biology, 2022, 23, 10.	8.8	20
21	Enhancer retargeting of <i>CDX2</i> and <i>UBTF::ATXN7L3</i> define a subtype of high-risk B-progenitor acute lymphoblastic leukemia. Blood, 2022, 139, 3519-3531.	1.4	20
22	Molecular Mechanisms of Disease Progression in Primary Cutaneous Diffuse Large B-Cell Lymphoma, Leg Type during Ibrutinib Therapy. International Journal of Molecular Sciences, 2018, 19, 1758.	4.1	19
23	ASXL1 c.1934dup;p.Gly646Trpfs*12—a true somatic alteration requiring a new approach. Blood Cancer Journal, 2017, 7, 656.	6.2	18
24	Incidental detection of germline variants of potential clinical significance by massively parallel sequencing in haematological malignancies. Journal of Clinical Pathology, 2018, 71, 84-87.	2.0	18
25	Analysis of the Mitogen-activated protein kinase kinase 4 (MAP2K4) tumor suppressor gene in ovarian cancer. BMC Cancer, 2011, 11, 173.	2.6	17
26	Bioinformatics Pipelines for Targeted Resequencing and Whole-Exome Sequencing of Human and Mouse Genomes: A Virtual Appliance Approach for Instant Deployment. PLoS ONE, 2014, 9, e95217.	2.5	17
27	CNspector: a web-based tool for visualisation and clinical diagnosis of copy number variation from next generation sequencing. Scientific Reports, 2019, 9, 6426.	3.3	17
28	Utility of clinical comprehensive genomic characterization for diagnostic categorization in patients presenting with hypocellular bone marrow failure syndromes. Haematologica, 2020, 106, 64-73.	3.5	14
29	A synonymous GATA2 variant underlying familial myeloid malignancy with striking intrafamilial phenotypic variability. British Journal of Haematology, 2020, 190, e297-e301.	2.5	14
30	Sensitive NPM1 Mutation Quantitation in Acute Myeloid Leukemia Using Ultradeep Next-Generation Sequencing in the Diagnostic Laboratory. Archives of Pathology and Laboratory Medicine, 2018, 142, 606-612.	2.5	8
31	Detection of clinically relevant early genomic lesions in Bâ€cell malignancies from circulating tumour <scp>DNA</scp> using a single hybridisationâ€based next generation sequencing assay. British Journal of Haematology, 2018, 183, 146-149.	2.5	8
32	Adaptive reprogramming of NK cells in X-linked lymphoproliferative syndrome. Blood, 2018, 131, 699-702.	1.4	5
33	Inotuzumab ozogamicin resistance associated with a novel <i>CD22</i> truncating mutation in a case of Bâ€acute lymphoblastic leukaemia. British Journal of Haematology, 2020, 191, 123-126.	2.5	5
34	T Cell Landscape of Immune Aplastic Anemia Reveals a Convergent Antigen-Specific Signature. Blood, 2019, 134, 108-108.	1.4	5
35	Canary: an atomic pipeline for clinical amplicon assays. BMC Bioinformatics, 2017, 18, 555.	2.6	4
36	Genomic Aberrations of BRCA1-Mutated Fallopian Tube Carcinomas. American Journal of Pathology, 2014, 184, 1871-1876.	3.8	2

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37	Comprehensive genomic characterization dissects the complex biology of a case of synchronous Burkitt lymphoma and myeloid malignancy with shared hematopoietic ancestry. Leukemia and Lymphoma, 2018, 59, 992-995.	1.3	2
38	Severe chemotherapy toxicity in a 10-year-old with T-acute lymphoblastic lymphoma harboring biallelic FANCM variants. Leukemia and Lymphoma, 2020, 61, 1257-1259.	1.3	2
39	T cell receptor beta locus sequencing early post-allogeneic stem cell transplant identifies patients at risk of initial and recurrent cytomegalovirus infection. Bone Marrow Transplantation, 2021, 56, 2582-2590.	2.4	2
40	Methylâ€CpG binding domain 4, DNA glycosylase (<scp>MBD4</scp>)â€associated neoplasia syndrome associated with a homozygous missense variant in <i>MBD4</i> : Expansion of an emerging phenotype. British Journal of Haematology, 2022, , .	2.5	2
41	Cryptic molecular lesion in acute promyelocytic leukemia with negative initial FISH. Leukemia and Lymphoma, 2021, 62, 3060-3062.	1.3	1
42	Clinical Determinants of T-Cell Receptor Diversity after Allogeneic Hematopoietic Stem Cell Transplantation for Acute Myeloid Leukemia. Blood, 2019, 134, 1997-1997.	1.4	1
43	Direct evidence of a clonal and tumor-directed T cell response to prostate cancer brachytherapy Journal of Clinical Oncology, 2019, 37, 22-22.	1.6	1
44	Abstract B08: Genomics analyses of less common epithelial ovarian cancer subtypes , 2016, , .		0
45	Providing Diagnoses in Bone Marrow Failure Syndromes through Multimodal Comprehensive Genomic Evaluation and Multidisciplinary Care: The Melbourne Genomics Health Alliance Bone Marrow Failure Flagship. Blood, 2018, 132, 3867-3867.	1.4	0
46	Cnspectorx - Copy Number Assessment at a Genome Level from Targeted Sequence Data Optimized for Hematological Malignancy. Blood, 2019, 134, 3378-3378.	1.4	0
47	Longitudinal Genomic Characterization Using Cell-Free DNA in Patients with Idiopathic Aplastic Anemia. Blood, 2020, 136, 5-6.	1.4	0
48	580â€High dose-rate brachytherapy of localized prostate cancer converts tumors from cold to hot. , 2020, , .		0