

Jean-Christophe Andrau

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

3,599
citations

236612

25
h-index

233125

45
g-index

47
all docs

47
docs citations

47
times ranked

6475
citing authors

#	ARTICLE	IF	CITATIONS
1	The control of transcriptional memory by stable mitotic bookmarking. <i>Nature Communications</i> , 2022, 13, 1176.	5.8	26
2	Notch-dependent and -independent functions of transcription factor RBPJ. <i>Nucleic Acids Research</i> , 2022, 50, 7925-7937.	6.5	7
3	Analyses of Promoter, Enhancer, and Nucleosome Organization in Mammalian Cells by MNase-Seq. <i>Methods in Molecular Biology</i> , 2021, 2351, 93-104.	0.4	5
4	Fra-1 regulates its target genes via binding to remote enhancers without exerting major control on chromatin architecture in triple negative breast cancers. <i>Nucleic Acids Research</i> , 2021, 49, 2488-2508.	6.5	15
5	Stochastic pausing at latent HIV-1 promoters generates transcriptional bursting. <i>Nature Communications</i> , 2021, 12, 4503.	5.8	38
6	Immunopathological manifestations in Kabuki syndrome: a registry study of 177 individuals. <i>Genetics in Medicine</i> , 2020, 22, 181-188.	1.1	30
7	Alternative Enhancer Usage and Targeted Polycomb Marking Hallmark Promoter Choice during T Cell Differentiation. <i>Cell Reports</i> , 2020, 32, 108048.	2.9	13
8	Integration of high-throughput reporter assays identify a critical enhancer of the <i>Ikzf1</i> gene. <i>PLoS ONE</i> , 2020, 15, e0233191.	1.1	4
9	Evaluation of DNA Methylation Episignatures for Diagnosis and Phenotype Correlations in 42 Mendelian Neurodevelopmental Disorders. <i>American Journal of Human Genetics</i> , 2020, 106, 356-370.	2.6	171
10	The Landscape of L1 Retrotransposons in the Human Genome Is Shaped by Pre-insertion Sequence Biases and Post-insertion Selection. <i>Molecular Cell</i> , 2019, 74, 555-570.e7.	4.5	107
11	Critical role for TRIM28 and HP1 ^{2/3} in the epigenetic control of T cell metabolic reprogramming and effector differentiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 25839-25849.	3.3	23
12	MIR sequences recruit zinc finger protein ZNF768 to expressed genes. <i>Nucleic Acids Research</i> , 2019, 47, 700-715.	6.5	14
13	Regulation of the positive transcriptional effect of PLZF through a non-canonical EZH2 activity. <i>Nucleic Acids Research</i> , 2018, 46, 3339-3350.	6.5	26
14	Tyrosine-1 of RNA Polymerase II CTD Controls Global Termination of Gene Transcription in Mammals. <i>Molecular Cell</i> , 2018, 69, 48-61.e6.	4.5	66
15	Two possible modes of pioneering associated with combinations of H2A.Z and p300/CBP at nucleosome-occupied enhancers. <i>Transcription</i> , 2017, 8, 179-184.	1.7	7
16	ARS2 is a general suppressor of pervasive transcription. <i>Nucleic Acids Research</i> , 2017, 45, 10229-10241.	6.5	53
17	A threshold level of NFATc1 activity facilitates thymocyte differentiation and opposes notch-driven leukaemia development. <i>Nature Communications</i> , 2016, 7, 11841.	5.8	23
18	Pasha: a versatile R package for piling chromatin HTS data. <i>Bioinformatics</i> , 2016, 32, 2528-2530.	1.8	21

