

Benjamin Barwick

List of Publications by Year in descending order

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Version: 2024-02-01

66
papers

2,818
citations

236833

25
h-index

189801

50
g-index

69
all docs

69
docs citations

69
times ranked

5819
citing authors

#	ARTICLE	IF	CITATIONS
1	PDZ Proteins SCRIB and DLG1 Regulate Myeloma Cell Surface CD86 Expression, Growth, and Survival. <i>Molecular Cancer Research</i> , 2022, 20, 1122-1136.	1.5	3
2	Multivariant Transcriptome Analysis Identifies Modules and Hub Genes Associated with Poor Outcomes in Newly Diagnosed Multiple Myeloma Patients. <i>Cancers</i> , 2022, 14, 2228.	1.7	3
3	Î² adrenergic signaling regulates hematopoietic stem and progenitor cell commitment and therapy sensitivity in multiple myeloma. <i>Haematologica</i> , 2022, 107, 2226-2231.	1.7	3
4	YAP1 Expression in SCLC Defines a Distinct Subtype With T-cellâ€œInflamed Phenotype. <i>Journal of Thoracic Oncology</i> , 2021, 16, 464-476.	0.5	93
5	Chromatin Accessibility Identifies Regulatory Elements Predictive of Gene Expression and Disease Outcome in Multiple Myeloma. <i>Clinical Cancer Research</i> , 2021, 27, 3178-3189.	3.2	15
6	Venetoclax sensitivity in multiple myeloma is associated with B-cell gene expression. <i>Blood</i> , 2021, 137, 3604-3615.	0.6	44
7	Acetylation of KLF5 maintains EMT and tumorigenicity to cause chemoresistant bone metastasis in prostate cancer. <i>Nature Communications</i> , 2021, 12, 1714.	5.8	70
8	Oncolytic herpes simplex virus infects myeloma cells inÂvitro and inÂvivo. <i>Molecular Therapy - Oncolytics</i> , 2021, 20, 519-531.	2.0	8
9	Ten-eleven translocation protein 1 modulates medulloblastoma progression. <i>Genome Biology</i> , 2021, 22, 125.	3.8	3
10	The Murine MHC Class II Super Enhancer <i>IA/IE-SE</i> Contains a Functionally Redundant CTCF-Binding Component and a Novel Element Critical for Maximal Expression. <i>Journal of Immunology</i> , 2021, 206, 2221-2232.	0.4	3
11	Wholeâ€œgenome analysis of TET dioxygenase function in regulatory T cells. <i>EMBO Reports</i> , 2021, 22, e52716.	2.0	19
12	Aberrant Extrafollicular B Cells, Immune Dysfunction, Myeloid Inflammation, and MyD88-Mutant Progenitors Precede Waldenstrom Macroglobulinemia. <i>Blood Cancer Discovery</i> , 2021, 2, 600-615.	2.6	15
13	P-073: PDZ proteins, SCRIB and DLG1, regulate CD86 surface expression, myeloma growth, and survival. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2021, 21, S79.	0.2	0
14	Functional Genomic and Immune Response Characterization of PTEN Loss: Therapeutic Implications for Myeloma. <i>Blood</i> , 2021, 138, 1612-1612.	0.6	0
15	Disrupting Ectopic Super-Enhancers to Treat Multiple Myeloma. <i>Blood</i> , 2021, 138, 1593-1593.	0.6	0
16	Disrupting Mitohormesis As a Novel Therapeutic Strategy for Multiple Myeloma (MM) Including Those with High Risk Disease and Proteasome Inhibitor Resistance. <i>Blood</i> , 2021, 138, 722-722.	0.6	3
17	BRAF Mutations and Inflammatory Gene Expression in Myeloma Cells from Patients with Renal Dysfunction. <i>Blood</i> , 2021, 138, 1624-1624.	0.6	0
18	Functional Oncogenomic and Immune Response Landscape for Genes Recurrently Mutated in Myeloma. <i>Blood</i> , 2021, 138, 1589-1589.	0.6	0

