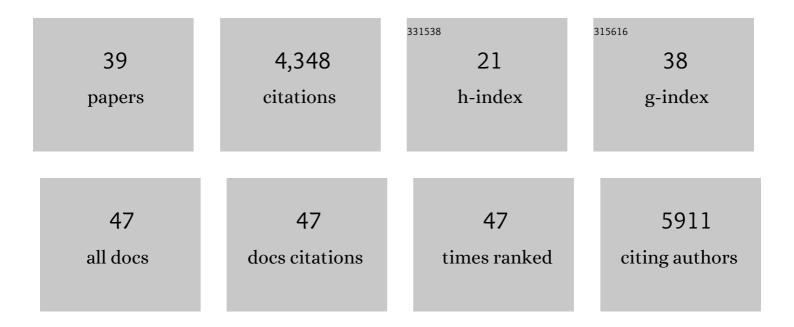
Felipe da Veiga Leprevost

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	MSFragger: ultrafast and comprehensive peptide identification in mass spectrometry–based proteomics. Nature Methods, 2017, 14, 513-520.	9.0	1,099
2	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. Cell, 2019, 179, 964-983.e31.	13.5	430
3	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. Cell, 2020, 182, 200-225.e35.	13.5	410
4	Integrated analysis of shotgun proteomic data with PatternLab for proteomics 4.0. Nature Protocols, 2016, 11, 102-117.	5.5	257
5	Philosopher: a versatile toolkit for shotgun proteomics data analysis. Nature Methods, 2020, 17, 869-870.	9.0	255
6	Proteogenomic characterization of pancreatic ductal adenocarcinoma. Cell, 2021, 184, 5031-5052.e26.	13.5	236
7	BioContainers: an open-source and community-driven framework for software standardization. Bioinformatics, 2017, 33, 2580-2582.	1.8	205
8	Proteogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell carcinoma. Cancer Cell, 2021, 39, 361-379.e16.	7.7	189
9	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. Cell, 2020, 183, 1962-1985.e31.	13.5	177
10	A proteogenomic portrait of lung squamous cell carcinoma. Cell, 2021, 184, 4348-4371.e40.	13.5	170
11	Discovering and linking public omics data sets using the Omics Discovery Index. Nature Biotechnology, 2017, 35, 406-409.	9.4	159
12	Ten Simple Rules for Taking Advantage of Git and GitHub. PLoS Computational Biology, 2016, 12, e1004947.	1.5	96
13	Quantitative proteomic landscape of metaplastic breast carcinoma pathological subtypes and their relationship to triple-negative tumors. Nature Communications, 2020, 11, 1723.	5.8	64
14	PTM-Shepherd: Analysis and Summarization of Post-Translational and Chemical Modifications From Open Search Results. Molecular and Cellular Proteomics, 2021, 20, 100018.	2.5	57
15	On best practices in the development of bioinformatics software. Frontiers in Genetics, 2014, 5, 199.	1.1	53
16	Reevaluating the Trypanosoma cruzi proteomic map: The shotgun description of bloodstream trypomastigotes. Journal of Proteomics, 2015, 115, 58-65.	1.2	44
17	Venomous extract protein profile of Brazilian tarantula Grammostola iheringi: searching for potential biotechnological applications. Journal of Proteomics, 2016, 136, 35-47.	1.2	41
18	The Ewing Sarcoma Secretome and Its Response to Activation of Wnt/beta-catenin Signaling. Molecular and Cellular Proteomics, 2018, 17, 901-912.	2.5	34

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#	Article	IF	CITATIONS
19	PepExplorer: A Similarity-driven Tool for Analyzing de Novo Sequencing Results. Molecular and Cellular Proteomics, 2014, 13, 2480-2489.	2.5	33
20	Recommendations for the packaging and containerizing of bioinformatics software. F1000Research, 2018, 7, 742.	0.8	29
21	Regulation of ALT-associated homology-directed repair by polyADP-ribosylation. Nature Structural and Molecular Biology, 2020, 27, 1152-1164.	3.6	27
22	Recommendations for the packaging and containerizing of bioinformatics software. F1000Research, 2018, 7, 742.	0.8	27
23	Deep Proteomics Using Two Dimensional Data Independent Acquisition Mass Spectrometry. Analytical Chemistry, 2020, 92, 4217-4225.	3.2	23
24	A multi-protease, multi-dissociation, bottom-up-to-top-down proteomic view of the Loxosceles intermedia venom. Scientific Data, 2017, 4, 170090.	2.4	21
25	Effectively addressing complex proteomic search spaces with peptide spectrum matching. Bioinformatics, 2013, 29, 1343-1344.	1.8	20
26	Computational proteomics pitfalls and challenges: HavanaBioinfo 2012 Workshop report. Journal of Proteomics, 2013, 87, 134-138.	1.2	19
27	Crystal-C: A Computational Tool for Refinement of Open Search Results. Journal of Proteome Research, 2020, 19, 2511-2515.	1.8	19
28	Quantitative proteomic analysis of the Saccharomyces cerevisiae industrial strains CAT-1 and PE-2. Journal of Proteomics, 2017, 151, 114-121.	1.2	18
29	Unveiling the partners of the DRBD2-mRNP complex, an RBP in Trypanosoma cruzi and ortholog to the yeast SR-protein Gbp2. BMC Microbiology, 2019, 19, 128.	1.3	17
30	GRASP55 regulates the unconventional secretion and aggregation of mutant huntingtin. Journal of Biological Chemistry, 2022, 298, 102219.	1.6	14
31	Pinpointing differentially expressed domains in complex protein mixtures with the cloud service of PatternLab for Proteomics. Journal of Proteomics, 2013, 89, 179-182.	1.2	11
32	Deep-Learning-Derived Evaluation Metrics Enable Effective Benchmarking of Computational Tools for Phosphopeptide Identification. Molecular and Cellular Proteomics, 2021, 20, 100171.	2.5	9
33	Proteomic Analyses of Vitreous in Proliferative Diabetic Retinopathy: Prior Studies and Future Outlook. Journal of Clinical Medicine, 2021, 10, 2309.	1.0	6
34	Using PepExplorer to Filter and Organize <i>De Novo</i> Peptide Sequencing Results. Current Protocols in Bioinformatics, 2015, 51, 13.27.1-13.27.9.	25.8	4
35	A validated analysis pipeline for mass spectrometry-based vitreous proteomics: new insights into proliferative diabetic retinopathy. Clinical Proteomics, 2021, 18, 28.	1.1	4
36	Differences in Extracellular Vesicle Protein Cargo Are Dependent on Head and Neck Squamous Cell Carcinoma Cell of Origin and Human Papillomavirus Status. Cancers, 2021, 13, 3714.	1.7	3

#	Article	IF	CITATIONS
37	Using MSFragger for ultrafast database searching. Protocol Exchange, 0, , .	0.3	1
38	Proteome Analysis of Formalin-Fixed Paraffin-Embedded Tissues from a Primary Gastric Melanoma and its Meningeal Metastasis: A Case Report. Current Topics in Medicinal Chemistry, 2014, 14, 382-387.	1.0	1
39	Abstract IA-003: Proteogenomic characterizations of pancreatic ductal adenocarcinoma. , 2021, , .		0