

Elizabeth Bartom

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.

78
papers

2,755
citations

27
h-index

52
g-index

95
ext. papers

3,690
ext. citations

9.5
avg, IF

5.13
L-index

#	Paper	IF	Citations
78	SF3B1 homeostasis is critical for survival and therapeutic response in T cell leukemia.. <i>Science Advances</i> , 2022 , 8, eabj8357	14.3	1
77	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	10.1	
76	Identification of the toxic 6mer seed consensus for human cancer cells.. <i>Scientific Reports</i> , 2022 , 12, 51304	4.9	1
75	Oncogenic and Tumor Suppressor Functions for Lymphoid Enhancer Factor 1 in T Acute Lymphoblastic Leukemia.. <i>Frontiers in Immunology</i> , 2022 , 13, 845488	8.4	1
74	SPOROS: A pipeline to analyze DISE/6mer seed toxicity.. <i>PLoS Computational Biology</i> , 2022 , 18, e1010023	3	0
73	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	11.5	
72	The transcriptional repressor ID2 supports natural killer cell maturation by controlling TCF1 amplitude. <i>Journal of Experimental Medicine</i> , 2021 , 218,	16.6	4
71	Epigenomic landscape and 3D genome structure in pediatric high-grade glioma. <i>Science Advances</i> , 2021 , 7,	14.3	8
70	The Ratio of Toxic-to-Nontoxic miRNAs Predicts Platinum Sensitivity in Ovarian Cancer. <i>Cancer Research</i> , 2021 , 81, 3985-4000	10.1	4
69	HGG-01. 3D GENOME STRUCTURE IMPACTS GENE EXPRESSION IN PEDIATRIC HIGH-GRADE GLIOMA. <i>Neuro-Oncology</i> , 2021 , 23, i17-i17	1	78
68	PAX9 Determines Epigenetic State Transition and Cell Fate in Cancer. <i>Cancer Research</i> , 2021 , 81, 4696-4708	10.1	3
67	EPCO-20. PEDIATRIC HIGH-GRADE GLIOMA EXHIBITS DISTINCT 3D GENOME STRUCTURE THAT IMPACTS TRANSCRIPTION REGULATION. <i>Neuro-Oncology</i> , 2021 , 23, vi6-vi6	1	
66	Elucidating the regulatory mechanism of Swi1 prion in global transcription and stress responses. <i>Scientific Reports</i> , 2020 , 10, 21838	4.9	1
65	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	36.3	38
64	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	5.3	2
63	HGG-26. H3G34V MUTATION AFFECTS GENOMIC H3K36 METHYLATION IN PEDIATRIC GLIOMA. <i>Neuro-Oncology</i> , 2020 , 22, iii348-iii348	1	78
62	6mer Seed Toxicity in Viral microRNAs. <i>IScience</i> , 2020 , 23, 100737	6.1	7

61	ASXL3 bridges BRD4 to BAP1 complex and governs enhancer activity in small cell lung cancer. <i>Genome Medicine</i> , 2020 , 12, 63	14.4	17
60	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	7.3	5
59	Quantitative and multiplexed chemical-genetic phenotyping in mammalian cells with QMAP-Seq. <i>Nature Communications</i> , 2020 , 11, 5722	17.4	1
58	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	5.7	12
57	Kaposi's Sarcoma-Associated Herpesvirus Drives a Super-Enhancer-Mediated Survival Gene Expression Program in Primary Effusion Lymphoma. <i>MBio</i> , 2020 , 11,	7.8	7
56	RACK1 evolved species-specific multifunctionality in translational control through sequence plasticity within a loop domain. <i>Journal of Cell Science</i> , 2019 , 132,	5.3	5
55	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	7.3	13
54	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	1	78
53	Cutting Edge: Lymphomyeloid-Primed Progenitor Cell Fates Are Controlled by the Transcription Factor Tal1. <i>Journal of Immunology</i> , 2019 , 202, 2837-2842	5.3	1
52	The Coincidence Between Increasing Age, Immunosuppression, and the Incidence of Patients With Glioblastoma. <i>Frontiers in Pharmacology</i> , 2019 , 10, 200	5.6	51
51	β-Catenin/Tcf7l2-dependent transcriptional regulation of GLUT1 gene expression by Zic family proteins in colon cancer. <i>Science Advances</i> , 2019 , 5, eaax0698	14.3	12
50	OS12.6 Intracranial GBM PDX Mutations Induced by Temozolomide Treatment. <i>Neuro-Oncology</i> , 2019 , 21, iii23-iii23	1	78
49	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	10.6	9
48	USP7 Cooperates with NOTCH1 to Drive the Oncogenic Transcriptional Program in T-Cell Leukemia. <i>Clinical Cancer Research</i> , 2019 , 25, 222-239	12.9	46
47	Regulation of MLL/COMPASS stability through its proteolytic cleavage by caspase1 as a possible approach for clinical therapy of leukemia. <i>Genes and Development</i> , 2019 , 33, 61-74	12.6	16
46	A Beginner's Guide to Analysis of RNA Sequencing Data. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2018 , 59, 145-157	5.7	38
45	Small interfering RNAs based on huntingtin trinucleotide repeats are highly toxic to cancer cells. <i>EMBO Reports</i> , 2018 , 19,	6.5	20
44	Transcriptional Profiling of Synovial Macrophages Using Minimally Invasive Ultrasound-Guided Synovial Biopsies in Rheumatoid Arthritis. <i>Arthritis and Rheumatology</i> , 2018 , 70, 841-854	9.5	27

