Darragh G Mcart

List of Publications by Year
in descending order

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Version: 2024-02-01

60 papers	5,879 citations	201575 27 h-index	138417 58 g-index
61 all docs	61 docs citations	61 times ranked	12158 citing authors

#	Article	IF	Citations
1	QuPath: Open source software for digital pathology image analysis. Scientific Reports, 2017, 7, 16878.	1.6	3,854
2	Digital pathology and image analysis in tissue biomarker research. Methods, 2014, 70, 59-73.	1.9	162
3	Challenging the Cancer Molecular Stratification Dogma: Intratumoral Heterogeneity Undermines Consensus Molecular Subtypes and Potential Diagnostic Value in Colorectal Cancer. Clinical Cancer Research, 2016, 22, 4095-4104.	3.2	135
4	Development and Validation of a 28-gene Hypoxia-related Prognostic Signature for Localized Prostate Cancer. EBioMedicine, 2018, 31, 182-189.	2.7	132
5	EphA2 Expression Is a Key Driver of Migration and Invasion and a Poor Prognostic Marker in Colorectal Cancer. Clinical Cancer Research, 2016, 22, 230-242.	3.2	97
6	AXL Is a Key Regulator of Inherent and Chemotherapy-Induced Invasion and Predicts a Poor Clinical Outcome in Early-Stage Colon Cancer. Clinical Cancer Research, 2014, 20, 164-175.	3.2	95
7	Validation of Next Generation Sequencing Technologies in Comparison to Current Diagnostic Gold Standards for BRAF, EGFR and KRAS Mutational Analysis. PLoS ONE, 2013, 8, e69604.	1.1	94
8	Validation of a Metastatic Assay using biopsies to improve risk stratification in patients with prostate cancer treated with radical radiation therapy. Annals of Oncology, 2018, 29, 215-222.	0.6	86
9	Integrated tumor identification and automated scoring minimizes pathologist involvement and provides new insights to key biomarkers in breast cancer. Laboratory Investigation, 2018, 98, 15-26.	1.7	81
10	Cancer-cell intrinsic gene expression signatures overcome intratumoural heterogeneity bias in colorectal cancer patient classification. Nature Communications, 2017, 8, 15657.	5.8	70
11	Prognostic and therapeutic relevance of FLIP and procaspase-8 overexpression in non-small cell lung cancer. Cell Death and Disease, 2013, 4, e951-e951.	2.7	59
12	The prognostic significance of the aberrant extremes of p53 immunophenotypes in breast cancer. Histopathology, 2014, 65, 340-352.	1.6	59
13	Prospective patient stratification into robust cancerâ€cell intrinsic subtypes from colorectal cancer biopsies. Journal of Pathology, 2018, 245, 19-28.	2.1	49
14	Transcriptional Subtyping and CD8 Immunohistochemistry Identifies Patients With Stage II and III Colorectal Cancer With Poor Prognosis Who Benefit From Adjuvant Chemotherapy. JCO Precision Oncology, 2018, 2018, 1-15.	1.5	45
15	Immune status is prognostic for poor survival in colorectal cancer patients and is associated with tumour hypoxia. British Journal of Cancer, 2020, 123, 1280-1288.	2.9	45
16	Automated Tumour Recognition and Digital Pathology Scoring Unravels New Role for PD-L1 in Predicting Good Outcome in ER-/HER2+ Breast Cancer. Journal of Oncology, 2018, 2018, 1-14.	0.6	44
17	Automated tumor analysis for molecular profiling in lung cancer. Oncotarget, 2015, 6, 27938-27952.	0.8	43
18	Comprehensive molecular pathology analysis of small bowel adenocarcinoma reveals novel targets with potential for clinical utility. Oncotarget, 2015, 6, 20863-20874.	0.8	41

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19	Quantification of HER2 heterogeneity in breast cancerâ€“implications for identification of sub-dominant clones for personalised treatment. Scientific Reports, 2016, 6, 23383.	1.6	38
20	TBX2 represses CST6 resulting in uncontrolled legumain activity to sustain breast cancer proliferation: a novel cancer-selective target pathway with therapeutic opportunities.. Oncotarget, 2014, 5, 1609-1620.	0.8	37
21	Epidermal growth factor receptor immunohistochemistry: new opportunities in metastatic colorectal cancer. Journal of Translational Medicine, 2015, 13, 217.	1.8	36
22	Transcriptional upregulation of c-MET is associated with invasion and tumor budding in colorectal cancer. Oncotarget, 2016, 7, 78932-78945.	0.8	36
23	Immune-Derived PD-L1 Gene Expression Defines a Subgroup of Stage II/III Colorectal Cancer Patients with Favorable Prognosis Who May Be Harmed by Adjuvant Chemotherapy. Cancer Immunology Research, 2016, 4, 582-591.	1.6	35
24	Building a â€˜Repository of Scienceâ€™: The importance ofÂintegrating biobanks within molecular pathology programmes. European Journal of Cancer, 2016, 67, 191-199.	1.3	31
25	Modelling the comet assay. Biochemical Society Transactions, 2009, 37, 914-917.	1.6	30
26	Identification of Candidate Small-Molecule Therapeutics to Cancer by Gene-Signature Perturbation in Connectivity Mapping. PLoS ONE, 2011, 6, e16382.	1.1	30
27	Analysis of wntless (WLS) expression in gastric, ovarian, and breast cancers reveals a strong association with HER2 overexpression. Modern Pathology, 2015, 28, 428-436.	2.9	27
28	Ultrasoundâ€Powered Implants: A Critical Review of Piezoelectric Material Selection and Applications. Advanced Healthcare Materials, 2021, 10, e2100986.	3.9	27
29	Comet sensitivity in assessing DNA damage and repair in different cell cycle stages. Mutagenesis, 2010, 25, 299-303.	1.0	25
30	cudaMap: a GPU accelerated program for gene expression connectivity mapping. BMC Bioinformatics, 2013, 14, 305.	1.2	25
31	QUADrATiC: scalable gene expression connectivity mapping for repurposing FDA-approved therapeutics. BMC Bioinformatics, 2016, 17, 198.	1.2	25
32	Natural killer-like signature observed post therapy in locally advanced rectal cancer is a determinant of pathological response and improved survival. Modern Pathology, 2017, 30, 1287-1298.	2.9	23
33	Depletion of DNMT1 in differentiated human cells highlights key classes of sensitive genes and an interplay with polycomb repression. Epigenetics and Chromatin, 2018, 11, 12.	1.8	18
34	Defining the molecular evolution of extrauterine high grade serous carcinoma. Gynecologic Oncology, 2019, 155, 305-317.	0.6	17
35	A Novel Role for Cathepsin S as a Potential Biomarker in Triple Negative Breast Cancer. Journal of Oncology, 2019, 2019, 1-12.	0.6	16
36	Connectivity Mapping for Candidate Therapeutics Identification Using Next Generation Sequencing RNA-Seq Data. PLoS ONE, 2013, 8, e66902.	1.1	16

