Frederik Otzen Bagger

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	An atlas of active enhancers across human cell types and tissues. Nature, 2014, 507, 455-461.	13.7	2,269
2	Classification of low quality cells from single-cell RNA-seq data. Genome Biology, 2016, 17, 29.	3.8	572
3	Single-cell RNA-seq and computational analysis using temporal mixture modeling resolves T _H 1/T _{FH} fate bifurcation in malaria. Science Immunology, 2017, 2, .	5.6	258
4	BloodSpot: a database of gene expression profiles and transcriptional programs for healthy and malignant haematopoiesis. Nucleic Acids Research, 2016, 44, D917-D924.	6.5	242
5	BloodSpot: a database of healthy and malignant haematopoiesis updated with purified and single cell mRNA sequencing profiles. Nucleic Acids Research, 2019, 47, D881-D885.	6.5	172
6	Comparing cancer vs normal gene expression profiles identifies new disease entities and common transcriptional programs in AML patients. Blood, 2014, 123, 894-904.	0.6	133
7	C/EBPα Is Required for Long-Term Self-Renewal and Lineage Priming of Hematopoietic Stem Cells and for the Maintenance of Epigenetic Configurations in Multipotent Progenitors. PLoS Genetics, 2014, 10, e1004079.	1.5	85
8	Telomerase Inhibition Effectively Targets Mouse and Human AML Stem Cells and Delays Relapse following Chemotherapy. Cell Stem Cell, 2014, 15, 775-790.	5.2	74
9	shRNA screening identifies JMJD1C as being required for leukemia maintenance. Blood, 2014, 123, 1870-1882.	0.6	73
10	ERG promotes the maintenance of hematopoietic stem cells by restricting their differentiation. Genes and Development, 2015, 29, 1915-1929.	2.7	71
11	Identification and validation of 174 COVID-19 vaccine candidate epitopes reveals low performance of common epitope prediction tools. Scientific Reports, 2020, 10, 20465.	1.6	66
12	HemaExplorer: a database of mRNA expression profiles in normal and malignant haematopoiesis. Nucleic Acids Research, 2013, 41, D1034-D1039.	6.5	65
13	A Gain-of-Function p53-Mutant Oncogene Promotes Cell Fate Plasticity and Myeloid Leukemia through the Pluripotency Factor FOXH1. Cancer Discovery, 2019, 9, 962-979.	7.7	58
14	The splicing factor RBM25 controls MYC activity in acute myeloid leukemia. Nature Communications, 2019, 10, 172.	5.8	42
15	Software-Supported USER Cloning Strategies for Site-Directed Mutagenesis and DNA Assembly. ACS Synthetic Biology, 2015, 4, 342-349.	1.9	41
16	SinaPlot: An Enhanced Chart for Simple and Truthful Representation of Single Observations Over Multiple Classes. Journal of Computational and Graphical Statistics, 2018, 27, 673-676.	0.9	37
17	Autophagy is required for stem cell mobilization by G-CSF. Blood, 2015, 125, 2933-2936.	0.6	36
18	Modification of T Cell Responses by Stem Cell Mobilization Requires Direct Signaling of the T Cell by G-CSF and IL-10. Journal of Immunology, 2014, 192, 3180-3189.	0.4	34

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19	HemaExplorer: a Web server for easy and fast visualization of gene expression in normal and malignant hematopoiesis. Blood, 2012, 119, 6394-6395.	0.6	32
20	A Comparison of Tools for Copy-Number Variation Detection in Germline Whole Exome and Whole Genome Sequencing Data. Cancers, 2021, 13, 6283.	1.7	31
21	Human erythroleukemia genetics and transcriptomes identify master transcription factors as functional disease drivers. Blood, 2020, 136, 698-714.	0.6	28
22	Amplification of pico-scale DNA mediated by bacterial carrier DNA for small-cell-number transcription factor ChIP-seq. BMC Genomics, 2015, 16, 46.	1.2	27
23	Peak-valley-peak pattern of histone modifications delineates active regulatory elements and their directionality. Nucleic Acids Research, 2016, 44, 4037-4051.	6.5	26
24	Deconvolution of autoencoders to learn biological regulatory modules from single cell mRNA sequencing data. BMC Bioinformatics, 2019, 20, 379.	1.2	22
25	Single mRNP Analysis Reveals that Small Cytoplasmic mRNP Granules Represent mRNA Singletons. Cell Reports, 2019, 29, 736-748.e4.	2.9	22
26	Nuclear interacting SET domain protein 1 inactivation impairs GATA1-regulated erythroid differentiation and causes erythroleukemia. Nature Communications, 2020, 11, 2807.	5.8	18
27	Deep sequencing of human papillomavirus positive loco-regionally advanced oropharyngeal squamous cell carcinomas reveals novel mutational signature. BMC Cancer, 2018, 18, 640.	1.1	14
28	H3K9 dimethylation safeguards cancer cells against activation of the interferon pathway. Science Advances, 2022, 8, eabf8627.	4.7	10
29	Single Cell Sequencing in Cancer Diagnostics. Advances in Experimental Medicine and Biology, 2020, 1255, 175-193.	0.8	9
30	Cellular origin of prognostic chromosomal aberrations in AML patients. Leukemia, 2015, 29, 1785-1789.	3.3	8
31	Unveiling mRNP composition by fluorescence correlation and cross-correlation spectroscopy using cell lysates. Nucleic Acids Research, 2021, 49, e119-e119.	6.5	3
32	Interpretable Autoencoders Trained on Single Cell Sequencing Data Can Transfer Directly to Data from Unseen Tissues. Cells, 2022, 11, 85.	1.8	3
33	Analysis of telomerase target gene expression effects from murine models in patient cohorts by homology translation and random survival forest modeling. Genomics Data, 2016, 7, 275-280.	1.3	1
34	Autophagy Is Required For Long-Term Hematopoietic Stem Cell (HSC) Function and G-CSF-Induced HSC Mobilization. Blood, 2013, 122, 892-892.	0.6	1
35	Inhibition of Telomerase with Imetelstat Is Detrimental to Leukemia Stem Cells in Acute Myeloid Leukemia (AML). Blood, 2014, 124, 2322-2322.	0.6	1
36	Bloodspot: A Web Resource Facilitating the Analysis of Transcriptional Programs in Normal and Malignant Hematopoiesis. Blood, 2015, 126, 2358-2358.	0.6	1

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37	Transformation Mechanisms of the Nfia-ETO2 Fusion Gene Associated with Pediatric Pure Acute Erythroleukemia. Blood, 2019, 134, 532-532.	0.6	1
38	Inhibition Of Telomerase Is a Novel and Effective Therapy In MLL-Rearranged Acute Myeloid Leukemia (AML). Blood, 2013, 122, 2887-2887.	0.6	0
39	Improving The Analysis Of Gene Expression Profiles By Comparing AML Blasts With Their Nearest Normal Counterparts. Blood, 2013, 122, 2568-2568.	0.6	0
40	Dissecting GATA1 Protein Interactions in Normal and Malignant Human Erythroblasts. Blood, 2021, 138, 3293-3293.	0.6	0
41	Modeling the Cellular Origin of EVI1 + MLL-AF9-Driven Acute Myeloid Leukemia (AML). Blood, 2021, 138, 2210-2210.	0.6	0