

Elizabeth Bartom

List of Publications by Year in descending order

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Version: 2024-02-01

81
papers

3,503
citations

249298

26
h-index

175968

55
g-index

95
all docs

95
docs citations

95
times ranked

8078
citing authors

#	ARTICLE	IF	CITATIONS
1	SF3B1 homeostasis is critical for survival and therapeutic response in T cell leukemia. <i>Science Advances</i> , 2022, 8, eabj8357.	4.7	16
2	Abstract P1-11-01: Modulation of the high risk postmenopausal breast tissue genomic profiles with licorice and its bioactive compounds. <i>Cancer Research</i> , 2022, 82, P1-11-01-P1-11-01.	0.4	0
3	Identification of the toxic 6mer seed consensus for human cancer cells. <i>Scientific Reports</i> , 2022, 12, 5130.	1.6	11
4	Oncogenic and Tumor Suppressor Functions for Lymphoid Enhancer Factor 1 in E2a-/- T Acute Lymphoblastic Leukemia. <i>Frontiers in Immunology</i> , 2022, 13, 845488.	2.2	8
5	SPOROS: A pipeline to analyze DISE/6mer seed toxicity. <i>PLoS Computational Biology</i> , 2022, 18, e1010022.	1.5	10
6	195â€f3D Genome Structure and Epigenetic Transcription Regulation in Pediatric High-Grade Glioma. <i>Neurosurgery</i> , 2022, 68, 59-59.	0.6	0
7	Placental dysfunction influences fetal monocyte subpopulation gene expression in preterm birth. <i>JCI Insight</i> , 2022, 7, .	2.3	4
8	A synthetic lethality screen reveals ING5 as a genetic dependency of catalytically dead Set1A/COMPASS in mouse embryonic stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2118385119.	3.3	3
9	The transcriptional repressor ID2 supports natural killer cell maturation by controlling TCF1 amplitude. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	17
10	Epigenomic landscape and 3D genome structure in pediatric high-grade glioma. <i>Science Advances</i> , 2021, 7, .	4.7	36
11	The Ratio of Toxic-to-Nontoxic miRNAs Predicts Platinum Sensitivity in Ovarian Cancer. <i>Cancer Research</i> , 2021, 81, 3985-4000.	0.4	14
12	HGG-01. 3D GENOME STRUCTURE IMPACTS GENE EXPRESSION IN PEDIATRIC HIGH-GRADE GLIOMA. <i>Neuro-Oncology</i> , 2021, 23, i17-i17.	0.6	0
13	PAX9 Determines Epigenetic State Transition and Cell Fate in Cancer. <i>Cancer Research</i> , 2021, 81, 4696-4708.	0.4	10
14	EPCO-20. PEDIATRIC HIGH-GRADE GLIOMA EXHIBITS DISTINCT 3D GENOME STRUCTURE THAT IMPACTS TRANSCRIPTION REGULATION. <i>Neuro-Oncology</i> , 2021, 23, vi6-vi6.	0.6	0
15	6mer Seed Toxicity in Viral microRNAs. <i>IScience</i> , 2020, 23, 100737.	1.9	13
16	ASXL3 bridges BRD4 to BAP1 complex and governs enhancer activity in small cell lung cancer. <i>Genome Medicine</i> , 2020, 12, 63.	3.6	34
17	Effects of H3.3G34V mutation on genomic H3K36 and H3K27 methylation patterns in isogenic pediatric glioma cells. <i>Acta Neuropathologica Communications</i> , 2020, 8, 219.	2.4	14
18	Quantitative and multiplexed chemical-genetic phenotyping in mammalian cells with QMAP-Seq. <i>Nature Communications</i> , 2020, 11, 5722.	5.8	1

