Nicolas Bellora

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/783503/publications.pdf

Version: 2024-02-01

40 papers

2,722 citations

304743

22

h-index

302126 39 g-index

52 all docs 52 docs citations

52 times ranked 5157 citing authors

#	Article	IF	Citations
1	Comprehensive phylogeny of ray-finned fishes (Actinopterygii) based on transcriptomic and genomic data. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 6249-6254.	7.1	445
2	Jagged1 is the pathological link between Wnt and Notch pathways in colorectal cancer. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 6315-6320.	7.1	338
3	The Genome Sequence of (i) Saccharomyces eubayanus (i) and the Domestication of Lager-Brewing Yeasts. Molecular Biology and Evolution, 2015, 32, 2818-2831.	8.9	217
4	Leveraging transcript quantification for fast computation of alternative splicing profiles. Rna, 2015, 21, 1521-1531.	3.5	213
5	Origin of Primate Orphan Genes: A Comparative Genomics Approach. Molecular Biology and Evolution, 2008, 26, 603-612.	8.9	201
6	Nuclear matrix protein Matrin3 regulates alternative splicing and forms overlapping regulatory networks with <scp>PTB</scp> . EMBO Journal, 2015, 34, 653-668.	7.8	124
7	Interferon- \hat{I}^3 Is a Critical Modulator of CB ₂ Cannabinoid Receptor Signaling during Neuropathic Pain. Journal of Neuroscience, 2008, 28, 12136-12145.	3.6	122
8	The translational landscape of the splicing factor SRSF1 and its role in mitosis. ELife, 2014, 3, e02028.	6.0	96
9	Argonaute-1 binds transcriptional enhancers and controls constitutive and alternative splicing in human cells. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15622-15629.	7.1	86
10	In mammalian foetal testes, SOX9 regulates expression of its target genes by binding to genomic regions with conserved signatures. Nucleic Acids Research, 2017, 45, 7191-7211.	14.5	77
11	Molecular bases of responses to abiotic stress in trees. Journal of Experimental Botany, 2020, 71, 3765-3779.	4.8	65
12	Housekeeping genes tend to show reduced upstream sequence conservation. Genome Biology, 2007, 8, R140.	9.6	64
13	Structural basis for the biological relevance of the invariant apical stem in IRES-mediated translation. Nucleic Acids Research, 2011, 39, 8572-8585.	14.5	58
14	A chromatin code for alternative splicing involving a putative association between CTCF and HP1 $\hat{l}\pm$ proteins. BMC Biology, 2015, 13, 31.	3.8	52
15	The alternative splicing program of differentiated smooth muscle cells involves concerted non-productive splicing of post-transcriptional regulators. Nucleic Acids Research, 2016, 44, 8933-8950.	14.5	47
16	Chromatin-Bound lîºBî± Regulates a Subset of Polycomb Target Genes in Differentiation and Cancer. Cancer Cell, 2013, 24, 151-166.	16.8	46
17	Lineage-specific roles of the cytoplasmic polyadenylation factor CPEB4 in the regulation of melanoma drivers. Nature Communications, 2016, 7, 13418.	12.8	46
18	Splicing-associated chromatin signatures: a combinatorial and position-dependent role for histone marks in splicing definition. Nature Communications, 2021, 12, 682.	12.8	43

#	Article	IF	Citations
19	Genomic content of a novel yeast species Hanseniaspora gamundiae sp. nov. from fungal stromata (Cyttaria) associated with a unique fermented beverage in Andean Patagonia, Argentina. PLoS ONE, 2019, 14, e0210792.	2.5	37
20	Comparative genomics provides new insights into the diversity, physiology, and sexuality of the only industrially exploited tremellomycete: Phaffia rhodozyma. BMC Genomics, 2016, 17, 901.	2.8	35
21	Evolution of primate orphan proteins. Biochemical Society Transactions, 2009, 37, 778-782.	3.4	31
22	Deciphering the modulation of gene expression by type I and II interferons combining 4sU-tagging, translational arrest and in silico promoter analysis. Nucleic Acids Research, 2013, 41, 8107-8125.	14.5	31
23	Nucleo-cytoplasmic shuttling of splicing factor SRSF1 is required for development and cilia function. ELife, 2021, 10, .	6.0	25
24	ILF3 contributes to the establishment of the antiviral type I interferon program. Nucleic Acids Research, 2020, 48, 116-129.	14.5	20
25	Positional bias of general and tissue-specific regulatory motifs in mouse gene promoters. BMC Genomics, 2007, 8, 459.	2.8	19
26	mRNA spindle localization and mitotic translational regulation by CPEB1 and CPEB4. Rna, 2021, 27, 291-302.	3.5	19
27	Preferential binding of a stable G3 <scp>BP</scp> ribonucleoprotein complex to intronâ€retaining transcripts in mouse brain and modulation of their expression in the cerebellum. Journal of Neurochemistry, 2016, 139, 349-368.	3.9	17
28	Tumor Necrosis Factor-Mediated Survival of CD169 ⁺ Cells Promotes Immune Activation during Vesicular Stomatitis Virus Infection. Journal of Virology, 2018, 92, .	3.4	16
29	PEAKS: identification of regulatory motifs by their position in DNA sequences. Bioinformatics, 2007, 23, 243-244.	4.1	15
30	Spontaneous circadian rhythms in a cold-adapted natural isolate of Aureobasidium pullulans. Scientific Reports, 2017, 7, 13837.	3.3	15
31	Unique genomic traits for cold adaptation in <i>Naganishia vishniacii</i> , a polyextremophile yeast isolated from Antarctica. FEMS Yeast Research, 2021, 21, .	2.3	14
32	Hanseniaspora smithiae sp. nov., a Novel Apiculate Yeast Species From Patagonian Forests That Lacks the Typical Genomic Domestication Signatures for Fermentative Environments. Frontiers in Microbiology, 2021, 12, 679894.	3.5	10
33	Chromatin topology defines estradiol-primed progesterone receptor and PAX2 binding in endometrial cancer cells. ELife, 2022, 11 , .	6.0	10
34	The Untapped Australasian Diversity of Astaxanthin-Producing Yeasts with Biotechnological Potential—Phaffia australis sp. nov. and Phaffia tasmanica sp. nov Microorganisms, 2020, 8, 1651.	3.6	9
35	High-throughput meta-analysis and validation of differentially expressed genes as potential biomarkers of ionizing radiation-response. Radiotherapy and Oncology, 2021, 154, 21-28.	0.6	7
36	Deciphering the transcriptomic regulation of heat stress responses in Nothofagus pumilio. PLoS ONE, 2021, 16, e0246615.	2.5	6

3

#	Article	IF	CITATIONS
37	A Quantitative Profiling Tool for Diverse Genomic Data Types Reveals Potential Associations between Chromatin and Pre-mRNA Processing. PLoS ONE, 2015, 10, e0132448.	2.5	5
38	Canonical ErbB-2 isoform and ErbB-2 variant c located in the nucleus drive triple negative breast cancer growth. Oncogene, 2020, 39, 6245-6262.	5.9	5
39	Novel yeast taxa from the cold: description of Cryolevonia giraudoae sp. nov. and Camptobasidium gelus sp. nov International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3711-3717.	1.7	4
40	Biotechnologically Relevant Yeasts from Patagonian Natural Environments., 2016,, 325-351.		3