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37	PICan: An integromics framework for dynamic cancer biomarker discovery. Molecular Oncology, 2015, 9, 1234-1240.	2.1	15
38	Stratified analysis reveals chemokine-like factor (CKLF) as a potential prognostic marker in the MSI-immune consensus molecular subtype CMS1 of colorectal cancer. Oncotarget, 2016, 7, 36632-36644.	0.8	15
39	The prognostic value of the stem-like group in colorectal cancer using a panel of immunohistochemistry markers. Oncotarget, 2015, 6, 12763-12773.	0.8	14
40	Glucose transporter 1 expression as a marker of prognosis in oesophageal adenocarcinoma. Oncotarget, 2018, 9, 18518-18528.	0.8	13
41	Systematic random sampling of the comet assay. Mutagenesis, 2009, 24, 373-378.	1.0	12
42	RALB GTPase: a critical regulator of DR5 expression and TRAIL sensitivity in KRAS mutant colorectal cancer. Cell Death and Disease, 2020, 11, 930.	2.7	12
43	samExploreR: exploring reproducibility and robustness of RNA-seq results based on SAM files. Bioinformatics, 2016, 32, 3345-3347.	1.8	11
44	Evolutionary genetic algorithm identifies IL2RB as a potential predictive biomarker for immune-checkpoint therapy in colorectal cancer. NAR Genomics and Bioinformatics, 2021, 3, lqab016.	1.5	10
45	Embracing an integromic approach to tissue biomarker research in cancer: Perspectives and lessons learned. Briefings in Bioinformatics, 2017, 18, bbw044.	3.2	9
46	KRAS mutant colorectal cancer gene signatures identified angiotensin II receptor blockers as potential therapies. Oncotarget, 2017, 8, 3206-3225.	0.8	9
47	Bcl-xL as a poor prognostic biomarker and predictor of response to adjuvant chemotherapy specifically in BRAF-mutant stage II and III colon cancer. Oncotarget, 2018, 9, 13834-13847.	0.8	9
48	p16 as a prognostic indicator in ovarian/tubal highâ€grade serous carcinoma. Histopathology, 2016, 68, 615-618.	1.6	8
49	Molecular classification of non-invasive breast lesions for personalised therapy and chemoprevention. Oncotarget, 2015, 6, 43244-43254.	0.8	8
50	ACE: A Workbench Using Evolutionary Genetic Algorithms for Analyzing Association in TCGA. Cancer Research, 2019, 79, 2072-2075.	0.4	6
51	Delivering a researchâ€enabled multistakeholder partnership for enhanced patient care at a population level: The Northern Ireland Comprehensive Cancer Program. Cancer, 2016, 122, 664-673.	2.0	5
52	IHC-based subcellular quantification provides new insights into prognostic relevance of FLIP and procaspase-8 in non-small-cell lung cancer. Cell Death Discovery, 2017, 3, 17050.	2.0	5
53	Repurposing FDA approved drugs as radiosensitizers for treating hypoxic prostate cancer. BMC Urology, 2021, 21, 96.	0.6	5
54	Clinically Actionable Insights into Initial and Matched Recurrent Glioblastomas to Inform Novel Treatment Approaches. Journal of Oncology, 2019, 2019, 1-14.	0.6	4

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55	Impact of Variable RNA-Sequencing Depth on Gene Expression Signatures and Target Compound Robustness: Case Study Examining Brain Tumor (Glioma) Disease Progression. JCO Precision Oncology, 2018, 2, 1-17.	1.5	3
56	Modelling the comet assay. BMC Systems Biology, 2007, 1, .	3.0	1
57	A strong correlation between expression of Wntless and of human epidermal growth factor receptor 2 in gastric, ovarian, and breast cancers suggests a novel-signalling pathway involving NFÎºB and STAT3. Lancet, The, 2013, 381, S106.	6.3	1
58	NUQA: Estimating Cancer Spatial and Temporal Heterogeneity and Evolution through Alignment-Free Methods. Molecular Biology and Evolution, 2019, 36, 2883-2889.	3.5	1
59	Patient stratification into robust cancer-cell intrinsic subtypes from colorectal cancer biopsies may inform prospective clinical trials. European Journal of Surgical Oncology, 2018, 44, S49.	0.5	0
60	Prostate cancer heterogeneity assessment with multi-regional sampling and alignment-free methods. NAR Genomics and Bioinformatics, 2020, 2, lqaa062.	1.5	0