

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	Age-associated DNA methylation in pediatric populations. <i>Genome Research</i> , 2012, 22, 623-632.	2.4	326
2	Wnt signaling in triple negative breast cancer is associated with metastasis. <i>BMC Cancer</i> , 2013, 13, 537.	1.1	210
3	Global DNA Methylation Remodeling Accompanies CD8 T Cell Effector Function. <i>Journal of Immunology</i> , 2013, 191, 3419-3429.	0.4	167
4	A heterozygous <i>IDH1</i> ^{R132H/WT} mutation induces genome-wide alterations in DNA methylation. <i>Genome Research</i> , 2012, 22, 2339-2355.	2.4	157
5	Epigenetic programming underpins B cell dysfunction in human SLE. <i>Nature Immunology</i> , 2019, 20, 1071-1082.	7.0	142
6	Plasma cell differentiation is coupled to division-dependent DNA hypomethylation and gene regulation. <i>Nature Immunology</i> , 2016, 17, 1216-1225.	7.0	124
7	Multiple myeloma immunoglobulin lambda translocations portend poor prognosis. <i>Nature Communications</i> , 2019, 10, 1911.	5.8	109
8	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
9	Cell of Origin and Genetic Alterations in the Pathogenesis of Multiple Myeloma. <i>Frontiers in Immunology</i> , 2019, 10, 1121.	2.2	103
10	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
11	B cell activation and plasma cell differentiation are inhibited by de novo DNA methylation. <i>Nature Communications</i> , 2018, 9, 1900.	5.8	94
12	Plasma cell differentiation is controlled by multiple cell division-coupled epigenetic programs. <i>Nature Communications</i> , 2018, 9, 1698.	5.8	93
13	YAP1 Expression in SCLC Defines a Distinct Subtype With T-cell "Inflamed Phenotype. <i>Journal of Thoracic Oncology</i> , 2021, 16, 464-476.	0.5	93
14	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
15	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
16	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
17	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
18	Prostate cancer genes associated with TMPRSS2-ERG gene fusion and prognostic of biochemical recurrence in multiple cohorts. <i>British Journal of Cancer</i> , 2010, 102, 570-576.	2.9	61

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19	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
20	LSD1 protects against hippocampal and cortical neurodegeneration. Nature Communications, 2017, 8, 805.	5.8	55
21	Venetoclax sensitivity in multiple myeloma is associated with B-cell gene expression. Blood, 2021, 137, 3604-3615.	0.6	44
22	The Histone Demethylase LSD1 Regulates B Cell Proliferation and Plasmablast Differentiation. Journal of Immunology, 2018, 201, 2799-2811.	0.4	43
23	Epigenetically heterogeneous tumor cells direct collective invasion through filopodia-driven fibronectin micropatterning. Science Advances, 2020, 6, eaaz6197.	4.7	41
24	Heterozygosity for Pten Promotes Tumorigenesis in a Mouse Model of Medulloblastoma. PLoS ONE, 2010, 5, e10849.	1.1	40
25	CD28 Regulates Metabolic Fitness for Long-Lived Plasma Cell Survival. Cell Reports, 2020, 31, 107815.	2.9	32
26	DNA Extraction from Formalin-Fixed, Paraffin-Embedded Tissue. Cold Spring Harbor Protocols, 2009, 2009, pdb.prot5138-pdb.prot5138.	0.2	28
27	Genome-wide CIITA-binding profile identifies sequence preferences that dictate function versus recruitment. Nucleic Acids Research, 2015, 43, 3128-3142.	6.5	28
28	Galactic Cosmic Radiation Induces Persistent Epigenome Alterations Relevant to Human Lung Cancer. Scientific Reports, 2018, 8, 6709.	1.6	26
29	Conserved Region C Functions To Regulate PD-1 Expression and Subsequent CD8 T Cell Memory. Journal of Immunology, 2017, 198, 205-217.	0.4	24
30	PD-1 Expression during Acute Infection Is Repressed through an LSD1-Blimp-1 Axis. Journal of Immunology, 2020, 204, 449-458.	0.4	24
31	Genetic heterogeneity within collective invasion packs drives leader and follower cell phenotypes. Journal of Cell Science, 2019, 132, .	1.2	23
32	Integrated phosphoproteomics and transcriptional classifiers reveal hidden RAS signaling dynamics in multiple myeloma. Blood Advances, 2019, 3, 3214-3227.	2.5	19
33	Whole-genome analysis of TET dioxygenase function in regulatory T cells. EMBO Reports, 2021, 22, e52716.	2.0	19
34	Common distal elements orchestrate CIITA isoform-specific expression in multiple cell types. Genes and Immunity, 2014, 15, 543-555.	2.2	16
35	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
36	CD86 regulates myeloma cell survival. Blood Advances, 2017, 1, 2307-2319.	2.5	15

