

Pierre-Ëtienne Jacques

List of Publications by Year in descending order

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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	MetaboAnalyst 5.0: narrowing the gap between raw spectra and functional insights. <i>Nucleic Acids Research</i> , 2021, 49, W388-W396.	14.5	2,221
2	The retrovirus HERVH is a long noncoding RNA required for human embryonic stem cell identity. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 423-425.	8.2	347
3	The Majority of Primate-Specific Regulatory Sequences Are Derived from Transposable Elements. <i>PLoS Genetics</i> , 2013, 9, e1003504.	3.5	293
4	Genome-Wide Replication-Independent Histone H3 Exchange Occurs Predominantly at Promoters and Implicates H3 K56 Acetylation and Asf1. <i>Molecular Cell</i> , 2007, 27, 393-405.	9.7	292
5	The σ factors of <i>Mycobacterium tuberculosis</i> . <i>FEMS Microbiology Reviews</i> , 2006, 30, 926-941.	8.6	191
6	A Universal RNA Polymerase II CTD Cycle Is Orchestrated by Complex Interplays between Kinase, Phosphatase, and Isomerase Enzymes along Genes. <i>Molecular Cell</i> , 2012, 45, 158-170.	9.7	186
7	Systematic identification of fragile sites via genome-wide location analysis of γ -H2AX. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 299-305.	8.2	167
8	Histone H2A.Z is essential for estrogen receptor signaling. <i>Genes and Development</i> , 2009, 23, 1522-1533.	5.9	133
9	DSIF and RNA Polymerase II CTD Phosphorylation Coordinate the Recruitment of Rpd3S to Actively Transcribed Genes. <i>PLoS Genetics</i> , 2010, 6, e1001173.	3.5	122
10	Dynamic Deposition of Histone Variant H3.3 Accompanies Developmental Remodeling of the Arabidopsis Transcriptome. <i>PLoS Genetics</i> , 2012, 8, e1002658.	3.5	118
11	The Euchromatic and Heterochromatic Landscapes Are Shaped by Antagonizing Effects of Transcription on H2A.Z Deposition. <i>PLoS Genetics</i> , 2009, 5, e1000687.	3.5	117
12	Novel <i>Mycobacterium tuberculosis</i> anti- σ factor antagonists control σ F activity by distinct mechanisms. <i>Molecular Microbiology</i> , 2002, 45, 1527-1540.	2.5	94
13	Translatome analysis of an NB-LRR immune response identifies important contributors to plant immunity in Arabidopsis. <i>Journal of Experimental Botany</i> , 2017, 68, 2333-2344.	4.8	88
14	Identification of <i>Mycobacterium tuberculosis</i> σ Factor Binding Sites by Chromatin Immunoprecipitation Assays. <i>Journal of Bacteriology</i> , 2007, 189, 1505-1513.	2.2	87
15	SON connects the splicing-regulatory network with pluripotency in human embryonic stem cells. <i>Nature Cell Biology</i> , 2013, 15, 1141-1152.	10.3	84
16	BOFdat: Generating biomass objective functions for genome-scale metabolic models from experimental data. <i>PLoS Computational Biology</i> , 2019, 15, e1006971.	3.2	83
17	The histone variant H2A.Z is an important regulator of enhancer activity. <i>Nucleic Acids Research</i> , 2015, 43, gkv825.	14.5	80
18	Control of Chromatin Structure by Spt6: Different Consequences in Coding and Regulatory Regions. <i>Molecular and Cellular Biology</i> , 2011, 31, 531-541.	2.3	68