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19	Role of Hypoxia-Inducible Factors in Regulating Right Ventricular Function and Remodeling during Chronic Hypoxia-induced Pulmonary Hypertension. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2020, 63, 652-664.	1.4	30
20	Kaposi's Sarcoma-Associated Herpesvirus Drives a Super-Enhancer-Mediated Survival Gene Expression Program in Primary Effusion Lymphoma. <i>MBio</i> , 2020, 11, .	1.8	13
21	Elucidating the regulatory mechanism of Swi1 prion in global transcription and stress responses. <i>Scientific Reports</i> , 2020, 10, 21838.	1.6	5
22	Uncoupling histone H3K4 trimethylation from developmental gene expression via an equilibrium of COMPASS, Polycomb and DNA methylation. <i>Nature Genetics</i> , 2020, 52, 615-625.	9.4	76
23	Ezh2 Represses Transcription of Innate Lymphoid Genes in B Lymphocyte Progenitors and Maintains the B-2 Cell Fate. <i>Journal of Immunology</i> , 2020, 204, 1760-1769.	0.4	3
24	HGG-26. H3G34V MUTATION AFFECTS GENOMIC H3K36 METHYLATION IN PEDIATRIC GLIOMA. <i>Neuro-Oncology</i> , 2020, 22, iii348-iii348.	0.6	0
25	β-Catenin/Tcf7l2-dependent transcriptional regulation of GLUT1 gene expression by Zic family proteins in colon cancer. <i>Science Advances</i> , 2019, 5, eaax0698.	4.7	28
26	OS12.6 Intracranial GBM PDX Mutations Induced by Temozolomide Treatment. <i>Neuro-Oncology</i> , 2019, 21, iii23-iii23.	0.6	0
27	RACK1 evolved species-specific multifunctionality in translational control through sequence plasticity in a loop domain. <i>Journal of Cell Science</i> , 2019, 132, .	1.2	10
28	Tenascin-C expression contributes to pediatric brainstem glioma tumor phenotype and represents a novel biomarker of disease. <i>Acta Neuropathologica Communications</i> , 2019, 7, 75.	2.4	24
29	HGG-10. HISTONE H3G34V MUTATION IS SUFFICIENT TO DRIVE DISTINCT GENOMIC H3K36 METHYLATION PATTERNS IN PEDIATRIC GLIOMA. <i>Neuro-Oncology</i> , 2019, 21, ii88-ii89.	0.6	0
30	Cutting Edge: Lymphomyeloid-Primed Progenitor Cell Fates Are Controlled by the Transcription Factor Tal1. <i>Journal of Immunology</i> , 2019, 202, 2837-2842.	0.4	4
31	The Coincidence Between Increasing Age, Immunosuppression, and the Incidence of Patients With Glioblastoma. <i>Frontiers in Pharmacology</i> , 2019, 10, 200.	1.6	82
32	The Oncogenic Kaposi's Sarcoma-Associated Herpesvirus Encodes a Mimic of the Tumor-Suppressive miR-15/16 miRNA Family. <i>Cell Reports</i> , 2019, 29, 2961-2969.e6.	2.9	14
33	USP7 Cooperates with NOTCH1 to Drive the Oncogenic Transcriptional Program in T-Cell Leukemia. <i>Clinical Cancer Research</i> , 2019, 25, 222-239.	3.2	66
34	Regulation of MLL/COMPASS stability through its proteolytic cleavage by <i>taspase1</i> as a possible approach for clinical therapy of leukemia. <i>Genes and Development</i> , 2019, 33, 61-74.	2.7	26
35	A Beginner's Guide to Analysis of RNA Sequencing Data. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2018, 59, 145-157.	1.4	78
36	Small interfering RNA s based on huntingtin trinucleotide repeats are highly toxic to cancer cells. <i>EMBO Reports</i> , 2018, 19, .	2.0	32

