## Francois-Michel Boisvert

List of Publications by Year in descending order

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66 papers

7,069 citations

34 h-index 65 g-index

70 all docs

70 docs citations

70 times ranked

9920 citing authors

#	Article	IF	CITATIONS
1	The multifunctional nucleolus. Nature Reviews Molecular Cell Biology, 2007, 8, 574-585.	37.0	1,306
2	The Nucleolus under Stress. Molecular Cell, 2010, 40, 216-227.	9.7	882
3	Identifying specific protein interaction partners using quantitative mass spectrometry and bead proteomes. Journal of Cell Biology, 2008, 183, 223-239.	5.2	404
4	A Quantitative Spatial Proteomics Analysis of Proteome Turnover in Human Cells. Molecular and Cellular Proteomics, 2012, 11, M111.011429.	3.8	332
5	A Proteomic Analysis of Arginine-methylated Protein Complexes. Molecular and Cellular Proteomics, 2003, 2, 1319-1330.	3.8	323
6	Promyelocytic Leukemia (Pml) Nuclear Bodies Are Protein Structures That Do Not Accumulate RNA. Journal of Cell Biology, 2000, 148, 283-292.	5.2	245
7	NOPdb: Nucleolar Proteome Database2008 update. Nucleic Acids Research, 2009, 37, D181-D184.	14.5	243
8	Sam68 RNA Binding Protein Is an In Vivo Substrate for Protein ArginineN-Methyltransferase 1. Molecular Biology of the Cell, 2003, 14, 274-287.	2.1	237
9	Direct Detection of Alternative Open Reading Frames Translation Products in Human Significantly Expands the Proteome. PLoS ONE, 2013, 8, e70698.	2.5	192
10	Arginine methylation of MRE11 by PRMT1 is required for DNA damage checkpoint control. Genes and Development, 2005, 19, 671-676.	5.9	181
11	Symmetrical dimethylarginine methylation is required for the localization of SMN in Cajal bodies and pre-mRNA splicing. Journal of Cell Biology, 2002, 159, 957-969.	5.2	175
12	Characterization and prediction of protein nucleolar localization sequences. Nucleic Acids Research, 2010, 38, 7388-7399.	14.5	167
13	A Quantitative Proteomics Analysis of Subcellular Proteome Localization and Changes Induced by DNA Damage. Molecular and Cellular Proteomics, 2010, 9, 457-470.	3.8	164
14	Glycogen Synthase Kinase-3 (GSK3) Inhibition Induces Prosurvival Autophagic Signals in Human Pancreatic Cancer Cells. Journal of Biological Chemistry, 2015, 290, 5592-5605.	3.4	145
15	The Transcription Coactivator Cbp Is a Dynamic Component of the Promyelocytic Leukemia Nuclear Body. Journal of Cell Biology, 2001, 152, 1099-1106.	5.2	141
16	A Role for the GSG Domain in Localizing Sam68 to Novel Nuclear Structures in Cancer Cell Lines. Molecular Biology of the Cell, 1999, 10, 3015-3033.	2.1	136
17	Two distinct arginine methyltransferases are required for biogenesis of Sm-class ribonucleoproteins. Journal of Cell Biology, 2007, 178, 733-740.	5.2	128
18	The GAR Motif of 53BP1 is Arginine Methylated by PRMT1 and is Necessary for 53BP1 DNA Binding Activity. Cell Cycle, 2005, 4, 1834-1841.	2.6	121

