Pierre-Étienne Jacques

List of Publications by Year
in descending order

44 papers	5,380 citations	236925 25 h-index	243625 44 g-index
45 all docs	45 docs citations	45 times ranked	7072 citing authors

#	ARTICLE	IF	CITATIONS
1	Human plasma pregnancy-associated miRNAs and their temporal variation within the first trimester of pregnancy. Reproductive Biology and Endocrinology, 2022, 20, 14.	3.3	17
2	First trimester plasma microRNAs levels predict Matsuda Index-estimated insulin sensitivity between 24th and 29th week of pregnancy. BMJ Open Diabetes Research and Care, 2022, 10, e002703.	2.8	6
3	Investigating the role of RNA structures in transcriptional pausing using in vitro assays and in silico analyses. RNA Biology, 2022, 19, 916-927.	3.1	0
4	Comparative epigenome-wide analysis highlights placenta-specific differentially methylated regions. Epigenomics, 2021, 13, 357-368.	2.1	5
5	MetaboAnalyst 5.0: narrowing the gap between raw spectra and functional insights. Nucleic Acids Research, 2021, 49, W388-W396.	14.5	2,221
6	Genome-scale metabolic modeling reveals key features of a minimal gene set. Molecular Systems Biology, 2021, 17, e10099.	7.2	15
7	Inactivation of the riboswitch-controlled GMP synthase GuaA in *Clostridioides difficile* is associated with severe growth defects and poor infectivity in a mouse model of infection. RNA Biology, 2021, 18, 699-710.	3.1	5
8	Nutrient-dependent control of RNA polymerase II elongation rate regulates specific gene expression programs by alternative polyadenylation. Genes and Development, 2020, 34, 883-897.	5.9	33
9	Molecular diagnosis of muscular diseases in outpatient clinics. Neurology: Genetics, 2020, 6, e408.	1.9	15
10	Integrative characterization of the near-minimal bacterium *Mesoplasma florum*. Molecular Systems Biology, 2020, 16, e9844.	7.2	12
11	The epiGenomic Efficient Correlator (epiGeEC) tool allows fast comparison of user datasets with thousands of public epigenomic datasets. Bioinformatics, 2019, 35, 674-676.	4.1	5
12	BOFdat: Generating biomass objective functions for genome-scale metabolic models from experimental data. PLoS Computational Biology, 2019, 15, e1006971.	3.2	83
13	Clinical validity of phenotype-driven analysis software PhenoVar as a diagnostic aid for clinical geneticists in the interpretation of whole-exome sequencing data. Genetics in Medicine, 2018, 20, 942-949.	2.4	15
14	The DNA double-strand "breakome" of mouse spermatids. Cellular and Molecular Life Sciences, 2018, 75, 2859-2872.	5.4	14
15	Common mechanism of transcription termination at coding and noncoding RNA genes in fission yeast. Nature Communications, 2018, 9, 4364.	12.8	35
16	Translatome analysis of an NB-LRR immune response identifies important contributors to plant immunity in Arabidopsis. Journal of Experimental Botany, 2017, 68, 2333-2344.	4.8	88
17	Global inhibition of transcription causes an increase in histone H2A.Z incorporation within gene bodies. Nucleic Acids Research, 2017, 45, 12715-12722.	14.5	28
18	High-Resolution Genome-Wide Mapping of Nucleosome Positioning and Occupancy Level Using Paired-End Sequencing Technology. Methods in Molecular Biology, 2017, 1528, 229-243.	0.9	4

