

Stéphane Le Crom

List of Publications by Year in descending order

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47
papers

4,791
citations

186265
28
h-index

214800
47
g-index

53
all docs

53
docs citations

53
times ranked

7582
citing authors

#	ARTICLE	IF	CITATIONS
1	Local Translation in Perisynaptic Astrocytic Processes Is Specific and Changes after Fear Conditioning. <i>Cell Reports</i> , 2020, 32, 108076.	6.4	53
2	Analysis of the genomic basis of functional diversity in dinoflagellates using a transcriptome-based sequence similarity network. <i>Molecular Ecology</i> , 2018, 27, 2365-2380.	3.9	12
3	Comparative Transcriptomics Highlights New Features of the Iron Starvation Response in the Human Pathogen <i>Candida glabrata</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 2689.	3.5	7
4	Connexin 43 Controls the Astrocyte Immunoregulatory Phenotype. <i>Brain Sciences</i> , 2018, 8, 50.	2.3	16
5	Cyclin G and the Polycomb Repressive complexes PRC1 and PR-DUB cooperate for developmental stability. <i>PLoS Genetics</i> , 2018, 14, e1007498.	3.5	7
6	Isolation and differential transcriptome of vascular smooth muscle cells and mid-capillary pericytes from the rat brain. <i>Scientific Reports</i> , 2018, 8, 12272.	3.3	55
7	Increased Fatty Acid Oxidation in Differentiated Proximal Tubular Cells Surviving a Reversible Episode of Acute Kidney Injury. <i>Cellular Physiology and Biochemistry</i> , 2018, 47, 1338-1351.	1.6	19
8	Meet-U: Educating through research immersion. <i>PLoS Computational Biology</i> , 2018, 14, e1005992.	3.2	4
9	Translation in astrocyte distal processes sets molecular heterogeneity at the gliovascular interface. <i>Cell Discovery</i> , 2017, 3, 17005.	6.7	130
10	Genome sequencing and transcriptome analysis of <i>Trichoderma reesei</i> QM9978 strain reveals a distal chromosome translocation to be responsible for loss of <i>vib1</i> expression and loss of cellulase induction. <i>Biotechnology for Biofuels</i> , 2017, 10, 209.	6.2	43
11	A Network of Paralogous Stress Response Transcription Factors in the Human Pathogen <i>Candida glabrata</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 645.	3.5	31
12	Genome sequencing of the <i>Trichoderma reesei</i> QM9136 mutant identifies a truncation of the transcriptional regulator XYR1 as the cause for its cellulase-negative phenotype. <i>BMC Genomics</i> , 2015, 16, 326.	2.8	31
13	Kinetic transcriptome analysis reveals an essentially intact induction system in a cellulase hyper-producer <i>Trichoderma reesei</i> strain. <i>Biotechnology for Biofuels</i> , 2014, 7, 173.	6.2	7
14	bPeaks: a bioinformatics tool to detect transcription factor binding sites from ChIPseq data in yeasts and other organisms with small genomes. <i>Yeast</i> , 2014, 31, 375-391.	1.7	23
15	B16 Mitogen And Stress-activated Kinase-1 Deficiency And Transcriptional Dysregulation In Huntington's Disease. <i>Journal of Neurology, Neurosurgery and Psychiatry</i> , 2014, 85, A14-A14.	1.9	0
16	Comparative transcriptomics reveals different strategies of <i>Trichoderma</i> mycoparasitism. <i>BMC Genomics</i> , 2013, 14, 121.	2.8	260
17	Insights into the role of DNA methylation in diatoms by genome-wide profiling in <i>Phaeodactylum tricornutum</i> . <i>Nature Communications</i> , 2013, 4, 2091.	12.8	113
18	A comprehensive evaluation of normalization methods for Illumina high-throughput RNA sequencing data analysis. <i>Briefings in Bioinformatics</i> , 2013, 14, 671-683.	6.5	1,064