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19	Mitochondrial Electron Transport Chain Inhibition Promotes Resistance to Proteasome Inhibitors in Multiple Myeloma. <i>Blood</i> , 2021, 138, 1611-1611.	0.6	0
20	PD-1 Expression during Acute Infection Is Repressed through an LSD1-Blimp-1 Axis. <i>Journal of Immunology</i> , 2020, 204, 449-458.	0.4	24
21	CD28 Regulates Metabolic Fitness for Long-Lived Plasma Cell Survival. <i>Cell Reports</i> , 2020, 31, 107815.	2.9	32
22	We need CD38 STAT-JAK. <i>Blood</i> , 2020, 136, 2246-2248.	0.6	0
23	Epigenetically heterogeneous tumor cells direct collective invasion through filopodia-driven fibronectin micropatterning. <i>Science Advances</i> , 2020, 6, eaaz6197.	4.7	41
24	Downregulation of PA28 \pm induces proteasome remodeling and results in resistance to proteasome inhibitors in multiple myeloma. <i>Blood Cancer Journal</i> , 2020, 10, 125.	2.8	7
25	Electron transport chain activity is a predictor and target for venetoclax sensitivity in multiple myeloma. <i>Nature Communications</i> , 2020, 11, 1228.	5.8	62
26	Increased DNA Repair Gene Expression Correlates with MYC Expression and Inferior Progression-Free Survival in Multiple Myeloma Patients. <i>Blood</i> , 2020, 136, 48-49.	0.6	1
27	Chromatin Accessibility Identifies Regulatory Elements Predictive of Oncogene Expression in Multiple Myeloma. <i>Blood</i> , 2020, 136, 31-32.	0.6	0
28	Epigenetic programming underpins B cell dysfunction in human SLE. <i>Nature Immunology</i> , 2019, 20, 1071-1082.	7.0	142
29	Genetic heterogeneity within collective invasion packs drives leader and follower cell phenotypes. <i>Journal of Cell Science</i> , 2019, 132, .	1.2	23
30	Cell of Origin and Genetic Alterations in the Pathogenesis of Multiple Myeloma. <i>Frontiers in Immunology</i> , 2019, 10, 1121.	2.2	103
31	Multiple myeloma immunoglobulin lambda translocations portend poor prognosis. <i>Nature Communications</i> , 2019, 10, 1911.	5.8	109
32	Integrated phosphoproteomics and transcriptional classifiers reveal hidden RAS signaling dynamics in multiple myeloma. <i>Blood Advances</i> , 2019, 3, 3214-3227.	2.5	19
33	Gain of Chromosome 1q is associated with early progression in multiple myeloma patients treated with lenalidomide, bortezomib, and dexamethasone. <i>Blood Cancer Journal</i> , 2019, 9, 94.	2.8	104
34	The Role of Proteasome Activator PA28 \pm in Multiple Myeloma. <i>Blood</i> , 2019, 134, 5499-5499.	0.6	0
35	Multiple Myeloma Epigenetic Programming Prognostic of Outcome Converges with Loci Reprogrammed in Relapsed/Refractory Disease. <i>Blood</i> , 2019, 134, 858-858.	0.6	2
36	EZH2 Represses the B Cell Transcriptional Program and Regulates Antibody-Secreting Cell Metabolism and Antibody Production. <i>Journal of Immunology</i> , 2018, 200, 1039-1052.	0.4	99

