

# CÃ©line Hernandez

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1755735/publications.pdf>

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	ExpASY: SIB bioinformatics resource portal. <i>Nucleic Acids Research</i> , 2012, 40, W597-W603.	14.5	1,737
2	Qualitative simulation of genetic regulatory networks using piecewise-linear models. <i>Bulletin of Mathematical Biology</i> , 2004, 66, 301-340.	1.9	309
3	RSAT 2015: Regulatory Sequence Analysis Tools. <i>Nucleic Acids Research</i> , 2015, 43, W50-W56.	14.5	263
4	Genetic Network Analyzer: qualitative simulation of genetic regulatory networks. <i>Bioinformatics</i> , 2003, 19, 336-344.	4.1	240
5	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
6	Cooperative development of logical modelling standards and tools with CoLoMoTo. <i>Bioinformatics</i> , 2015, 31, 1154-1159.	4.1	98
7	Benchmarking joint multi-omics dimensionality reduction approaches for the study of cancer. <i>Nature Communications</i> , 2021, 12, 124.	12.8	89
8	Qualitative simulation of the initiation of sporulation in. <i>Bulletin of Mathematical Biology</i> , 2004, 66, 261-299.	1.9	81
9	Logical Modeling and Analysis of Cellular Regulatory Networks With GINsim 3.0. <i>Frontiers in Physiology</i> , 2018, 9, 646.	2.8	75
10	The CoLoMoTo Interactive Notebook: Accessible and Reproducible Computational Analyses for Qualitative Biological Networks. <i>Frontiers in Physiology</i> , 2018, 9, 680.	2.8	67
11	Dynamic Impacts of the Inhibition of the Molecular Chaperone Hsp90 on the T-Cell Proteome Have Implications for Anti-Cancer Therapy. <i>PLoS ONE</i> , 2013, 8, e80425.	2.5	44
12	A Novel Pulse-Chase SILAC Strategy Measures Changes in Protein Decay and Synthesis Rates Induced by Perturbation of Proteostasis with an Hsp90 Inhibitor. <i>PLoS ONE</i> , 2013, 8, e80423.	2.5	42
13	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
14	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
15	Addressing Trypsin Bias in Large Scale (Phospho)proteome Analysis by Size Exclusion Chromatography and Secondary Digestion of Large Post-Trypsin Peptides. <i>Journal of Proteome Research</i> , 2011, 10, 800-811.	3.7	35
16	Hybrid Modeling and Simulation of Genetic Regulatory Networks: A Qualitative Approach. <i>Lecture Notes in Computer Science</i> , 2003, , 267-282.	1.3	32
17	Histone Chaperone SSRP1 is Essential for Wnt Signaling Pathway Activity During Osteoblast Differentiation. <i>Stem Cells</i> , 2016, 34, 1369-1376.	3.2	32
18	The purinergic P2Y14 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

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19	Proteo-Transcriptomic Dynamics of Cellular Response to HIV-1 Infection. <i>Scientific Reports</i> , 2019, 9, 213.	3.3	24
20	Contribution of ROS and metabolic status to neonatal and adult CD8+ T cell activation. <i>PLoS ONE</i> , 2019, 14, e0226388.	2.5	21
21	Krox20 hindbrain regulation incorporates multiple modes of cooperation between cis-acting elements. <i>PLoS Genetics</i> , 2017, 13, e1006903.	3.5	18
22	Computational Verification of Large Logical Modelsâ€™ Application to the Prediction of T Cell Response to Checkpoint Inhibitors. <i>Frontiers in Physiology</i> , 2020, 11, 558606.	2.8	18
23	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
24	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
25	SwissPIT: An workflowâ€based platform for analyzing tandemâ€MS spectra using the Grid. <i>Proteomics</i> , 2009, 9, 2648-2655.	2.2	15
26	Early activation of the fatty acid metabolism pathway by chronic high glucose exposure in rat insulin secretory Î²â€cells. <i>Proteomics</i> , 2010, 10, 59-71.	2.2	14
27	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
28	Labeling of <i>Bifidobacterium longum</i> Cells with 13 C-Substituted Leucine for Quantitative Proteomic Analyses. <i>Applied and Environmental Microbiology</i> , 2007, 73, 5653-5656.	3.1	11
29	pICarver: A Software Tool and Strategy for Peptides Isoelectric Focusing. <i>Journal of Proteome Research</i> , 2008, 7, 4336-4345.	3.7	11
30	swissPIT: a novel approach for pipelined analysis of mass spectrometry data. <i>Bioinformatics</i> , 2008, 24, 1416-1417.	4.1	7
31	Deciphering and modelling the TGF-Î² signalling interplays specifying the dorsal-ventral axis of the sea urchin embryo. <i>Development (Cambridge)</i> , 2020, 148, .	2.5	4