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19	Transfer activation of SXT/R391 integrative and conjugative elements: unraveling the SetCD regulon. Nucleic Acids Research, 2015, 43, 2045-2056.	14.5	48
20	Aggregate and Heatmap Representations of Genome-Wide Localization Data Using VAP, a Versatile Aggregate Profiler. Methods in Molecular Biology, 2015, 1334, 273-298.	0.9	17
21	The histone variant H2A.Z is an important regulator of enhancer activity. Nucleic Acids Research, 2015, 43, gkv825.	14.5	80
22	Systems consequences of amplicon formation in human breast cancer. Genome Research, 2014, 24, 1559-1571.	5.5	32
23	VAP: a versatile aggregate profiler for efficient genome-wide data representation and discovery. Nucleic Acids Research, 2014, 42, W485-W493.	14.5	33
24	The retrovirus HERVH is a long noncoding RNA required for human embryonic stem cell identity. Nature Structural and Molecular Biology, 2014, 21, 423-425.	8.2	347
25	The Switch from Fermentation to Respiration in <i>Saccharomyces cerevisiae</i> Is Regulated by the Ert1 Transcriptional Activator/Repressor. Genetics, 2014, 198, 547-560.	2.9	31
26	SON connects the splicing-regulatory network with pluripotency in human embryonic stem cells. Nature Cell Biology, 2013, 15, 1141-1152.	10.3	84
27	The Majority of Primate-Specific Regulatory Sequences Are Derived from Transposable Elements. PLoS Genetics, 2013, 9, e1003504.	3.5	293
28	A Positive Feedback Loop Links Opposing Functions of P-TEFb/Cdk9 and Histone H2B Ubiquitylation to Regulate Transcript Elongation in Fission Yeast. PLoS Genetics, 2012, 8, e1002822.	3.5	53
29	Dynamic Deposition of Histone Variant H3.3 Accompanies Developmental Remodeling of the Arabidopsis Transcriptome. PLoS Genetics, 2012, 8, e1002658.	3.5	118
30	A Universal RNA Polymerase II CTD Cycle Is Orchestrated by Complex Interplays between Kinase, Phosphatase, and Isomerase Enzymes along Genes. Molecular Cell, 2012, 45, 158-170.	9.7	186
31	Control of Chromatin Structure by Spt6: Different Consequences in Coding and Regulatory Regions. Molecular and Cellular Biology, 2011, 31, 531-541.	2.3	68
32	The Peptidyl Prolyl Isomerase Rrd1 Regulates the Elongation of RNA Polymerase II during Transcriptional Stresses. PLoS ONE, 2011, 6, e23159.	2.5	20
33	Systematic identification of fragile sites via genome-wide location analysis of Î³-H2AX. Nature Structural and Molecular Biology, 2010, 17, 299-305.	8.2	167
34	DSIF and RNA Polymerase II CTD Phosphorylation Coordinate the Recruitment of Rpd3S to Actively Transcribed Genes. PLoS Genetics, 2010, 6, e1001173.	3.5	122
35	Cytosine Deaminase as a Negative Selection Marker for Gene Disruption and Replacement in the Genus <i>Streptomyces</i> and Other Actinobacteria. Applied and Environmental Microbiology, 2009, 75, 1211-1214.	3.1	45
36	The Euchromatic and Heterochromatic Landscapes Are Shaped by Antagonizing Effects of Transcription on H2A.Z Deposition. PLoS Genetics, 2009, 5, e1000687.	3.5	117

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37	Histone H2A.Z is essential for estrogen receptor signaling. Genes and Development, 2009, 23, 1522-1533.	5.9	133
38	Yeast RNase III Triggers Polyadenylation-Independent Transcription Termination. Molecular Cell, 2009, 36, 99-109.	9.7	48
39	Identification of Mycobacterial Ïƒ Factor Binding Sites by Chromatin Immunoprecipitation Assays. Journal of Bacteriology, 2007, 189, 1505-1513.	2.2	87
40	Genome-Wide Replication-Independent Histone H3 Exchange Occurs Predominantly at Promoters and Implicates H3 K56 Acetylation and Asf1. Molecular Cell, 2007, 27, 393-405.	9.7	292
41	The Ïƒ factors ofMycobacterium tuberculosis. FEMS Microbiology Reviews, 2006, 30, 926-941.	8.6	191
42	Detection of prokaryotic promoters from the genomic distribution of hexanucleotide pairs. BMC Bioinformatics, 2006, 7, 423.	2.6	28
43	MtbRegList, a database dedicated to the analysis of transcriptional regulation in Mycobacterium tuberculosis. Bioinformatics, 2005, 21, 2563-2565.	4.1	42
44	Novel Mycobacterium tuberculosis anti-Ïƒ factor antagonists control ÏƒF activity by distinct mechanisms. Molecular Microbiology, 2002, 45, 1527-1540.	2.5	94