

Mathieu Lavallée-Adam

List of Publications by Year in descending order

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Version: 2024-02-01

41
papers

1,800
citations

331259

21
h-index

288905

40
g-index

49
all docs

49
docs citations

49
times ranked

3750
citing authors

#	ARTICLE	IF	CITATIONS
1	Ddp1 Cooperates with Ppx1 to Counter a Stress Response Initiated by Nonvacuolar Polyphosphate. <i>MBio</i> , 2022, 13, .	1.8	10
2	Identification of novel lipid droplet factors that regulate lipophagy and cholesterol efflux in macrophage foam cells. <i>Autophagy</i> , 2021, 17, 3671-3689.	4.3	90
3	Proteomics characterization of mitochondrial-derived vesicles under oxidative stress. <i>FASEB Journal</i> , 2021, 35, e21278.	0.2	36
4	PIGNON: a protein-protein interaction-guided functional enrichment analysis for quantitative proteomics. <i>BMC Bioinformatics</i> , 2021, 22, 302.	1.2	4
5	Proximity Interactome Map of the Vac14-Fig4 Complex Using BioID. <i>Journal of Proteome Research</i> , 2021, 20, 4959-4973.	1.8	4
6	Studying the Temporal Dynamics of the Gut Microbiota Using Metabolic Stable Isotope Labeling and Metaproteomics. <i>Analytical Chemistry</i> , 2020, 92, 15711-15718.	3.2	5
7	Computational Identification of Human Biological Processes and Protein Sequence Motifs Putatively Targeted by SARS-CoV-2 Proteins Using Protein-Protein Interaction Networks. <i>Journal of Proteome Research</i> , 2020, 19, 4553-4566.	1.8	13
8	Quantitative analysis of global protein stability rates in tissues. <i>Scientific Reports</i> , 2020, 10, 15983.	1.6	13
9	A functional ecological network based on metaproteomics responses of individual gut microbiomes to resistant starches. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3833-3842.	1.9	15
10	A Broad Response to Intracellular Long-Chain Polyphosphate in Human Cells. <i>Cell Reports</i> , 2020, 33, 108318.	2.9	33
11	pepFunk: a tool for peptide-centric functional analysis of metaproteomic human gut microbiome studies. <i>Bioinformatics</i> , 2020, 36, 4171-4179.	1.8	7
12	MealTime-MS: A Machine Learning-Guided Real-Time Mass Spectrometry Analysis for Protein Identification and Efficient Dynamic Exclusion. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 1459-1472.	1.2	5
13	Comparison of CRISPR Genomic Tagging for Affinity Purification and Endogenous Immunoprecipitation Coupled with Quantitative Mass Spectrometry To Identify the Dynamic AMPK \pm 2 Interactome. <i>Journal of Proteome Research</i> , 2019, 18, 3703-3714.	1.8	6
14	Proteomics INTEGRator (PINT): An Online Tool To Store, Query, and Visualize Large Proteomics Experiment Results. <i>Journal of Proteome Research</i> , 2019, 18, 2999-3008.	1.8	0
15	Proteomic analyses reveal misregulation of LIN28 expression and delayed timing of glial differentiation in human iPS cells with MECP2 loss-of-function. <i>PLoS ONE</i> , 2019, 14, e0212553.	1.1	23
16	Increased proteomic complexity in <i>Drosophila</i> hybrids during development. <i>Science Advances</i> , 2018, 4, eaao3424.	4.7	12
17	Proteomic and Metaproteomic Approaches to Understand Host-Microbe Interactions. <i>Analytical Chemistry</i> , 2018, 90, 86-109.	3.2	44
18	A complex of C9ORF72 and p62 uses arginine methylation to eliminate stress granules by autophagy. <i>Nature Communications</i> , 2018, 9, 2794.	5.8	126