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37	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
38	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
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	Factors affecting the persistence of drug-induced reprogramming of the cancer methylome. <i>Epigenetics</i> , 2016, 11, 273-287.	1.3	8
41	Oncolytic herpes simplex virus infects myeloma cells in vitro and in vivo. <i>Molecular Therapy - Oncolytics</i> , 2021, 20, 519-531.	2.0	8
42	Downregulation of PA28 β induces proteasome remodeling and results in resistance to proteasome inhibitors in multiple myeloma. <i>Blood Cancer Journal</i> , 2020, 10, 125.	2.8	7
43	Ten-eleven translocation protein 1 modulates medulloblastoma progression. <i>Genome Biology</i> , 2021, 22, 125.	3.8	3
44	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
45	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
46	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
47	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
48	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
49	β 2 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
50	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. <i>Blood</i> , 2008, 112, 5167-5167.	0.6	2
51	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
52	PROTEIN-CODING AND MICRORNA BIOMARKER GENE PANELS PREDICTIVE OF CLINICAL RECURRENCE IN PROSTATE CANCER. <i>Journal of Urology</i> , 2009, 181, 776-776.	0.2	1
53	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
54	We need CD38 STAT-JAK. <i>Blood</i> , 2020, 136, 2246-2248.	0.6	0

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55	Discovery of a novel set of prostate cancer-related genes associated with the prognostically important TMPRSS2:ERG fusion gene. <i>Journal of Clinical Oncology</i> , 2008, 26, 5056-5056.	0.8	0
56	Whole Genome DNA Methylation Analysis of Compass Identifies Biomarkers of Multiple Myeloma Survival. <i>Blood</i> , 2018, 132, 3174-3174.	0.6	0
57	A Role for Syntenin-1 in Multiple Myeloma Cell Survival. <i>Blood</i> , 2018, 132, 1008-1008.	0.6	0
58	The Role of Proteasome Activator PA28 $\hat{\pm}$ in Multiple Myeloma. <i>Blood</i> , 2019, 134, 5499-5499.	0.6	0
59	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
60	Functional Genomic and Immune Response Characterization of PTEN Loss: Therapeutic Implications for Myeloma. <i>Blood</i> , 2021, 138, 1612-1612.	0.6	0
61	Disrupting Ectopic Super-Enhancers to Treat Multiple Myeloma. <i>Blood</i> , 2021, 138, 1593-1593.	0.6	0
62	BRAF Mutations and Inflammatory Gene Expression in Myeloma Cells from Patients with Renal Dysfunction. <i>Blood</i> , 2021, 138, 1624-1624.	0.6	0
63	Functional Oncogenomic and Immune Response Landscape for Genes Recurrently Mutated in Myeloma. <i>Blood</i> , 2021, 138, 1589-1589.	0.6	0
64	Mitochondrial Electron Transport Chain Inhibition Promotes Resistance to Proteasome Inhibitors in Multiple Myeloma. <i>Blood</i> , 2021, 138, 1611-1611.	0.6	0
65	Chromatin Accessibility Identifies Regulatory Elements Predictive of Oncogene Expression in Multiple Myeloma. <i>Blood</i> , 2020, 136, 31-32.	0.6	0
66	Invited Keynote Talk: Data Mining and Statistical Methods for Analyzing Microarray Experiments. , 2008, , 444-444.		0