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19	Quantitative Proteomics and Dynamic Imaging of the Nucleolus Reveal Distinct Responses to UV and Ionizing Radiation. Molecular and Cellular Proteomics, 2011, 10, M111.009241.	3.8	110
20	Protein Interfaces in Signaling Regulated by Arginine Methylation. Science Signaling, 2005, 2005, re2-re2.	3.6	105
21	Human ING1 Proteins Differentially Regulate Histone Acetylation. Journal of Biological Chemistry, 2002, 277, 29832-29839.	3.4	91
22	Proteomics methods for subcellular proteome analysis. FEBS Journal, 2013, 280, 5626-5634.	4.7	87
23	Aven recognition of RNA G-quadruplexes regulates translation of the mixed lineage leukemia protooncogenes. ELife, 2015, 4, .	6.0	83
24	OpenProt: a more comprehensive guide to explore eukaryotic coding potential and proteomes. Nucleic Acids Research, 2019, 47, D403-D410.	14.5	71
25	OpenProt 2021: deeper functional annotation of the coding potential of eukaryotic genomes. Nucleic Acids Research, 2021, 49, D380-D388.	14.5	71
26	Methylation of MRE11 Regulates its Nuclear Compartmentalization. Cell Cycle, 2005, 4, 981-989.	2.6	70
27	The Product of the Survival of Motor Neuron(SMN) Gene is a Human Telomerase-associated Protein. Molecular Biology of the Cell, 2002, 13, 3192-3202.	2.1	60
28	Loss of functional caveolae during senescence of human fibroblasts. Journal of Cellular Physiology, 2001, 187, 226-235.	4.1	53
29	p53â€Dependent subcellular proteome localization following DNA damage. Proteomics, 2010, 10, 4087-4097.	2.2	51
30	Systematic Analysis of Protein Pools, Isoforms, and Modifications Affecting Turnover and Subcellular Localization. Molecular and Cellular Proteomics, 2012, 11, M111.013680.	3.8	48
31	APEX2â€mediated RAB proximity labeling identifies a role for RAB21 in clathrinâ€independent cargo sorting. EMBO Reports, 2019, 20, .	4.5	44
32	The response to neoadjuvant chemoradiotherapy with 5-fluorouracil in locally advanced rectal cancer patients: a predictive proteomic signature. Clinical Proteomics, 2018, 15, 16.	2.1	43
33	Compartmentalization of regulatory proteins in the cell nucleus. Journal of Steroid Biochemistry and Molecular Biology, 2001, 76, 9-21.	2.5	41
34	RRP1B Targets PP1 to Mammalian Cell Nucleoli and Is Associated with Pre-60S Ribosomal Subunits. Molecular Biology of the Cell, 2010, 21, 4212-4226.	2.1	39
35	Quantitative Proteomics Reveals Dynamic Interactions of the Minichromosome Maintenance Complex (MCM) in the Cellular Response to Etoposide Induced DNA Damage*. Molecular and Cellular Proteomics, 2015, 14, 2002-2013.	3.8	37
36	UBB pseudogene 4 encodes functional ubiquitin variants. Nature Communications, 2020, 11, 1306.	12.8	34