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37	Galactic Cosmic Radiation Induces Persistent Epigenome Alterations Relevant to Human Lung Cancer. <i>Scientific Reports</i> , 2018, 8, 6709.	1.6	26
38	Plasma cell differentiation is controlled by multiple cell division-coupled epigenetic programs. <i>Nature Communications</i> , 2018, 9, 1698.	5.8	93
39	14-3-3 σ binds the proteasome, limits proteolytic function and enhances sensitivity to proteasome inhibitors. <i>Leukemia</i> , 2018, 32, 744-751.	3.3	12
40	The Histone Demethylase LSD1 Regulates B Cell Proliferation and Plasmablast Differentiation. <i>Journal of Immunology</i> , 2018, 201, 2799-2811.	0.4	43
41	B cell activation and plasma cell differentiation are inhibited by de novo DNA methylation. <i>Nature Communications</i> , 2018, 9, 1900.	5.8	94
42	Immunoglobulin Lambda Translocations Identify Poor Outcome and IMiD Resistance in Multiple Myeloma and Co-Occur with Hyperdiploidy. <i>Blood</i> , 2018, 132, 405-405.	0.6	3
43	Whole Genome DNA Methylation Analysis of Compass Identifies Biomarkers of Multiple Myeloma Survival. <i>Blood</i> , 2018, 132, 3174-3174.	0.6	0
44	A Role for Syntenin-1 in Multiple Myeloma Cell Survival. <i>Blood</i> , 2018, 132, 1008-1008.	0.6	0
45	Conserved Region C Functions To Regulate PD-1 Expression and Subsequent CD8 T Cell Memory. <i>Journal of Immunology</i> , 2017, 198, 205-217.	0.4	24
46	MAX is an epigenetic sensor of 5-carboxylcytosine and is altered in multiple myeloma. <i>Nucleic Acids Research</i> , 2017, 45, 2396-2407.	6.5	69
47	LSD1 protects against hippocampal and cortical neurodegeneration. <i>Nature Communications</i> , 2017, 8, 805.	5.8	55
48	CD86 regulates myeloma cell survival. <i>Blood Advances</i> , 2017, 1, 2307-2319.	2.5	15
49	ATAC-seq on biobanked specimens defines a unique chromatin accessibility structure in naïve SLE B cells. <i>Scientific Reports</i> , 2016, 6, 27030.	1.6	88
50	Factors affecting the persistence of drug-induced reprogramming of the cancer methylome. <i>Epigenetics</i> , 2016, 11, 273-287.	1.3	8
51	Plasma cell differentiation is coupled to division-dependent DNA hypomethylation and gene regulation. <i>Nature Immunology</i> , 2016, 17, 1216-1225.	7.0	124
52	Genome-wide CIITA-binding profile identifies sequence preferences that dictate function versus recruitment. <i>Nucleic Acids Research</i> , 2015, 43, 3128-3142.	6.5	28
53	Common distal elements orchestrate CIITA isoform-specific expression in multiple cell types. <i>Genes and Immunity</i> , 2014, 15, 543-555.	2.2	16
54	Global DNA Methylation Remodeling Accompanies CD8 T Cell Effector Function. <i>Journal of Immunology</i> , 2013, 191, 3419-3429.	0.4	167

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55	Wnt signaling in triple negative breast cancer is associated with metastasis. BMC Cancer, 2013, 13, 537.	1.1	210
56	Differential Activation of Wnt- β -Catenin Pathway in Triple Negative Breast Cancer Increases MMP7 in a PTEN Dependent Manner. PLoS ONE, 2013, 8, e77425.	1.1	61
57	A heterozygous <i>IDH1</i> ^{R132H/WT} mutation induces genome-wide alterations in DNA methylation. Genome Research, 2012, 22, 2339-2355.	2.4	157
58	Age-associated DNA methylation in pediatric populations. Genome Research, 2012, 22, 623-632.	2.4	326
59	Molecular characterisation of formalin-fixed paraffin-embedded (FFPE) breast tumour specimens using a custom 512-gene breast cancer bead array-based platform. British Journal of Cancer, 2011, 105, 1574-1581.	2.9	15
60	Prostate cancer genes associated with TMPRSS2-ERG gene fusion and prognostic of biochemical recurrence in multiple cohorts. British Journal of Cancer, 2010, 102, 570-576.	2.9	61
61	Heterozygosity for Pten Promotes Tumorigenesis in a Mouse Model of Medulloblastoma. PLoS ONE, 2010, 5, e10849.	1.1	40
62	DNA Extraction from Formalin-Fixed, Paraffin-Embedded Tissue. Cold Spring Harbor Protocols, 2009, 2009, pdb.prot5138-pdb.prot5138.	0.2	28
63	PROTEIN-CODING AND MICRORNA BIOMARKER GENE PANELS PREDICTIVE OF CLINICAL RECURRENCE IN PROSTATE CANCER. Journal of Urology, 2009, 181, 776-776.	0.2	1
64	Discovery of a novel set of prostate cancer-related genes associated with the prognostically important TMPRSS2:ERG fusion gene. Journal of Clinical Oncology, 2008, 26, 5056-5056.	0.8	0
65	SF1126, a Novel PI3K Inhibitor Results in Downstream Inhibition of the PI3K Axis and Displays Sequence Specific Synergy When Combined with Bortezomib in Multiple Myeloma Cells. Blood, 2008, 112, 5167-5167.	0.6	2
66	Invited Keynote Talk: Data Mining and Statistical Methods for Analyzing Microarray Experiments. , 2008, , 444-444.		0