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19	High infestation levels of <i>Schizotetranychus oryzae</i> severely affects rice metabolism. <i>Journal of Plant Physiology</i> , 2017, 219, 100-111.	1.6	23
20	Quantitative Analysis of the Proteome Response to the Histone Deacetylase Inhibitor (HDACi) Vorinostat in Niemann-Pick Type C1 disease. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1938-1957.	2.5	26
21	Amyloid Accumulation Drives Proteome-wide Alterations in Mouse Models of Alzheimer's Disease-like Pathology. <i>Cell Reports</i> , 2017, 21, 2614-2627.	2.9	56
22	Functional 5' UTR motif discovery with LESMoN: Local Enrichment of Sequence Motifs in biological Networks. <i>Nucleic Acids Research</i> , 2017, 45, 10415-10427.	6.5	9
23	Using PSEA-Quant for Protein Set Enrichment Analysis of Quantitative Mass Spectrometry-Based Proteomics. <i>Current Protocols in Bioinformatics</i> , 2016, 53, 13.28.1-13.28.16.	25.8	8
24	Physiological and Molecular Alterations Promoted by <i>Schizotetranychus oryzae</i> Mite Infestation in Rice Leaves. <i>Journal of Proteome Research</i> , 2016, 15, 431-446.	1.8	22
25	Curation of the Mammalian Palmitoylome Indicates a Pivotal Role for Palmitoylation in Diseases and Disorders of the Nervous System and Cancers. <i>PLoS Computational Biology</i> , 2015, 11, e1004405.	1.5	120
26	From Raw Data to Biological Discoveries: A Computational Analysis Pipeline for Mass Spectrometry-Based Proteomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2015, 26, 1820-1826.	1.2	17
27	Quantitative Proteomics of Human Fibroblasts with I1061T Mutation in Niemann-Pick C1 (NPC1) Protein Provides Insights into the Disease Pathogenesis*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1734-1749.	2.5	41
28	Recessive mutations in POLR1C cause a leukodystrophy by impairing biogenesis of RNA polymerase III. <i>Nature Communications</i> , 2015, 6, 7623.	5.8	127
29	The Sorting Receptor SorCS1 Regulates Trafficking of Neurexin and AMPA Receptors. <i>Neuron</i> , 2015, 87, 764-780.	3.8	71
30	5F08 CFTR interactome remodelling promotes rescue of cystic fibrosis. <i>Nature</i> , 2015, 528, 510-516.	13.7	225
31	Sheathless Capillary Electrophoresis-Tandem Mass Spectrometry for Top-Down Characterization of <i>Pyrococcus furiosus</i> Proteins on a Proteome Scale. <i>Analytical Chemistry</i> , 2014, 86, 11006-11012.	3.2	66
32	Methylation of the DNA/RNA-binding protein Kin17 by METTL22 affects its association with chromatin. <i>Journal of Proteomics</i> , 2014, 100, 115-124.	1.2	36
33	PSEA-Quant: A Protein Set Enrichment Analysis on Label-Free and Label-Based Protein Quantification Data. <i>Journal of Proteome Research</i> , 2014, 13, 5496-5509.	1.8	57
34	Discovery of Cell Compartment Specific Protein-Protein Interactions using Affinity Purification Combined with Tandem Mass Spectrometry. <i>Journal of Proteome Research</i> , 2013, 12, 272-281.	1.8	28
35	A Newly Uncovered Group of Distantly Related Lysine Methyltransferases Preferentially Interact with Molecular Chaperones to Regulate Their Activity. <i>PLoS Genetics</i> , 2013, 9, e1003210.	1.5	138
36	Nuclear import of RNA polymerase II is coupled with nucleocytoplasmic shuttling of the RNA polymerase II-associated protein 2. <i>Nucleic Acids Research</i> , 2013, 41, 6881-6891.	6.5	50

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37	Modeling Contaminants in AP-MS/MS Experiments. Journal of Proteome Research, 2011, 10, 886-895.	1.8	45
38	The Protein Interaction Network of the Human Transcription Machinery Reveals a Role for the Conserved GTPase RPAP4/GPN1 and Microtubule Assembly in Nuclear Import and Biogenesis of RNA Polymerase II. Molecular and Cellular Proteomics, 2010, 9, 2827-2839.	2.5	96
39	Detection of Locally Over-Represented GO Terms in Protein-Protein Interaction Networks. Journal of Computational Biology, 2010, 17, 443-457.	0.8	12
40	High-resolution mapping of the protein interaction network for the human transcription machinery and affinity purification of RNA polymerase II-associated complexes. Methods, 2009, 48, 381-386.	1.9	77
41	Detection of Locally Over-Represented GO Terms in Protein-Protein Interaction Networks. Lecture Notes in Computer Science, 2009, , 302-320.	1.0	3