

Touati Benoukraf

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

2,198
citations

304602

22
h-index

243529

44
g-index

51
all docs

51
docs citations

51
times ranked

4634
citing authors

#	ARTICLE	IF	CITATIONS
1	E2F and STAT3 provide transcriptional synergy for histone variant H2AZ activation to sustain glioblastoma chromatin accessibility and tumorigenicity. <i>Cell Death and Differentiation</i> , 2022, 29, 1379-1394.	5.0	9
2	Autosomal dominant non-syndromic hearing loss maps to DFNA33 (13q34) and co-segregates with splice and frameshift variants in ATP11A, a phospholipid flippase gene. <i>Human Genetics</i> , 2022, 141, 431-444.	1.8	7
3	Hepatocellular carcinoma organoid co-cultures mimic angiocrine crosstalk to generate inflammatory tumor microenvironment. <i>Biomaterials</i> , 2022, 284, 121527.	5.7	30
4	ZNF143 mediates CTCF-bound promoter-enhancer loops required for murine hematopoietic stem and progenitor cell function. <i>Nature Communications</i> , 2021, 12, 43.	5.8	45
5	A chemical biology approach reveals a dependency of glioblastoma on biotin distribution. <i>Science Advances</i> , 2021, 7, eabf6033.	4.7	10
6	Hydrogel-based colorectal cancer organoid co-culture models. <i>Acta Biomaterialia</i> , 2021, 132, 461-472.	4.1	72
7	Phosphorylation of Tet3 by cdk5 is critical for robust activation of BRN2 during neuronal differentiation. <i>Nucleic Acids Research</i> , 2020, 48, 1225-1238.	6.5	14
8	TFregulomeR reveals transcription factors' context-specific features and functions. <i>Nucleic Acids Research</i> , 2020, 48, e10-e10.	6.5	27
9	Targeted Inhibition of Purine Metabolism Is Effective in Suppressing Hepatocellular Carcinoma Progression. <i>Hepatology Communications</i> , 2020, 4, 1362-1381.	2.0	22
10	β -Catenin/TCF/LEF signaling promotes steady-state and emergency granulopoiesis via G-CSF receptor upregulation. <i>Blood</i> , 2020, 136, 2574-2587.	0.6	35
11	Hematopoietic stem cells acquire survival advantage by loss of RUNX1 methylation identified in familial leukemia. <i>Blood</i> , 2020, 136, 1919-1932.	0.6	20
12	Lysine acetyltransferase Tip60 is required for hematopoietic stem cell maintenance. <i>Blood</i> , 2020, 136, 1735-1747.	0.6	33
13	NanoVar: accurate characterization of patients' genomic structural variants using low-depth nanopore sequencing. <i>Genome Biology</i> , 2020, 21, 56.	3.8	73
14	Increased intron retention is a post-transcriptional signature associated with progressive aging and Alzheimer's disease. <i>Aging Cell</i> , 2019, 18, e12928.	3.0	80
15	MethMotif: an integrative cell specific database of transcription factor binding motifs coupled with DNA methylation profiles. <i>Nucleic Acids Research</i> , 2019, 47, D145-D154.	6.5	52
16	β -Catenin-Tcf/Lef Signaling Promotes Steady State and Emergency Granulopoiesis through G-CSF Receptor Upregulation. <i>Blood</i> , 2019, 134, 1193-1193.	0.6	0
17	The basic helix-loop-helix transcription factor SHARP1 is an oncogenic driver in MLL-AF6 acute myelogenous leukemia. <i>Nature Communications</i> , 2018, 9, 1622.	5.8	20
18	Generation of matched patient-derived xenograft in vitro-in vivo models using 3D macroporous hydrogels for the study of liver cancer. <i>Biomaterials</i> , 2018, 159, 229-240.	5.7	56