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37	Transcriptional Profiling of Synovial Macrophages Using Minimally Invasive Ultrasound-Guided Synovial Biopsies in Rheumatoid Arthritis. <i>Arthritis and Rheumatology</i> , 2018, 70, 841-854.	2.9	44
38	A Carcinogen-induced mouse model recapitulates the molecular alterations of human muscle invasive bladder cancer. <i>Oncogene</i> , 2018, 37, 1911-1925.	2.6	102
39	ZNF598 Plays Distinct Roles in Interferon-Stimulated Gene Expression and Poxvirus Protein Synthesis. <i>Cell Reports</i> , 2018, 23, 1249-1258.	2.9	33
40	PDTM-39. HISTONE H3 MUTATION EFFECTS ON CHROMATIN STRUCTURE AND REGULATION OF GENE TRANSCRIPTION IN PEDIATRIC GLIOMA. <i>Neuro-Oncology</i> , 2018, 20, vi212-vi212.	0.6	0
41	A CHAF1B-Dependent Molecular Switch in Hematopoiesis and Leukemia Pathogenesis. <i>Cancer Cell</i> , 2018, 34, 707-723.e7.	7.7	68
42	6mer seed toxicity in tumor suppressive microRNAs. <i>Nature Communications</i> , 2018, 9, 4504.	5.8	37
43	A CHAF1B-Dependent Molecular Switch in Hematopoiesis and Leukemia. <i>Experimental Hematology</i> , 2018, 64, S26-S27.	0.2	0
44	CD95/Fas ligand mRNA is toxic to cells. <i>ELife</i> , 2018, 7, .	2.8	32
45	Abstract 4391: CD95L mRNA is toxic to cancer cells. , 2018, , .		0
46	Abstract LB-401: Induction of DISE by tumor suppressive microRNAs. , 2018, , .		0
47	Abstract 4387: Triplet nucleotide repeat-based siRNAs are highly toxic to cancer cells. , 2018, , .		0
48	Not All H3K4 Methylations Are Created Equal: Mll2/COMPASS Dependency in Primordial Germ Cell Specification. <i>Molecular Cell</i> , 2017, 65, 460-475.e6.	4.5	81
49	Quantitation of Cell Type-Specific Responses to Brassinosteroid by Deep Sequencing of Polysome-Associated Polyadenylated RNA. <i>Methods in Molecular Biology</i> , 2017, 1564, 81-102.	0.4	1
50	Therapeutic targeting of polycomb and BET bromodomain proteins in diffuse intrinsic pontine gliomas. <i>Nature Medicine</i> , 2017, 23, 493-500.	15.2	332
51	EZH2 Regulates the Developmental Timing of Effectors of the Pre-“Antigen Receptor Checkpoints. <i>Journal of Immunology</i> , 2017, 198, 4682-4691.	0.4	29
52	SET1A/COMPASS and shadow enhancers in the regulation of homeotic gene expression. <i>Genes and Development</i> , 2017, 31, 787-801.	2.7	48
53	DIPG-24. EPIGENETIC ANALYSIS OF FORMALIN-FIXED PARAFFIN-EMBEDDED PEDIATRIC GLIOMA TISSUE. <i>Neuro-Oncology</i> , 2017, 19, iv9-iv10.	0.6	0
54	Cancer-Associated IDH1 Promotes Growth and Resistance to Targeted Therapies in the Absence of Mutation. <i>Cell Reports</i> , 2017, 19, 1858-1873.	2.9	164

