Georgina L Ryland

List of Publications by Year
in descending order

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48	2,056	430874	254184
papers	citations	18 h-index	43 g-index

52	52	52	5227
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	JAFFAL: detecting fusion genes with long-read transcriptome sequencing. Genome Biology, 2022, 23, 10.	8.8	20
2	Enhancer retargeting of CDX2 and UBTF::ATXN7L3 define a subtype of high-risk B-progenitor acute lymphoblastic leukemia. Blood, 2022, 139, 3519-3531.	1.4	20
3	Methylâ€CpG binding domain 4, DNA glycosylase (<scp>MBD4</scp>)â€associated neoplasia syndrome associated with a homozygous missense variant in MBD4 : Expansion of an emerging phenotype. British Journal of Haematology, 2022, , .	2.5	2
4	ALLSorts: an RNA-Seq subtype classifier for B-cell acute lymphoblastic leukemia. Blood Advances, 2022, 6, 4093-4097.	5.2	25
5	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
6	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
7	Cryptic molecular lesion in acute promyelocytic leukemia with negative initial FISH. Leukemia and Lymphoma, 2021, 62, 3060-3062.	1.3	1
8	Therapeutic options for mucinous ovarian carcinoma. Gynecologic Oncology, 2020, 156, 552-560.	1.4	49
9	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
10	A synonymous GATA2 variant underlying familial myeloid malignancy with striking intrafamilial phenotypic variability. British Journal of Haematology, 2020, 190, e297-e301.	2.5	14
11	High dose-rate brachytherapy of localized prostate cancer converts tumors from cold to hot. , 2020, 8, e000792.		45
12	Inotuzumab ozogamicin resistance associated with a novel CD22 truncating mutation in a case of Bâ€acute lymphoblastic leukaemia. British Journal of Haematology, 2020, 191, 123-126.	2.5	5
13	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
14	Longitudinal Genomic Characterization Using Cell-Free DNA in Patients with Idiopathic Aplastic Anemia. Blood, 2020, 136, 5-6.	1.4	0
15	580â€...High dose-rate brachytherapy of localized prostate cancer converts tumors from cold to hot. , 2020, , .		0
16	The molecular origin and taxonomy of mucinous ovarian carcinoma. Nature Communications, 2019, 10, 3935.	12.8	110
17	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
18	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

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19	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
20	T Cell Landscape of Immune Aplastic Anemia Reveals a Convergent Antigen-Specific Signature. Blood, 2019, 134, 108-108.	1.4	5
21	Cnspectorx - Copy Number Assessment at a Genome Level from Targeted Sequence Data Optimized for Hematological Malignancy. Blood, 2019, 134, 3378-3378.	1.4	0
22	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
23	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
24	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
25	Adaptive reprogramming of NK cells in X-linked lymphoproliferative syndrome. Blood, 2018, 131, 699-702.	1.4	5
26	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
27	Novel genomic findings in multiple myeloma identified through routine diagnostic sequencing. Journal of Clinical Pathology, 2018, 71, 895-899.	2.0	28
28	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
29	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
30	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
31	Multiplexed transcriptome analysis to detect ALK, ROS1 and RET rearrangements in lung cancer. Scientific Reports, 2017, 7, 42259.	3.3	49
32	ASXL1 c.1934dup;p.Gly646Trpfs*12â€"a true somatic alteration requiring a new approach. Blood Cancer Journal, 2017, 7, 656.	6.2	18
33	Canary: an atomic pipeline for clinical amplicon assays. BMC Bioinformatics, 2017, 18, 555.	2.6	4
34	Abstract B08: Genomics analyses of less common epithelial ovarian cancer subtypes.. , 2016, , .		0
35	Mutational landscape of mucinous ovarian carcinoma and its neoplastic precursors. Genome Medicine, 2015, 7, 87.	8.2	126
36	Molecular profiling of low grade serous ovarian tumours identifies novel candidate driver genes. Oncotarget, 2015, 6, 37663-37677.	1.8	142

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37	Loss of heterozygosity: what is it good for?. BMC Medical Genomics, 2015, 8, 45.	1.5	85
38	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
39	Inferring copy number and genotype in tumour exome data. BMC Genomics, 2014, 15, 732.	2.8	102
40	Genomic Aberrations of BRCA1-Mutated Fallopian Tube Carcinomas. American Journal of Pathology, 2014, 184, 1871-1876.	3.8	2
41	A simple consensus approach improves somatic mutation prediction accuracy. Genome Medicine, 2013, 5, 90.	8.2	33
42	<scp>RNF43</scp> is a tumour suppressor gene mutated in mucinous tumours of the ovary. Journal of Pathology, 2013, 229, 469-476.	4.5	102
43	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
44	CONTRA: copy number analysis for targeted resequencing. Bioinformatics, 2012, 28, 1307-1313.	4.1	308
45	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
46	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
47	MicroRNA Genes and Their Target 3â€²-Untranslated Regions Are Infrequently Somatically Mutated in Ovarian Cancers. PLoS ONE, 2012, 7, e35805.	2.5	27
48	Analysis of the Mitogen-activated protein kinase kinase 4 (MAP2K4) tumor suppressor gene in ovarian cancer. BMC Cancer, 2011, 11, 173.	2.6	17