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19	Datasets describing the growth and molecular features of hepatocellular carcinoma patient-derived xenograft cells grown in a three-dimensional macroporous hydrogel. <i>Data in Brief</i> , 2018, 18, 594-606.	0.5	3
20	TIP60 represses activation of endogenous retroviral elements. <i>Nucleic Acids Research</i> , 2018, 46, 9456-9470.	6.5	33
21	miREM: an expectation-maximization approach for prioritizing miRNAs associated with gene-set. <i>BMC Bioinformatics</i> , 2018, 19, 299.	1.2	3
22	Loss of USP28-mediated BRAF degradation drives resistance to RAF cancer therapies. <i>Journal of Experimental Medicine</i> , 2018, 215, 1913-1928.	4.2	41
23	EVI2B is a C/EBP β target gene required for granulocytic differentiation and functionality of hematopoietic progenitors. <i>Cell Death and Differentiation</i> , 2017, 24, 705-716.	5.0	25
24	LPS independent activation of the pro-inflammatory receptor Trem1 by C/EBP β in granulocytes. <i>Scientific Reports</i> , 2017, 7, 46440.	1.6	9
25	Wanted DEAD/H or Alive: Helicases Winding Up in Cancers. <i>Journal of the National Cancer Institute</i> , 2017, 109, djw278.	3.0	79
26	NicE-seq: high resolution open chromatin profiling. <i>Genome Biology</i> , 2017, 18, 122.	3.8	45
27	Disruption of the C/EBP β -miR-182 balance impairs granulocytic differentiation. <i>Nature Communications</i> , 2017, 8, 46.	5.8	38
28	Whole genome DNA methylation: beyond genes silencing. <i>Oncotarget</i> , 2017, 8, 5629-5637.	0.8	105
29	Pasha: a versatile R package for piling chromatin HTS data. <i>Bioinformatics</i> , 2016, 32, 2528-2530.	1.8	21
30	Acquired resistance to combination treatment through loss of synergy with MEK and PI3K inhibitors in colorectal cancer. <i>Oncotarget</i> , 2016, 7, 29187-29198.	0.8	4
31	Methodological aspects of whole-genome bisulfite sequencing analysis. <i>Briefings in Bioinformatics</i> , 2015, 16, 369-379.	3.2	63
32	Feasibility of Low-Throughput Next Generation Sequencing for Germline DNA Screening. <i>Clinical Chemistry</i> , 2014, 60, 1549-1557.	1.5	7
33	The gene signature in CCAAT-enhancer-binding protein β dysfunctional acute myeloid leukemia predicts responsiveness to histone deacetylase inhibitors. <i>Haematologica</i> , 2014, 99, 697-705.	1.7	13
34	Transposon mutagenesis identifies genes driving hepatocellular carcinoma in a chronic hepatitis B mouse model. <i>Nature Genetics</i> , 2014, 46, 24-32.	9.4	105
35	DNMT1-interacting RNAs block gene-specific DNA methylation. <i>Nature</i> , 2013, 503, 371-376.	13.7	446
36	GBSA: a comprehensive software for analysing whole genome bisulfite sequencing data. <i>Nucleic Acids Research</i> , 2013, 41, e55-e55.	6.5	31

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37	C/EBP β is required for development of dendritic cell progenitors. <i>Blood</i> , 2013, 121, 4073-4081.	0.6	28
38	Processing ChIP-Chip Data: From the Scanner to the Browser. <i>Methods in Molecular Biology</i> , 2011, 719, 251-268.	0.4	2
39	H3K4 tri-methylation provides an epigenetic signature of active enhancers. <i>EMBO Journal</i> , 2011, 30, 4198-4210.	3.5	265
40	Characterisation of Genome-Wide PLZF/RARA Target Genes. <i>PLoS ONE</i> , 2011, 6, e24176.	1.1	22
41	Assessing the efficiency and significance of Methylated DNA Immunoprecipitation (MeDIP) assays in using in vitro methylated genomic DNA. <i>BMC Research Notes</i> , 2010, 3, 240.	0.6	17
42	A unique H3K4me2 profile marks tissue-specific gene regulation. <i>Genome Research</i> , 2010, 20, 1493-1502.	2.4	117
43	Initiation of V(D)J Recombination by D β 2-Associated Recombination Signal Sequences: A Critical Control Point in TCR β Gene Assembly. <i>PLoS ONE</i> , 2009, 4, e4575.	1.1	17
44	Duality of Enhancer Functioning Mode Revealed in a Reduced TCR β Gene Enhancer Knockin Mouse Model. <i>Journal of Immunology</i> , 2009, 183, 7939-7948.	0.4	13
45	CoCAS: a ChIP-on-chip analysis suite. <i>Bioinformatics</i> , 2009, 25, 954-955.	1.8	25