43	A Carcinogen-induced mouse model recapitulates the molecular alterations of human muscle invasive bladder cancer. <i>Oncogene</i> , 2018 , 37, 1911-1925	9.2	66
42	ZNF598 Plays Distinct Roles in Interferon-Stimulated Gene Expression and Poxvirus Protein Synthesis. <i>Cell Reports</i> , 2018 , 23, 1249-1258	10.6	16
41	CD95/Fas ligand mRNA is toxic to cells. <i>ELife</i> , 2018 , 7,	8.9	19
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	1	78
39	A CHAF1B-Dependent Molecular Switch in Hematopoiesis and Leukemia Pathogenesis. <i>Cancer Cell</i> , 2018 , 34, 707-723.e7	24.3	36
38	6mer seed toxicity in tumor suppressive microRNAs. <i>Nature Communications</i> , 2018 , 9, 4504	17.4	18
37	Not All H3K4 Methylations Are Created Equal: Mll2/COMPASS Dependency in Primordial Germ Cell Specification. <i>Molecular Cell</i> , 2017 , 65, 460-475.e6	17.6	53
36	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	1.4	1
35	Therapeutic targeting of polycomb and BET bromodomain proteins in diffuse intrinsic pontine gliomas. <i>Nature Medicine</i> , 2017 , 23, 493-500	50.5	225
34	EZH2 Regulates the Developmental Timing of Effectors of the Pre-Antigen Receptor Checkpoints. <i>Journal of Immunology</i> , 2017 , 198, 4682-4691	5.3	16
33	SET1A/COMPASS and shadow enhancers in the regulation of homeotic gene expression. <i>Genes and Development</i> , 2017 , 31, 787-801	12.6	33
32	DIPG-24. EPIGENETIC ANALYSIS OF FORMALIN-FIXED PARAFFIN-EMBEDDED PEDIATRIC GLIOMA TISSUE. <i>Neuro-Oncology</i> , 2017 , 19, iv9-iv10	1	78
31	Cancer-Associated IDH1 Promotes Growth and Resistance to Targeted Therapies in the Absence of Mutation. <i>Cell Reports</i> , 2017 , 19, 1858-1873	10.6	104
30	Therapeutic Targeting of MLL Degradation Pathways in MLL-Rearranged Leukemia. <i>Cell</i> , 2017 , 168, 59-73.e13	36.13	72
29	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	36.3	97
28	Many si/shRNAs can kill cancer cells by targeting multiple survival genes through an off-target mechanism. <i>ELife</i> , 2017 , 6,	8.9	35
27	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	16.6	434
26	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	1	78

25	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	1	2
24	Disease Specific Signatures Identified by RNA-seq of Sorted Lung Cellular Populations. <i>FASEB Journal</i> , 2017 , 31, 656.4	0.9	
23	Regulation of the imprinted Dlk1-Dio3 locus by allele-specific enhancer activity. <i>Genes and Development</i> , 2016 , 30, 92-101	12.6	40
22	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, e232-6	6.6	11
21	Transcriptomic signatures decode Th17 cell pathogenicity. <i>Cellular and Molecular Immunology</i> , 2016 , 13, 557-9	15.4	0
20	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, 923-8	11.5	92
19	ExScalibur: A High-Performance Cloud-Enabled Suite for Whole Exome Germline and Somatic Mutation Identification. <i>PLoS ONE</i> , 2015 , 10, e0135800	3.7	11
18	Plaques 2013 , 356-357		1
17	Comparison of the genome sequences of "Candidatus Portiera aleyrodidarum" primary endosymbionts of the whitefly Bemisia tabaci B and Q biotypes. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 1757-9	4.8	20
16	CUX1 is a haploinsufficient tumor suppressor gene on chromosome 7 frequently inactivated in acute myeloid leukemia. <i>Blood</i> , 2013 , 121, 975-83	2.2	111
15	Multiplicity of Infection 2013 , 509-510		1
14	Genome sequences of the primary endosymbiont "Candidatus Portiera aleyrodidarum" in the whitefly Bemisia tabaci B and Q biotypes. <i>Journal of Bacteriology</i> , 2012 , 194, 6678-9	3.5	22
13	Epigenetic repression of the Igk locus by STAT5-mediated recruitment of the histone methyltransferase Ezh2. <i>Nature Immunology</i> , 2011 , 12, 1212-20	19.1	138
12	Genetic pathways leading to therapy-related myeloid neoplasms. <i>Mediterranean Journal of Hematology and Infectious Diseases</i> , 2011 , 3, e2011019	3.2	12
11	Short, local duplications in eukaryotic genomes. <i>Current Opinion in Genetics and Development</i> , 2005 , 15, 640-4	4.9	23
10	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, 10349-54	11.5	21
9	Exploring the characteristics of sequence elements in proximal promoters of human genes. <i>Genomics</i> , 2004 , 84, 929-40	4.3	19
8	Annotating large genomes with exact word matches. <i>Genome Research</i> , 2003 , 13, 2306-15	9.7	53

7	The microsatellites of Escherichia coli: rapidly evolving repetitive DNAs in a non-pathogenic prokaryote. <i>Molecular Microbiology</i> , 2001 , 39, 183-90	4-1	34
6	MAGPIE/EGRET annotation of the 2.9-Mb Drosophila melanogaster Adh region. <i>Genome Research</i> , 2000 , 10, 502-10	9-7	15
5	6mer Seed Toxicity Determines Strand Selection in miRNAs		1
4	Identification of the toxic 6mer seed consensus in human cancer cells		2
3	USP7 cooperates with NOTCH1 to drive the oncogenic transcriptional program in T cell leukemia		1
2	The balance between toxic versus nontoxic microRNAs determines platinum sensitivity in ovarian cancer		1
1	SPOROS: A pipeline to analyze DISE/6mer seed toxicity		1