

Darragh G Mcart

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

59
papers

2,797
citations

25
h-index

52
g-index

61
ext. papers

4,381
ext. citations

6.4
avg, IF

4.68
L-index

#	Paper	IF	Citations
59	Evolutionary genetic algorithm identifies as a potential predictive biomarker for immune-checkpoint therapy in colorectal cancer. <i>NAR Genomics and Bioinformatics</i> , 2021 , 3, lqab016	3.7	3
58	Ultrasound-Powered Implants: A Critical Review of Piezoelectric Material Selection and Applications. <i>Advanced Healthcare Materials</i> , 2021 , 10, e2100986	10.1	4
57	Repurposing FDA approved drugs as radiosensitizers for treating hypoxic prostate cancer. <i>BMC Urology</i> , 2021 , 21, 96	2.2	1
56	RALB GTPase: a critical regulator of DR5 expression and TRAIL sensitivity in KRAS mutant colorectal cancer. <i>Cell Death and Disease</i> , 2020 , 11, 930	9.8	8
55	Prostate cancer heterogeneity assessment with multi-regional sampling and alignment-free methods. <i>NAR Genomics and Bioinformatics</i> , 2020 , 2, lqaa062	3.7	
54	Immune status is prognostic for poor survival in colorectal cancer patients and is associated with tumour hypoxia. <i>British Journal of Cancer</i> , 2020 , 123, 1280-1288	8.7	22
53	Defining the molecular evolution of extrauterine high grade serous carcinoma. <i>Gynecologic Oncology</i> , 2019 , 155, 305-317	4.9	8
52	NUQA: Estimating Cancer Spatial and Temporal Heterogeneity and Evolution through Alignment-Free Methods. <i>Molecular Biology and Evolution</i> , 2019 , 36, 2883-2889	8.3	1
51	A Novel Role for Cathepsin S as a Potential Biomarker in Triple Negative Breast Cancer. <i>Journal of Oncology</i> , 2019 , 2019, 3980273	4.5	10
50	ACE: A Workbench Using Evolutionary Genetic Algorithms for Analyzing Association in TCGA. <i>Cancer Research</i> , 2019 , 79, 2072-2075	10.1	2
49	Clinically Actionable Insights into Initial and Matched Recurrent Glioblastomas to Inform Novel Treatment Approaches. <i>Journal of Oncology</i> , 2019 , 2019, 4878547	4.5	3
48	Prospective patient stratification into robust cancer-cell intrinsic subtypes from colorectal cancer biopsies. <i>Journal of Pathology</i> , 2018 , 245, 19-28	9.4	37
47	Integrated tumor identification and automated scoring minimizes pathologist involvement and provides new insights to key biomarkers in breast cancer. <i>Laboratory Investigation</i> , 2018 , 98, 15-26	5.9	47
46	Development and Validation of a 28-gene Hypoxia-related Prognostic Signature for Localized Prostate Cancer. <i>EBioMedicine</i> , 2018 , 31, 182-189	8.8	67
45	Validation of a Metastatic Assay using biopsies to improve risk stratification in patients with prostate cancer treated with radical radiation therapy. <i>Annals of Oncology</i> , 2018 , 29, 215-222	10.3	27
44	Depletion of DNMT1 in differentiated human cells highlights key classes of sensitive genes and an interplay with polycomb repression. <i>Epigenetics and Chromatin</i> , 2018 , 11, 12	5.8	16
43	as a poor prognostic biomarker and predictor of response to adjuvant chemotherapy specifically in -mutant stage II and III colon cancer. <i>Oncotarget</i> , 2018 , 9, 13834-13847	3.3	4

42	Glucose transporter 1 expression as a marker of prognosis in oesophageal adenocarcinoma. <i>Oncotarget</i> , 2018 , 9, 18518-18528	3.3	12
41	Transcriptional subtyping and CD8 immunohistochemistry identifies poor prognosis stage II/III colorectal cancer patients who benefit from adjuvant chemotherapy. <i>JCO Precision Oncology</i> , 2018 , 2018,	3.6	31
40	Automated Tumour Recognition and Digital Pathology Scoring Unravels New Role for PD-L1 in Predicting Good Outcome in ER-/HER2+ Breast Cancer. <i>Journal of Oncology</i> , 2018 , 2018, 2937012	4.5	25
39	Impact of Variable RNA-Sequencing Depth on Gene Expression Signatures and Target Compound Robustness: Case Study Examining Brain Tumor (Glioma) Disease Progression. <i>JCO Precision Oncology</i> , 2018 , 2,	3.6	3
38	Natural killer-like signature observed post therapy in locally advanced rectal cancer is a determinant of pathological response and improved survival. <i>Modern Pathology</i> , 2017 , 30, 1287-1298	9.8	14
37	Cancer-cell intrinsic gene expression signatures overcome intratumoural heterogeneity bias in colorectal cancer patient classification. <i>Nature Communications</i> , 2017 , 8, 15657	17.4	45
36	Embracing an integromic approach to tissue biomarker research in cancer: Perspectives and lessons learned. <i>Briefings in Bioinformatics</i> , 2017 , 18, 634-646	13.4	6
35	IHC-based subcellular quantification provides new insights into prognostic relevance of FLIP and procaspase-8 in non-small-cell lung cancer. <i>Cell Death Discovery</i> , 2017 , 3, 17050	6.9	3
34	QuPath: Open source software for digital pathology image analysis. <i>Scientific Reports</i> , 2017 , 7, 16878	4.9	1369
33	KRAS mutant colorectal cancer gene signatures identified angiotensin II receptor blockers as potential therapies. <i>Oncotarget</i> , 2017 , 8, 3206-3225	3.3	7
32	EphA2 Expression Is a Key Driver of Migration and Invasion and a Poor Prognostic Marker in Colorectal Cancer. <i>Clinical Cancer Research</i> , 2016 , 22, 230-242	12.9	73
31	QUADrATiC: scalable gene expression connectivity mapping for repurposing FDA-approved therapeutics. <i>BMC Bioinformatics</i> , 2016 , 17, 198	3.6	21
30	Transcriptional upregulation of c-MET is associated with invasion and tumor budding in colorectal cancer. <i>Oncotarget</i> , 2016 , 7, 78932-78945	3.3	31
29	Stratified analysis reveals chemokine-like factor (CKLF) as a potential prognostic marker in the MSI-immune consensus molecular subtype CMS1 of colorectal cancer. <i>Oncotarget</i> , 2016 , 7, 36632-36644	3.3	10
28	samExploreR: exploring reproducibility and robustness of RNA-seq results based on SAM files. <i>Bioinformatics</i> , 2016 , 32, 3345-3347	7.2	7
27	p16 as a prognostic indicator in ovarian/tubal high-grade serous carcinoma. <i>Histopathology</i> , 2016 , 68, 615-8	7.3	7
26	Quantification of HER2 heterogeneity in breast cancer-implications for identification of sub-dominant clones for personalised treatment. <i>Scientific Reports</i> , 2016 , 6, 23383	4.9	26
25	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. <i>Cancer Immunology Research</i> , 2016 , 4, 582-91	12.5	31