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19	A Positive Feedback Loop Links Opposing Functions of P-TEFb/Cdk9 and Histone H2B Ubiquitylation to Regulate Transcript Elongation in Fission Yeast. <i>PLoS Genetics</i> , 2012, 8, e1002822.	3.5	53
20	Yeast RNase III Triggers Polyadenylation-Independent Transcription Termination. <i>Molecular Cell</i> , 2009, 36, 99-109.	9.7	48
21	Transfer activation of SXT/R391 integrative and conjugative elements: unraveling the SetCD regulon. <i>Nucleic Acids Research</i> , 2015, 43, 2045-2056.	14.5	48
22	Cytosine Deaminase as a Negative Selection Marker for Gene Disruption and Replacement in the Genus <i>Streptomyces</i> and Other Actinobacteria. <i>Applied and Environmental Microbiology</i> , 2009, 75, 1211-1214.	3.1	45
23	MtbRegList, a database dedicated to the analysis of transcriptional regulation in <i>Mycobacterium tuberculosis</i> . <i>Bioinformatics</i> , 2005, 21, 2563-2565.	4.1	42
24	Common mechanism of transcription termination at coding and noncoding RNA genes in fission yeast. <i>Nature Communications</i> , 2018, 9, 4364.	12.8	35
25	VAP: a versatile aggregate profiler for efficient genome-wide data representation and discovery. <i>Nucleic Acids Research</i> , 2014, 42, W485-W493.	14.5	33
26	Nutrient-dependent control of RNA polymerase II elongation rate regulates specific gene expression programs by alternative polyadenylation. <i>Genes and Development</i> , 2020, 34, 883-897.	5.9	33
27	Systems consequences of amplicon formation in human breast cancer. <i>Genome Research</i> , 2014, 24, 1559-1571.	5.5	32
28	The Switch from Fermentation to Respiration in <i>Saccharomyces cerevisiae</i> Is Regulated by the Ert1 Transcriptional Activator/Repressor. <i>Genetics</i> , 2014, 198, 547-560.	2.9	31
29	Detection of prokaryotic promoters from the genomic distribution of hexanucleotide pairs. <i>BMC Bioinformatics</i> , 2006, 7, 423.	2.6	28
30	Global inhibition of transcription causes an increase in histone H2A.Z incorporation within gene bodies. <i>Nucleic Acids Research</i> , 2017, 45, 12715-12722.	14.5	28
31	The Peptidyl Prolyl Isomerase Rrd1 Regulates the Elongation of RNA Polymerase II during Transcriptional Stresses. <i>PLoS ONE</i> , 2011, 6, e23159.	2.5	20
32	Aggregate and Heatmap Representations of Genome-Wide Localization Data Using VAP, a Versatile Aggregate Profiler. <i>Methods in Molecular Biology</i> , 2015, 1334, 273-298.	0.9	17
33	Human plasma pregnancy-associated miRNAs and their temporal variation within the first trimester of pregnancy. <i>Reproductive Biology and Endocrinology</i> , 2022, 20, 14.	3.3	17
34	Clinical validity of phenotype-driven analysis software PhenoVar as a diagnostic aid for clinical geneticists in the interpretation of whole-exome sequencing data. <i>Genetics in Medicine</i> , 2018, 20, 942-949.	2.4	15
35	Molecular diagnosis of muscular diseases in outpatient clinics. <i>Neurology: Genetics</i> , 2020, 6, e408.	1.9	15
36	Genome-scale metabolic modeling reveals key features of a minimal gene set. <i>Molecular Systems Biology</i> , 2021, 17, e10099.	7.2	15

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37	The DNA double-strand breakome of mouse spermatids. <i>Cellular and Molecular Life Sciences</i> , 2018, 75, 2859-2872.	5.4	14
38	Integrative characterization of the near-minimal bacterium <i>Mesoplasma florum</i> . <i>Molecular Systems Biology</i> , 2020, 16, e9844.	7.2	12
39	First trimester plasma microRNAs levels predict Matsuda Index-estimated insulin sensitivity between 24th and 29th week of pregnancy. <i>BMJ Open Diabetes Research and Care</i> , 2022, 10, e002703.	2.8	6
40	The epiGenomic Efficient Correlator (epiGeEC) tool allows fast comparison of user datasets with thousands of public epigenomic datasets. <i>Bioinformatics</i> , 2019, 35, 674-676.	4.1	5
41	Comparative epigenome-wide analysis highlights placenta-specific differentially methylated regions. <i>Epigenomics</i> , 2021, 13, 357-368.	2.1	5
42	Inactivation of the riboswitch-controlled GMP synthase GuaA in <i>Clostridioides difficile</i> is associated with severe growth defects and poor infectivity in a mouse model of infection. <i>RNA Biology</i> , 2021, 18, 699-710.	3.1	5
43	High-Resolution Genome-Wide Mapping of Nucleosome Positioning and Occupancy Level Using Paired-End Sequencing Technology. <i>Methods in Molecular Biology</i> , 2017, 1528, 229-243.	0.9	4
44	Investigating the role of RNA structures in transcriptional pausing using in vitro assays and in silico analyses. <i>RNA Biology</i> , 2022, 19, 916-927.	3.1	0