

Felipe da Veiga Leprevost
Research Investigator
Department of Pathology
1301 Catherine St, Ann Arbor, MI
Phone: 734 436 1805
Email: felipevl@umich.edu

Education and Training

Education

02/2003-01/2006	BSc, Biology, Positivo University, Curitiba, Parana Brazil
02/2006-01/2009	MS, Molecular & Cellular Biology, Fiocruz, Rio de Janeiro, RJ Brazil
02/2010-01/2013	BSc, Positivo University, Curitiba, Parana Brazil
02/2010-01/2014	PhD, Computational Proteomics, Fiocruz, Curitiba, Parana Brazil

PostDoctoral Training

02/2014-02/2015	Research Fellow, Computational Proteomics, Fiocruz, Curitiba, Parana Brazil
03/2015-06/2019	Research Fellow, Computational Proteomics, University of Michigan, Ann Arbor, Michigan

Academic, Administrative, Clinical, Research and Military Appointments

Academic Appointments

06/2019-present	Research Investigator, University of Michigan, Ann Arbor, MI
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Research Interests

- Recent advances in the molecular biology field, more specifically related to the omics sciences, are creating a necessity for better analysis methodologies. Much of my work centers on the development of bioinformatics software for proteomics and exploratory data analysis. As a system analyst & developer I have been promoting the good practices in developing computational tools for the life sciences while at the same time, applying my knowledge to create and share open-source libraries and software that other can use on their projects. As a molecular biologist, my interest centers on how to properly analyse and interpret biological data, more specifically proteomics. My focus lies mainly on developing better exploratory data analysis and techniques for protein functional analysis, aiming for better characterizations of biological phenomena. More recently, I started working with protein post-translational modification (PTM) annotation systems, seeking to develop a robust annotation pipeline for big data sets. By applying different methodologies like open-searches, in landscape scenarios, we hope to shed more light on misinterpreted peptide mass spectra.

Grants

Submitted Grants

Common Fund Data Supplement: Unraveling the functional impact of genomic rearrangements in cancer by bridging and augmenting Common Fund and CPTAC data resources NIH-DHHS-US- 20-PAF00307
Co-I with Effort (Principal Investigator: Nesvizhskii, Alexey;Chinnaiyan, Arul M;Dhanasekaran, Saravana M)
09/2019-08/2020. \$304,533

Memberships in Professional Societies

2014-2015	Member, Brazilian Proteomics Society
2015-present	Member, American Society for Mass Spectrometry
2018-present	Member, Human Proteome Organization

Editorial Positions, Boards, and Peer-Review Service

Journal Reviewer

2013-present	Bioinformatics (Ad Hoc)
2013-present	Frontiers in Genetics (Ad Hoc)

2013-present	Journal of Proteomics (Ad Hoc)
2013-present	Proteomics (Ad Hoc)
2014-present	Current Topics in Medicinal Chemistry (Ad Hoc)
2014-present	Frontiers in Bioengineering and Biotechnology (Ad Hoc)
2014-present	Journal of Proteomics Research (Ad Hoc)

Teaching

Undergraduate Student

02/2014-03/2015 Marlon Dias Mariano dos Santos, Bsc. Biotechnology, Fiocruz

Committee and Administrative Services

Committee Services

International

2013 Yet Another Perl Conference::Brasil, Chair of the Bioinformatics section
 2014 Yet Another Perl Conference::Brasil, President

