

# Felipe da Veiga Leprevost

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

36  
papers

1,717  
citations

19  
h-index

41  
g-index

47  
ext. papers

3,016  
ext. citations

15.8  
avg, IF

4.48  
L-index

#	Paper	IF	Citations
36	A validated analysis pipeline for mass spectrometry-based vitreous proteomics: new insights into proliferative diabetic retinopathy. <i>Clinical Proteomics</i> , <b>2021</b> , 18, 28	5	2
35	Deep-Learning-Derived Evaluation Metrics Enable Effective Benchmarking of Computational Tools for Phosphopeptide Identification. <i>Molecular and Cellular Proteomics</i> , <b>2021</b> , 20, 100171	7.6	1
34	Proteomic Analyses of Vitreous in Proliferative Diabetic Retinopathy: Prior Studies and Future Outlook. <i>Journal of Clinical Medicine</i> , <b>2021</b> , 10,	5.1	1
33	Proteogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell carcinoma. <i>Cancer Cell</i> , <b>2021</b> , 39, 361-379.e16	24.3	50
32	A proteogenomic portrait of lung squamous cell carcinoma. <i>Cell</i> , <b>2021</b> , 184, 4348-4371.e40	56.2	15
31	Proteogenomic characterization of pancreatic ductal adenocarcinoma. <i>Cell</i> , <b>2021</b> , 184, 5031-5052.e26	56.2	26
30	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. <i>Cell</i> , <b>2020</b> , 182, 200-225.e35	56.2	139
29	Deep Proteomics Using Two Dimensional Data Independent Acquisition Mass Spectrometry. <i>Analytical Chemistry</i> , <b>2020</b> , 92, 4217-4225	7.8	15
28	Quantitative proteomic landscape of metaplastic breast carcinoma pathological subtypes and their relationship to triple-negative tumors. <i>Nature Communications</i> , <b>2020</b> , 11, 1723	17.4	18
27	Crystal-C: A Computational Tool for Refinement of Open Search Results. <i>Journal of Proteome Research</i> , <b>2020</b> , 19, 2511-2515	5.6	8
26	Regulation of ALT-associated homology-directed repair by polyADP-ribosylation. <i>Nature Structural and Molecular Biology</i> , <b>2020</b> , 27, 1152-1164	17.6	14
25	Philosopher: a versatile toolkit for shotgun proteomics data analysis. <i>Nature Methods</i> , <b>2020</b> , 17, 869-870.e16	21.6	50
24	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. <i>Cell</i> , <b>2020</b> , 183, 1962-1985.e31	56.2	45
23	PTM-Shepherd: Analysis and Summarization of Post-Translational and Chemical Modifications From Open Search Results. <i>Molecular and Cellular Proteomics</i> , <b>2020</b> , 20, 100018	7.6	19
22	Unveiling the partners of the DRBD2-mRNP complex, an RBP in <i>Trypanosoma cruzi</i> and ortholog to the yeast SR-protein Gbp2. <i>BMC Microbiology</i> , <b>2019</b> , 19, 128	4.5	9
21	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , <b>2019</b> , 179, 964-983.e31	56.2	173
20	The Ewing Sarcoma Secretome and Its Response to Activation of Wnt/beta-catenin Signaling. <i>Molecular and Cellular Proteomics</i> , <b>2018</b> , 17, 901-912	7.6	20

19	Recommendations for the packaging and containerizing of bioinformatics software. <i>F1000Research</i> , <b>2018</b> , 7,	3.6	17
18	Recommendations for the packaging and containerizing of bioinformatics software. <i>F1000Research</i> , <b>2018</b> , 7, 742	3.6	13
17	MSFragger: ultrafast and comprehensive peptide identification in mass spectrometry-based proteomics. <i>Nature Methods</i> , <b>2017</b> , 14, 513-520	21.6	402
16	Discovering and linking public omics data sets using the Omics Discovery Index. <i>Nature Biotechnology</i> , <b>2017</b> , 35, 406-409	44.5	105
15	BioContainers: an open-source and community-driven framework for software standardization. <i>Bioinformatics</i> , <b>2017</b> , 33, 2580-2582	7.2	123
14	A multi-protease, multi-dissociation, bottom-up-to-top-down proteomic view of the <i>Loxosceles intermedia</i> venom. <i>Scientific Data</i> , <b>2017</b> , 4, 170090	8.2	19
13	Quantitative proteomic analysis of the <i>Saccharomyces cerevisiae</i> industrial strains CAT-1 and PE-2. <i>Journal of Proteomics</i> , <b>2017</b> , 151, 114-121	3.9	11
12	Integrated analysis of shotgun proteomic data with PatternLab for proteomics 4.0. <i>Nature Protocols</i> , <b>2016</b> , 11, 102-17	18.8	156
11	Venomous extract protein profile of Brazilian tarantula <i>Grammostola iheringi</i> : searching for potential biotechnological applications. <i>Journal of Proteomics</i> , <b>2016</b> , 136, 35-47	3.9	19
10	Reevaluating the <i>Trypanosoma cruzi</i> proteomic map: The shotgun description of bloodstream trypomastigotes. <i>Journal of Proteomics</i> , <b>2015</b> , 115, 58-65	3.9	38
9	Using PepExplorer to Filter and Organize De Novo Peptide Sequencing Results. <i>Current Protocols in Bioinformatics</i> , <b>2015</b> , 51, 13.27.1-13.27.9	24.2	2
8	PepExplorer: a similarity-driven tool for analyzing de novo sequencing results. <i>Molecular and Cellular Proteomics</i> , <b>2014</b> , 13, 2480-9	7.6	30
7	On best practices in the development of bioinformatics software. <i>Frontiers in Genetics</i> , <b>2014</b> , 5, 199	4.5	34
6	Proteome analysis of formalin-fixed paraffin-embedded tissues from a primary gastric melanoma and its meningeal metastasis: a case report. <i>Current Topics in Medicinal Chemistry</i> , <b>2014</b> , 14, 382-7	3	1
5	Computational proteomics pitfalls and challenges: HavanaBioinfo 2012 workshop report. <i>Journal of Proteomics</i> , <b>2013</b> , 87, 134-8	3.9	17
4	Pinpointing differentially expressed domains in complex protein mixtures with the cloud service of PatternLab for Proteomics. <i>Journal of Proteomics</i> , <b>2013</b> , 89, 179-82	3.9	11
3	Effectively addressing complex proteomic search spaces with peptide spectrum matching. <i>Bioinformatics</i> , <b>2013</b> , 29, 1343-4	7.2	19
2	Omics Discovery Index - Discovering and Linking Public Omics Datasets		2

1	PTM-Shepherd: analysis and summarization of post-translational and chemical modifications from open search results	4
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