24	Challenging the Cancer Molecular Stratification Dogma: Intratumoral Heterogeneity Undermines Consensus Molecular Subtypes and Potential Diagnostic Value in Colorectal Cancer. <i>Clinical Cancer Research</i> , 2016 , 22, 4095-104	12.9	88
23	Building a Repository of Science: The importance of integrating biobanks within molecular pathology programmes. <i>European Journal of Cancer</i> , 2016 , 67, 191-199	7.5	26
22	Delivering a research-enabled multistakeholder partnership for enhanced patient care at a population level: The Northern Ireland Comprehensive Cancer Program. <i>Cancer</i> , 2016 , 122, 664-73	6.4	3
21	PICan: An integromics framework for dynamic cancer biomarker discovery. <i>Molecular Oncology</i> , 2015 , 9, 1234-40	7.9	13
20	Analysis of wntless (WLS) expression in gastric, ovarian, and breast cancers reveals a strong association with HER2 overexpression. <i>Modern Pathology</i> , 2015 , 28, 428-36	9.8	25
19	Epidermal growth factor receptor immunohistochemistry: new opportunities in metastatic colorectal cancer. <i>Journal of Translational Medicine</i> , 2015 , 13, 217	8.5	30
18	Automated tumor analysis for molecular profiling in lung cancer. <i>Oncotarget</i> , 2015 , 6, 27938-52	3.3	30
17	The prognostic value of the stem-like group in colorectal cancer using a panel of immunohistochemistry markers. <i>Oncotarget</i> , 2015 , 6, 12763-73	3.3	14
16	Comprehensive molecular pathology analysis of small bowel adenocarcinoma reveals novel targets with potential for clinical utility. <i>Oncotarget</i> , 2015 , 6, 20863-74	3.3	31
15	Molecular classification of non-invasive breast lesions for personalised therapy and chemoprevention. <i>Oncotarget</i> , 2015 , 6, 43244-54	3.3	6
14	The prognostic significance of the aberrant extremes of p53 immunophenotypes in breast cancer. <i>Histopathology</i> , 2014 , 65, 340-52	7.3	54
13	AXL is a key regulator of inherent and chemotherapy-induced invasion and predicts a poor clinical outcome in early-stage colon cancer. <i>Clinical Cancer Research</i> , 2014 , 20, 164-75	12.9	83
12	Digital pathology and image analysis in tissue biomarker research. <i>Methods</i> , 2014 , 70, 59-73	4.6	120
11	TBX2 represses CST6 resulting in uncontrolled legumain activity to sustain breast cancer proliferation: a novel cancer-selective target pathway with therapeutic opportunities. <i>Oncotarget</i> , 2014 , 5, 1609-20	3.3	28
10	cudaMap: a GPU accelerated program for gene expression connectivity mapping. <i>BMC Bioinformatics</i> , 2013 , 14, 305	3.6	21
9	Prognostic and therapeutic relevance of FLIP and procaspase-8 overexpression in non-small cell lung cancer. <i>Cell Death and Disease</i> , 2013 , 4, e951	9.8	48
8	Validation of next generation sequencing technologies in comparison to current diagnostic gold standards for BRAF, EGFR and KRAS mutational analysis. <i>PLoS ONE</i> , 2013 , 8, e69604	3.7	86
7	Connectivity Mapping for Candidate Therapeutics Identification Using Next Generation Sequencing RNA-Seq Data. <i>PLoS ONE</i> , 2013 , 8, e66902	3.7	13

6	Identification of candidate small-molecule therapeutics to cancer by gene-signature perturbation in connectivity mapping. <i>PLoS ONE</i> , 2011 , 6, e16382	3.7	29
5	Comet sensitivity in assessing DNA damage and repair in different cell cycle stages. <i>Mutagenesis</i> , 2010 , 25, 299-303	2.8	21
4	Systematic random sampling of the comet assay. <i>Mutagenesis</i> , 2009 , 24, 373-8	2.8	10
3	Modelling the comet assay. <i>Biochemical Society Transactions</i> , 2009 , 37, 914-7	5.1	27
2	Modelling the comet assay. <i>BMC Systems Biology</i> , 2007 , 1,	3.5	1
1	QuPath: Open source software for digital pathology image analysis		8