

# CÃ©line Hernandez

## List of Publications by Year in descending order

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Version: 2024-02-01

31  
papers

3,558  
citations

394421

19  
h-index

434195

31  
g-index

38  
all docs

38  
docs citations

38  
times ranked

6303  
citing authors

#	ARTICLE	IF	CITATIONS
1	The purinergic P2Y <sub>14</sub> receptor links hepatocyte death to hepatic stellate cell activation and fibrogenesis in the liver. <i>Science Translational Medicine</i> , 2022, 14, eabe5795.	12.4	25
2	Benchmarking joint multi-omics dimensionality reduction approaches for the study of cancer. <i>Nature Communications</i> , 2021, 12, 124.	12.8	89
3	Deciphering and modelling the TGF- $\beta$ signalling interplays specifying the dorsal-ventral axis of the sea urchin embryo. <i>Development (Cambridge)</i> , 2020, 148, .	2.5	4
4	Computational Verification of Large Logical Models Application to the Prediction of T Cell Response to Checkpoint Inhibitors. <i>Frontiers in Physiology</i> , 2020, 11, 558606.	2.8	18
5	Proteo-Transcriptomic Dynamics of Cellular Response to HIV-1 Infection. <i>Scientific Reports</i> , 2019, 9, 213.	3.3	24
6	Cooperation between T cell receptor and Toll-like receptor 5 signaling for CD4 <sup>+</sup> T cell activation. <i>Science Signaling</i> , 2019, 12, .	3.6	38
7	Contribution of ROS and metabolic status to neonatal and adult CD8 <sup>+</sup> T cell activation. <i>PLoS ONE</i> , 2019, 14, e0226388.	2.5	21
8	Logical Modeling and Analysis of Cellular Regulatory Networks With GINsim 3.0. <i>Frontiers in Physiology</i> , 2018, 9, 646.	2.8	75
9	The CoLoMoTo Interactive Notebook: Accessible and Reproducible Computational Analyses for Qualitative Biological Networks. <i>Frontiers in Physiology</i> , 2018, 9, 680.	2.8	67
10	Prediction of Mutations to Control Pathways Enabling Tumor Cell Invasion with the CoLoMoTo Interactive Notebook (Tutorial). <i>Frontiers in Physiology</i> , 2018, 9, 787.	2.8	13
11	Krox20 hindbrain regulation incorporates multiple modes of cooperation between cis-acting elements. <i>PLoS Genetics</i> , 2017, 13, e1006903.	3.5	18
12	Histone Chaperone SSRP1 is Essential for Wnt Signaling Pathway Activity During Osteoblast Differentiation. <i>Stem Cells</i> , 2016, 34, 1369-1376.	3.2	32
13	ChIP-exo signal associated with DNA-binding motifs provides insight into the genomic binding of the glucocorticoid receptor and cooperating transcription factors. <i>Genome Research</i> , 2015, 25, 825-835.	5.5	113
14	RSAT 2015: Regulatory Sequence Analysis Tools. <i>Nucleic Acids Research</i> , 2015, 43, W50-W56.	14.5	263
15	Cooperative development of logical modelling standards and tools with CoLoMoTo. <i>Bioinformatics</i> , 2015, 31, 1154-1159.	4.1	98
16	Shotgun Ecotoxicoproteomics of <i>Daphnia pulex</i> : Biochemical Effects of the Anticancer Drug Tamoxifen. <i>Journal of Proteome Research</i> , 2015, 14, 279-291.	3.7	16
17	Quantitative proteomics identifies the membrane-associated peroxidase GPx8 as a cellular substrate of the hepatitis C virus NS3-4A protease. <i>Hepatology</i> , 2014, 59, 423-433.	7.3	41
18	Database Construction and Peptide Identification Strategies for Proteogenomic Studies on Sequenced Genomes. <i>Current Topics in Medicinal Chemistry</i> , 2014, 14, 425-434.	2.1	17

#	ARTICLE	IF	CITATIONS
19	A Novel Pulse-Chase SILAC Strategy Measures Changes in Protein Decay and Synthesis Rates Induced by Perturbation of Proteostasis with an Hsp90 Inhibitor. PLoS ONE, 2013, 8, e80423.	2.5	42
20	Dynamic Impacts of the Inhibition of the Molecular Chaperone Hsp90 on the T-Cell Proteome Have Implications for Anti-Cancer Therapy. PLoS ONE, 2013, 8, e80425.	2.5	44
21	ExPASy: SIB bioinformatics resource portal. Nucleic Acids Research, 2012, 40, W597-W603.	14.5	1,737
22	Addressing Trypsin Bias in Large Scale (Phospho)proteome Analysis by Size Exclusion Chromatography and Secondary Digestion of Large Post-Trypsin Peptides. Journal of Proteome Research, 2011, 10, 800-811.	3.7	35
23	Early activation of the fatty acid metabolism pathway by chronic high glucose exposure in rat insulin secretory $\beta$ cells. Proteomics, 2010, 10, 59-71.	2.2	14
24	SwissPIT: An workflow-based platform for analyzing tandem-MS spectra using the Grid. Proteomics, 2009, 9, 2648-2655.	2.2	15
25	pICarver: A Software Tool and Strategy for Peptides Isoelectric Focusing. Journal of Proteome Research, 2008, 7, 4336-4345.	3.7	11
26	swissPIT: a novel approach for pipelined analysis of mass spectrometry data. Bioinformatics, 2008, 24, 1416-1417.	4.1	7
27	Labeling of Bifidobacterium longum Cells with $^{13}$ C-Substituted Leucine for Quantitative Proteomic Analyses. Applied and Environmental Microbiology, 2007, 73, 5653-5656.	3.1	11
28	Qualitative simulation of the initiation of sporulation in. Bulletin of Mathematical Biology, 2004, 66, 261-299.	1.9	81
29	Qualitative simulation of genetic regulatory networks using piecewise-linear models. Bulletin of Mathematical Biology, 2004, 66, 301-340.	1.9	309
30	Genetic Network Analyzer: qualitative simulation of genetic regulatory networks. Bioinformatics, 2003, 19, 336-344.	4.1	240
31	Hybrid Modeling and Simulation of Genetic Regulatory Networks: A Qualitative Approach. Lecture Notes in Computer Science, 2003, , 267-282.	1.3	32