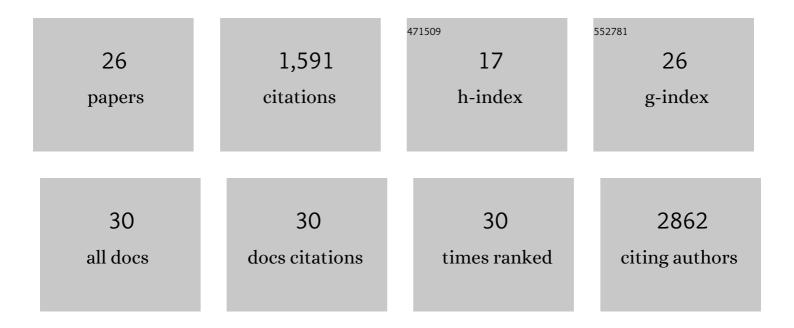
IvÃ;n D'Orso

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3070118/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Global landscape of HIV–human protein complexes. Nature, 2012, 481, 365-370.	27.8	651
2	CDK9: a signaling hub for transcriptional control. Transcription, 2019, 10, 57-75.	3.1	131
3	RNA-mediated displacement of an inhibitory snRNP complex activates transcription elongation. Nature Structural and Molecular Biology, 2010, 17, 815-821.	8.2	115
4	KAP1 Recruitment of the 7SK snRNP Complex to Promoters Enables Transcription Elongation by RNA Polymerase II. Molecular Cell, 2016, 61, 39-53.	9.7	109
5	Transcription Factors Mediate the Enzymatic Disassembly of Promoter-Bound 7SK snRNP to Locally Recruit P-TEFb for Transcription Elongation. Cell Reports, 2013, 5, 1256-1268.	6.4	74
6	Tat acetylation modulates assembly of a viral-host RNA–protein transcription complex. Proceedings of the United States of America, 2009, 106, 3101-3106.	7.1	59
7	Purification and characterization of HIV \hat{a} \in "human protein complexes. Methods, 2011, 53, 13-19.	3.8	56
8	HIV Tat controls RNA Polymerase II and the epigenetic landscape to transcriptionally reprogram target immune cells. ELife, 2015, 4, .	6.0	47
9	Transition Step during Assembly of HIV Tat:P-TEFb Transcription Complexes and Transfer to TAR RNA. Molecular and Cellular Biology, 2012, 32, 4780-4793.	2.3	46
10	PPM1G Binds 7SK RNA and Hexim1 To Block P-TEFb Assembly into the 7SK snRNP and Sustain Transcription Elongation. Molecular and Cellular Biology, 2015, 35, 3810-3828.	2.3	40
11	Transcription elongation control by the 7SK snRNP complex: Releasing the pause. Cell Cycle, 2016, 15, 2115-2123.	2.6	34
12	HIV-1 Proviral Transcription and Latency in the New Era. Viruses, 2020, 12, 555.	3.3	29
13	The HIV-1 Tat protein recruits a ubiquitin ligase to reorganize the 7SK snRNP for transcriptional activation. ELife, 2018, 7, .	6.0	29
14	KAP1 Is a Chromatin Reader that Couples Steps of RNA Polymerase II Transcription to Sustain Oncogenic Programs. Molecular Cell, 2020, 78, 1133-1151.e14.	9.7	26
15	CIPHER: a flexible and extensive workflow platform for integrative next-generation sequencing data analysis and genomic regulatory element prediction. BMC Bioinformatics, 2017, 18, 363.	2.6	25
16	Transcriptional Circuit Fragility Influences HIV Proviral Fate. Cell Reports, 2019, 27, 154-171.e9.	6.4	24
17	Transcription control by long non-coding RNAs. Transcription, 2012, 3, 78-86.	3.1	23
18	7SKiing on chromatin: Move globally, act locally. RNA Biology, 2016, 13, 545-553.	3.1	21

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#	Article	IF	CITATIONS
19	HIV-1 Tat: Its Dependence on Host Factors is Crystal Clear. Viruses, 2010, 2, 2226-2234.	3.3	19
20	Genome-wide analysis of KAP1, the 7SK snRNP complex, and RNA polymerase II. Genomics Data, 2016, 7, 250-255.	1.3	12
21	The ARF tumor suppressor targets PPM1G/PP2CÎ ³ to counteract NF-κB transcription tuning cell survival and the inflammatory response. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 32594-32605.	7.1	8
22	Tandem Affinity Purification of Protein Complexes from Eukaryotic Cells. Journal of Visualized Experiments, 2017, , .	0.3	6
23	Cleavage and Polyadenylation Specificity Factor 6 Is Required for Efficient HIV-1 Latency Reversal. MBio, 2021, 12, e0109821.	4.1	2
24	ADAP1 promotes latent HIV-1 reactivation by selectively tuning KRAS–ERK–AP-1 T cell signaling-transcriptional axis. Nature Communications, 2022, 13, 1109.	12.8	2
25	Nascent RNA: Friend or foe of the chromatin bound?. Molecular Cell, 2021, 81, 2871-2872.	9.7	1
26	Decoding Human Genome Regulatory Features That Influence HIV-1 Proviral Expression and Fate Through an Integrated Genomics Approach. Bioinformatics and Biology Insights, 2022, 16, 117793222110723.	2.0	1

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