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19	New Partners in Regulation of Gene Expression: The Enhancer of Trithorax and Polycomb Corto Interacts with Methylated Ribosomal Protein L12 Via Its Chromodomain. <i>PLoS Genetics</i> , 2012, 8, e1003006.	3.5	18
20	Eoulsan: a cloud computing-based framework facilitating high throughput sequencing analyses. <i>Bioinformatics</i> , 2012, 28, 1542-1543.	4.1	135
21	RNA sequencing revealed novel actors of the acquisition of drug resistance in <i>Candida albicans</i> . <i>BMC Genomics</i> , 2012, 13, 396.	2.8	30
22	Comparative genome sequence analysis underscores mycoparasitism as the ancestral life style of <i>Trichoderma</i> . <i>Genome Biology</i> , 2011, 12, R40.	8.8	594
23	The CRE1 carbon catabolite repressor of the fungus <i>Trichoderma reesei</i> : a master regulator of carbon assimilation. <i>BMC Genomics</i> , 2011, 12, 269.	2.8	180
24	Dok4 is involved in Schwann cell myelination and axonal interaction in vitro. <i>Glia</i> , 2011, 59, 351-362.	4.9	11
25	Differential Regulation of the Cellulase Transcription Factors XYR1, ACE2, and ACE1 in <i>Trichoderma reesei</i> Strains Producing High and Low Levels of Cellulase. <i>Eukaryotic Cell</i> , 2011, 10, 262-271.	3.4	136
26	Teolenn: an efficient and customizable workflow to design high-quality probes for microarray experiments. <i>Nucleic Acids Research</i> , 2010, 38, e117-e117.	14.5	23
27	Tracking the roots of cellulase hyperproduction by the fungus <i>Trichoderma reesei</i> using massively parallel DNA sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 16151-16156.	7.1	190
28	Selection of oligonucleotides for whole-genome microarrays with semi-automatic update. <i>Bioinformatics</i> , 2009, 25, 128-129.	4.1	48
29	An evaluation of custom microarray applications: the oligonucleotide design challenge. <i>Nucleic Acids Research</i> , 2009, 37, 1726-1739.	14.5	41
30	Novel features of boundary cap cells revealed by the analysis of newly identified molecular markers. <i>Glia</i> , 2009, 57, 1450-1457.	4.9	55
31	Genome-Wide Transcriptome Analyses of Silicon Metabolism in <i>Phaeodactylum tricornutum</i> Reveal the Multilevel Regulation of Silicic Acid Transporters. <i>PLoS ONE</i> , 2009, 4, e7458.	2.5	101
32	Identification of Phox2b-regulated genes by expression profiling of cranial motoneuron precursors. <i>Neural Development</i> , 2008, 3, 14.	2.4	16
33	Yeast Mitochondrial Biogenesis: A Role for the PUF RNA-Binding Protein Puf3p in mRNA Localization. <i>PLoS ONE</i> , 2008, 3, e2293.	2.5	208
34	The Central Role of PDR1 in the Foundation of Yeast Drug Resistance. <i>Journal of Biological Chemistry</i> , 2007, 282, 5063-5074.	3.4	64
35	Cross-Species Comparison Using Expression Data. , 2007, , 147-159.		1
36	Goulphar: rapid access and expertise for standard two-color microarray normalization methods. <i>BMC Bioinformatics</i> , 2006, 7, 467.	2.6	58

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37	Role of heat-shock factor 2 in cerebral cortex formation and as a regulator of p35 expression. <i>Genes and Development</i> , 2006, 20, 836-847.	5.9	85
38	Doelan: a solution for quality control monitoring of microarray production. <i>Bioinformatics</i> , 2005, 21, 4194-4195.	4.1	1
39	yMGV: a cross-species expression data mining tool. <i>Nucleic Acids Research</i> , 2004, 32, 323D-325.	14.5	6
40	Delineation of the conserved functional properties of D1A, D1B and D1C dopamine receptor subtypes in vertebrates. <i>Biology of the Cell</i> , 2004, 96, 383-394.	2.0	10
41	Dopamine receptors for every species: Gene duplications and functional diversification in Craniates. <i>Journal of Structural and Functional Genomics</i> , 2003, 3, 161-176.	1.2	46
42	Evolution and cell biology of dopamine receptors in vertebrates. <i>Biology of the Cell</i> , 2003, 95, 489-502.	2.0	159
43	yMGV: helping biologists with yeast microarray data mining. <i>Nucleic Acids Research</i> , 2002, 30, 76-79.	14.5	27
44	New Insights into the Pleiotropic Drug Resistance Network from Genome-Wide Characterization of the YRR1 Transcription Factor Regulation System. <i>Molecular and Cellular Biology</i> , 2002, 22, 2642-2649.	2.3	95
45	Ammonia Pulses and Metabolic Oscillations Guide Yeast Colony Development. <i>Molecular Biology of the Cell</i> , 2002, 13, 3901-3914.	2.1	131
46	Autocrine activation of adenosine A1 receptors blocks D1A but not D1B dopamine receptor desensitization. <i>Journal of Neurochemistry</i> , 2002, 82, 1549-1552.	3.9	19
47	Dopamine D1 and adenosine A1 receptors form functionally interacting heteromeric complexes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 8606-8611.	7.1	419