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55	Therapeutic Targeting of MLL Degradation Pathways in MLL-Rearranged Leukemia. <i>Cell</i> , 2017, 168, 59-72.e13.	13.5	99
56	Histone H3K4 monomethylation catalyzed by Trr and mammalian COMPASS-like proteins at enhancers is dispensable for development and viability. <i>Nature Genetics</i> , 2017, 49, 1647-1653.	9.4	168
57	Monocyte-derived alveolar macrophages drive lung fibrosis and persist in the lung over the life span. <i>Journal of Experimental Medicine</i> , 2017, 214, 2387-2404.	4.2	755
58	PDTM-02. NEXT-GENERATION SEQUENCING OF DIFFUSE INTRINSIC PONTINE GLIOMA CELLS REVEALS ALTERED EPIGENETIC REGULATION AND DISTINCT TUMOR SUBGROUPS. <i>Neuro-Oncology</i> , 2017, 19, vi189-vi190.	0.6	0
59	PDTM-28. TARGETED INHIBITION OF EZH2 AND BET BROMODOMAIN PROTEINS FOR THE TREATMENT OF DIFFUSE INTRINSIC PONTINE GLIOMAS. <i>Neuro-Oncology</i> , 2017, 19, vi196-vi196.	0.6	2
60	Many si/shRNAs can kill cancer cells by targeting multiple survival genes through an off-target mechanism. <i>ELife</i> , 2017, 6, .	2.8	62
61	Disease Specific Signatures Identified by RNA-seq of Sorted Lung Cellular Populations. <i>FASEB Journal</i> , 2017, 31, 656.4.	0.2	0
62	PDTB-14. INVESTIGATING HISTONE H3 POST-TRANSLATIONAL MODIFICATIONS USING PARAFFIN-EMBEDDED PEDIATRIC GLIOMA TISSUE SAMPLES. <i>Neuro-Oncology</i> , 2016, 18, vi152-vi153.	0.6	0
63	Retroviral insertional mutagenesis identifies the del(5q) genes, CXXC5, TIFAB and ETF1, as well as the Wnt pathway, as potential targets in del(5q) myeloid neoplasms. <i>Haematologica</i> , 2016, 101, e232-e236.	1.7	13
64	Transcriptomic signatures decode Th17 cell pathogenicity. <i>Cellular and Molecular Immunology</i> , 2016, 13, 557-559.	4.8	1
65	Regulation of the imprinted <i>Dlk1-Dio3</i> locus by allele-specific enhancer activity. <i>Genes and Development</i> , 2016, 30, 92-101.	2.7	55
66	Translatome analyses capture of opposing tissue-specific brassinosteroid signals orchestrating root meristem differentiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 923-928.	3.3	113
67	ExScalibur: A High-Performance Cloud-Enabled Suite for Whole Exome Germline and Somatic Mutation Identification. <i>PLoS ONE</i> , 2015, 10, e0135800.	1.1	12
68	Plaques. , 2013, , 356-357.		1
69	Comparison of the Genome Sequences of <i>Candidatus Portiera aleyrodidarum</i> Primary Endosymbionts of the Whitefly <i>Bemisia tabaci</i> B and Q Biotypes. <i>Applied and Environmental Microbiology</i> , 2013, 79, 1757-1759.	1.4	25
70	CUX1 is a haploinsufficient tumor suppressor gene on chromosome 7 frequently inactivated in acute myeloid leukemia. <i>Blood</i> , 2013, 121, 975-983.	0.6	130
71	Multiplicity of Infection. , 2013, , 509-510.		5
72	Retroviral Insertional Mutagenesis In <i>Egr1</i> +/- mice, Haploinsufficient For a Human Del(5q) Myeloid Leukemia Gene, Develop Myeloid Neoplasms With Proviral Insertions In Genes Syntenic To Human 5q. <i>Blood</i> , 2013, 122, 1275-1275.	0.6	0

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73	Genome Sequences of the Primary Endosymbiont <i>Candidatus Portiera aleyrodidarum</i> in the Whitefly <i>Bemisia tabaci</i> B and Q Biotypes. <i>Journal of Bacteriology</i> , 2012, 194, 6678-6679.	1.0	29
74	Epigenetic repression of the Igk locus by STAT5-mediated recruitment of the histone methyltransferase Ezh2. <i>Nature Immunology</i> , 2011, 12, 1212-1220.	7.0	169
75	GENETIC PATHWAYS LEADING TO THERAPY-RELATED MYELOID NEOPLASMS. <i>Mediterranean Journal of Hematology and Infectious Diseases</i> , 2011, 3, e2011019.	0.5	13
76	Short, local duplications in eukaryotic genomes. <i>Current Opinion in Genetics and Development</i> , 2005, 15, 640-644.	1.5	23
77	Distribution of short paired duplications in mammalian genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 10349-10354.	3.3	23
78	Exploring the characteristics of sequence elements in proximal promoters of human genes. <i>Genomics</i> , 2004, 84, 929-940.	1.3	24
79	Annotating Large Genomes With Exact Word Matches. <i>Genome Research</i> , 2003, 13, 2306-2315.	2.4	62
80	The microsatellites of <i>Escherichia coli</i> : rapidly evolving repetitive DNAs in a non-pathogenic prokaryote. <i>Molecular Microbiology</i> , 2001, 39, 183-190.	1.2	36
81	MAGPIE/EGRET Annotation of the 2.9-Mb <i>Drosophila melanogaster</i> Adh Region. <i>Genome Research</i> , 2000, 10, 502-510.	2.4	19