

Aurelien A Serandour

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

1,684
citations

623734

14
h-index

677142

22
g-index

28
all docs

28
docs citations

28
times ranked

3600
citing authors

#	ARTICLE	IF	CITATIONS
1	ETV6-RUNX1 and RUNX1 directly regulate RAG1 expression: one more step in the understanding of childhood B-cell acute lymphoblastic leukemia leukemogenesis. <i>Leukemia</i> , 2022, 36, 549-554.	7.2	11
2	The conundrum of the functional relationship between transcription factors and chromatin. <i>Epigenomics</i> , 2022, , .	2.1	0
3	Reduction of RUNX1 transcription factor activity by a CBFA2T3-mimicking peptide: application to B cell precursor acute lymphoblastic leukemia. <i>Journal of Hematology and Oncology</i> , 2021, 14, 47.	17.0	7
4	The hydroxymethylome of multiple myeloma identifies FAM72D as a 1q21 marker linked to proliferation. <i>Haematologica</i> , 2020, 105, 774-783.	3.5	23
5	DNA hydroxymethylation is associated with disease severity and persists at enhancers of oncogenic regions in multiple myeloma. <i>Clinical Epigenetics</i> , 2020, 12, 163.	4.1	9
6	Proteogenomic analysis of Inhibitor of Differentiation 4 (ID4) in basal-like breast cancer. <i>Breast Cancer Research</i> , 2020, 22, 63.	5.0	8
7	Interplay between transcription regulators RUNX1 and FUBP1 activates an enhancer of the oncogene KIT and amplifies cell proliferation. <i>Nucleic Acids Research</i> , 2018, 46, 11214-11228.	14.5	28
8	TRPS1 regulates oestrogen receptor binding and histone acetylation at enhancers. <i>Oncogene</i> , 2018, 37, 5281-5291.	5.9	24
9	Coupling Exonuclease Digestion with Selective Chemical Labeling for Base-resolution Mapping of 5-Hydroxymethylcytosine in Genomic DNA. <i>Bio-protocol</i> , 2018, 8, e2747.	0.4	2
10	Cytosine modifications modulate the chromatin architecture of transcriptional enhancers. <i>Genome Research</i> , 2017, 27, 947-958.	5.5	34
11	The logic of transcriptional regulator recruitment architecture at cis-regulatory modules controlling liver functions. <i>Genome Research</i> , 2017, 27, 985-996.	5.5	22
12	ERR α induces H3K9 demethylation by LSD1 to promote cell invasion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 3909-3914.	7.1	66
13	Two hematopoietic transcription factors, RUNX1 and FUBP1, control the expression of KIT oncogene in pre-B lymphoblasts. <i>Experimental Hematology</i> , 2017, 53, S112.	0.4	0
14	5-hydroxymethylcytosine marks postmitotic neural cells in the adult and developing vertebrate central nervous system. <i>Journal of Comparative Neurology</i> , 2017, 525, 478-497.	1.6	15
15	FOXA1 Directs H3K4 Monomethylation at Enhancers via Recruitment of the Methyltransferase MLL3. <i>Cell Reports</i> , 2016, 17, 2715-2723.	6.4	122
16	Single-CpG resolution mapping of 5-hydroxymethylcytosine by chemical labeling and exonuclease digestion identifies evolutionarily unconserved CpGs as TET targets. <i>Genome Biology</i> , 2016, 17, 56.	8.8	14
17	Progesterone receptor modulates ER α action in breast cancer. <i>Nature</i> , 2015, 523, 313-317.	27.8	504
18	Dynamic Estrogen Receptor Interactomes Control Estrogen-Responsive Trefoil Factor (TFF) Locus Cell-Specific Activities. <i>Molecular and Cellular Biology</i> , 2014, 34, 2418-2436.	2.3	20

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19	Normal RUNX1 and Pathogenic ETV6/RUNX1 Compete Genome-Wide for Chromatin Binding in Pre-B Acute Lymphoblastic Leukemia. <i>Blood</i> , 2014, 124, 3544-3544.	1.4	4
20	Endogenous Purification Reveals GREB1 as a Key Estrogen Receptor Regulatory Factor. <i>Cell Reports</i> , 2013, 3, 342-349.	6.4	319
21	Development of an Illumina-based ChIP-exonuclease method provides insight into FoxA1-DNA binding properties. <i>Genome Biology</i> , 2013, 14, R147.	9.6	76
22	Dynamic hydroxymethylation of deoxyribonucleic acid marks differentiation-associated enhancers. <i>Nucleic Acids Research</i> , 2012, 40, 8255-8265.	14.5	166
23	Epigenetic switch involved in activation of pioneer factor FOXA1-dependent enhancers. <i>Genome Research</i> , 2011, 21, 555-565.	5.5	196