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37	Clinical Proteomics in Colorectal Cancer, a Promising Tool for Improving Personalised Medicine. Proteomes, 2018, 6, 49.	3.5	31
38	Human Hepatocyte Nuclear Factor $4\hat{l}\pm$ Encodes Isoforms with Distinct Transcriptional Functions. Molecular and Cellular Proteomics, 2020, 19, 808-827.	3.8	31
39	Phenotypic Analysis of Organoids by Proteomics. Proteomics, 2017, 17, 1700023.	2.2	29
40	A Screen for Novel Phosphoinositide 3-kinase Effector Proteins. Molecular and Cellular Proteomics, 2011, 10, M110.003178.	3.8	26
41	A SILAC-Based Method for Quantitative Proteomic Analysis of Intestinal Organoids. Scientific Reports, 2016, 6, 38195.	3.3	24
42	Efficient extraction of nucleolar proteins for interactome analyses. Proteomics, 2010, 10, 3045-3050.	2.2	22
43	The Nucleolus: Structure and Function. , 2016, , 29-49.		20
44	Destabilization of the MiniChromosome Maintenance (MCM) complex modulates the cellular response to DNA double strand breaks. Cell Cycle, 2018, 17, 2593-2609.	2.6	20
45	Comprehensive Characterization of Minichromosome Maintenance Complex (MCM) Protein Interactions Using Affinity and Proximity Purifications Coupled to Mass Spectrometry. Journal of Proteome Research, 2016, 15, 2924-2934.	3.7	18
46	Human PDCD2L Is an Export Substrate of CRM1 That Associates with 40S Ribosomal Subunit Precursors. Molecular and Cellular Biology, 2016, 36, 3019-3032.	2.3	17
47	Loss of histone deacetylase Hdac1 disrupts metabolic processes in intestinal epithelial cells. FEBS Letters, 2015, 589, 2776-2783.	2.8	14
48	Proteomic Profiling of Mitochondrial-Derived Vesicles in Brain Reveals Enrichment of Respiratory Complex Sub-assemblies and Small TIM Chaperones. Journal of Proteome Research, 2021, 20, 506-517.	3.7	14
49	Proteomic profiling and functional characterization of post-translational modifications of the fission yeast RNA exosome. Nucleic Acids Research, 2018, 46, 11169-11183.	14.5	13
50	Quantitative Proteomics Identifies DNA Repair as a Novel Biological Function for Hepatocyte Nuclear Factor $4\hat{l}_{\pm}$ in Colorectal Cancer Cells. Cancers, 2019, 11, 626.	3.7	13
51	Identification of Mitofusin 1 and Complement Component 1q Subcomponent Binding Protein as Mitochondrial Targets in Systemic Lupus Erythematosus. Arthritis and Rheumatology, 2022, 74, 1193-1203.	5 <b>.</b> 6	13
52	Protein interaction network of alternatively spliced NudCD1 isoforms. Scientific Reports, 2017, 7, 12987.	3.3	12
53	Subcellular proteomics analysis of different stages of colorectal cancer cell lines. Proteomics, 2016, 16, 3009-3018.	2.2	11
54	Proteolytic Processing of the Epithelial Adherens Junction Molecule E-Cadherin by Neutrophil Elastase Generates Short Peptides With Novel Wound-Healing Bioactivity. Cellular and Molecular Gastroenterology and Hepatology, 2019, 7, 483-486.e8.	4.5	10

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55	Arginine Methylation Regulates the Cytokine Response. Molecular Cell, 2004, 15, 492-494.	9.7	9
56	Downregulation of KRAB zinc finger proteins in 5-fluorouracil resistant colorectal cancer cells. BMC Cancer, 2022, 22, 363.	2.6	9
57	PNAC: a protein nucleolar association classifier. BMC Genomics, 2011, 12, 74.	2.8	8
58	Proteomics Analysis of Colorectal Cancer Cells. Methods in Molecular Biology, 2018, 1765, 155-166.	0.9	8
59	Silencing PEX26 as an unconventional mode to kill drug-resistant cancer cells and forestall drug resistance. Autophagy, 2022, 18, 540-558.	9.1	7
60	The prefoldin complex stabilizes the von Hippel-Lindau protein against aggregation and degradation. PLoS Genetics, 2020, 16, e1009183.	3.5	6
61	Hypomorphic GINS3 variants alter DNA replication and cause Meier-Gorlin syndrome. JCI Insight, 2022, 7, .	5.0	6
62	C-terminal deletion of NOTCH1 intracellular domain (N1ICD) increases its stability but does not amplify and recapitulate N1ICD-dependent signalling. Scientific Reports, 2017, 7, 5034.	3.3	5
63	Rab21 in enterocytes participates in intestinal epithelium maintenance. Molecular Biology of the Cell, 2022, 33, mbcE21030139.	2.1	4
64	SILAC proteomics implicates SOCS1 in modulating cellular macromolecular complexes and the ubiquitin conjugating enzyme UBE2D involved in MET receptor tyrosine kinase downregulation. Biochimie, 2021, 182, 185-196.	2.6	2
65	Loss of functional caveolae during senescence of human fibroblasts. Journal of Cellular Physiology, 2001, 187, 226-235.	4.1	2
66	The Dynamic Proteome of the Nucleolus. , 2011, , 29-42.		0