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19	Dynamic recruitment of Ets1 to both nucleosome-occupied and -depleted enhancer regions mediates a transcriptional program switch during early T-cell differentiation. <i>Nucleic Acids Research</i> , 2016, 44, 3567-3585.	6.5	39
20	The chromatin environment shapes DNA replication origin organization and defines origin classes. <i>Genome Research</i> , 2015, 25, 1873-1885.	2.4	149
21	Site- and allele-specific polycomb dysregulation in T-cell leukaemia. <i>Nature Communications</i> , 2015, 6, 6094.	5.8	47
22	High-throughput and quantitative assessment of enhancer activity in mammals by CapStarr-seq. <i>Nature Communications</i> , 2015, 6, 6905.	5.8	138
23	Transcription-Dependent Generation of a Specialized Chromatin Structure at the TCR β Locus. <i>Journal of Immunology</i> , 2015, 194, 3432-3443.	0.4	10
24	Site-specific methylation and acetylation of lysine residues in the C-terminal domain (CTD) of RNA polymerase II. <i>Transcription</i> , 2015, 6, 91-101.	1.7	22
25	Architecture and Expression of the Nfatc1 Gene in Lymphocytes. <i>Frontiers in Immunology</i> , 2014, 5, 21.	2.2	19
26	Tyrosine phosphorylation of RNA polymerase II CTD is associated with antisense promoter transcription and active enhancers in mammalian cells. <i>ELife</i> , 2014, 3, e02105.	2.8	76
27	Divergent transcription is associated with promoters of transcriptional regulators. <i>BMC Genomics</i> , 2013, 14, 914.	1.2	95
28	Editorial for "Diversity of the non-coding transcriptomes revealed by RNA-seq technologies". <i>Methods</i> , 2013, 63, 1-2.	1.9	2
29	An update on recent methods applied for deciphering the diversity of the noncoding RNA genome structure and function. <i>Methods</i> , 2013, 63, 3-17.	1.9	11
30	Noncoding Transcription at Enhancers: General Principles and Functional Models. <i>Annual Review of Genetics</i> , 2012, 46, 1-19.	3.2	348
31	CpG islands and GC content dictate nucleosome depletion in a transcription-independent manner at mammalian promoters. <i>Genome Research</i> , 2012, 22, 2399-2408.	2.4	197
32	Argonaute proteins couple chromatin silencing to alternative splicing. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 998-1004.	3.6	245
33	Threonine-4 of mammalian RNA polymerase II CTD is targeted by Polo-like kinase 3 and required for transcriptional elongation. <i>EMBO Journal</i> , 2012, 31, 2784-2797.	3.5	123
34	Splicing enhances recruitment of methyltransferase HYPB/Setd2 and methylation of histone H3 Lys36. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 977-983.	3.6	204
35	H3K4 tri-methylation provides an epigenetic signature of active enhancers. <i>EMBO Journal</i> , 2011, 30, 4198-4210.	3.5	265
36	Transcription initiation platforms and GTF recruitment at tissue-specific enhancers and promoters. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 956-963.	3.6	296

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37	Initiating RNA Polymerase II and TIPs as hallmarks of enhancer activity and tissue-specificity. <i>Transcription</i> , 2011, 2, 263-268.	1.7	33
38	The Ccr4â€“Not Deadenylase Subunits CNOT7 and CNOT8 Have Overlapping Roles and Modulate Cell Proliferation. <i>Molecular Biology of the Cell</i> , 2009, 20, 3840-3850.	0.9	92
39	CoCAS: a ChIP-on-chip analysis suite. <i>Bioinformatics</i> , 2009, 25, 954-955.	1.8	25
40	Genome-wide RNA polymerase II: not genes only!. <i>Trends in Biochemical Sciences</i> , 2008, 33, 265-273.	3.7	63
41	Genome-Wide Location of the Coactivator Mediator: Binding without Activation and Transient Cdk8 Interaction on DNA. <i>Molecular Cell</i> , 2006, 22, 179-192.	4.5	138
42	Genome-Wide Analyses Reveal RNA Polymerase II Located Upstream of Genes Poised for Rapid Response upon <i>S. cerevisiae</i> Stationary Phase Exit. <i>Molecular Cell</i> , 2005, 18, 171-183.	4.5	192
43	Mot1p is essential for TBP recruitment to selected promoters during in vivo gene activation. <i>EMBO Journal</i> , 2002, 21, 5173-5183.	3.5	55
44	Bâ€³-associated factor(s) involved in RNA polymerase III preinitiation complex formation and start-site selection. <i>FEBS Journal</i> , 2001, 268, 5167-5175.	0.2	12
45	Mutagenesis of yeast TFIIB70 reveals C-terminal residues critical for interaction with TBP and C34 1 Edited by M. Yaniv. <i>Journal of Molecular Biology</i> , 1999, 288, 511-520.	2.0	49