National

2013-2015 Curitiba Perl Mongers, President

Bibliography

Peer-Reviewed Journals and Publications

1. Perez-Riverol Y, Hermjakob H, Kohlbacher O, Martens L, Creasy D, Cox J, Leprevost F, Shan BP, Pérez-Nuño VI, Blazejczyk M, Punta M, Vierlinger K, Valiente PA, Leon K, Chinea G, Guiole O, Bringas R, Cabrera G, Guillen G, Padron G, Gonzalez LJ, Besada V: Computational proteomics pitfalls and challenges: HavanaBioinfo 2012 workshop report. *J Proteomics* 87: 134-8, 2013. PM23376229
2. Borges D, Perez-Riverol Y, Nogueira FC, Domont GB, Noda J, da Veiga Leprevost F, Besada V, França FM, Barbosa VC, Sánchez A, Carvalho PC: Effectively addressing complex proteomic search spaces with peptide spectrum matching. *Bioinformatics* 29(10): 1343-4, 2013. PM23446294
3. Leprevost FV, Lima DB, Crestani J, Perez-Riverol Y, Zanchin N, Barbosa VC, Carvalho PC: Pinpointing differentially expressed domains in complex protein mixtures with the cloud service of PatternLab for Proteomics. *J Proteomics* 89: 179-82, 2013. PM23796493
4. Leprevost FV, Valente RH, Lima DB, Perales J, Melani R, Yates JR 3rd, Barbosa VC, Junqueira M, Carvalho PC: PepExplorer: a similarity-driven tool for analyzing de novo sequencing results. *Mol Cell Proteomics* 13(9): 2480-9, 2014. PM24878498/PMC4159663
5. Fischer Jde S, Canedo NH, Goncalves KM, Chimelli LM, Franca M, Leprevost FV, Aquino PF, Carvalho PC, Carvalho Mda G: Proteome analysis of formalin-fixed paraffin-embedded tissues from a primary gastric melanoma and its meningeal metastasis: a case report. *Curr Top Med Chem* 14(3): 382-7, 2014. PM24304316
6. Leprevost Fda V, Barbosa VC, Francisco EL, Perez-Riverol Y, Carvalho PC: On best practices in the development of bioinformatics software. *Front Genet* 5: 199, 2014. PM25071829/PMC4078907
7. da Veiga Leprevost F, Barbosa VC, Carvalho PC: Using PepExplorer to Filter and Organize De Novo Peptide Sequencing Results. *Curr Protoc Bioinformatics* 51: 13.27.1-9, 2015. PM26334921
8. Brunoro GV, Caminha MA, Ferreira AT, Leprevost Fda V, Carvalho PC, Perales J, Valente RH, Menna-Barreto RF: Reevaluating the Trypanosoma cruzi proteomic map: The shotgun description of bloodstream trypomastigotes. *J Proteomics* 115: 58-65, 2015. PM25534883
9. Carvalho PC, Lima DB, Leprevost FV, Santos MD, Fischer JS, Aquino PF, Moresco JJ, Yates JR 3rd, Barbosa VC: Integrated analysis of shotgun proteomic data with PatternLab for proteomics 4.0. *Nat Protoc* 11(1): 102-17, 2016. PM26658470/PMC5722229
10. Perez-Riverol Y, Gatto L, Wang R, Sachsenberg T, Uszkoreit J, Leprevost Fda V, Fufezan C, Ternent T, Eglen SJ, Katz DS, Pollard TJ, Kononov A, Flight RM, Blin K, Vizcaino JA: Ten Simple Rules for Taking Advantage of Git and GitHub. *PLoS Comput Biol* 12(7): e1004947, 2016. PM27415786/PMC4945047

11. Borges MH, Figueiredo SG, Leprevost FV, De Lima ME, Cordeiro Mdo N, Diniz MR, Moresco J, Carvalho PC, Yates JR: Venomous extract protein profile of Brazilian tarantula *Grammostola iheringi*: searching for potential biotechnological applications. *J Proteomics* 136: 35-47, 2016. PM26828374
12. Kong AT, Leprevost FV, Avtonomov DM, Mellacheruvu D, Nesvizhskii AI: MSFragger: ultrafast and comprehensive peptide identification in mass spectrometry-based proteomics. *Nat Methods* 14(5): 513-520, 2017. PM28394336/PMC5409104
13. Perez-Riverol Y, Bai M, da Veiga Leprevost F, Squizzato S, Park YM, Haug K, Carroll AJ, Spalding D, Paschall J, Wang M, Del-Toro N, Ternent T, Zhang P, Buso N, Bandeira N, Deutsch EW, Campbell DS, Beavis RC, Salek RM, Sarkans U, Petryszak R, Keays M, Fahy E, Sud M, Subramaniam S, Barbera A, Jiménez RC, Nesvizhskii AI, Sansone SA, Steinbeck C, Lopez R, Vizcaíno JA, Ping P, Hermjakob H: Discovering and linking public omics data sets using the Omics Discovery Index. *Nat Biotechnol* 35(5): 406-409, 2017. PM28486464/PMC5831141
14. Trevisan-Silva D, Bednaski AV, Fischer JSG, Veiga SS, Bandeira N, Guthals A, Marchini FK, Leprevost FV, Barbosa VC, Senff-Ribeiro A, Carvalho PC: A multi-protease, multi-dissociation, bottom-up-to-top-down proteomic view of the *Loxosceles intermedia* venom. *Sci Data* 4: 170090, 2017. PM28696408 /PMC5505115
15. da Veiga Leprevost F, Grüning BA, Alves Aflitos S, Röst HL, Uszkoreit J, Barsnes H, Vaudel M, Moreno P, Gatto L, Weber J, Bai M, Jimenez RC, Sachsenberg T, Pfeuffer J, Vera Alvarez R, Griss J, Nesvizhskii AI, Perez-Riverol Y: BioContainers: an open-source and community-driven framework for software standardization. *Bioinformatics* 33(16): 2580-2582, 2017. PM28379341/PMC5870671
16. Santos RM, Nogueira FC, Brasil AA, Carvalho PC, Leprevost FV, Domont GB, Eleutherio EC: Quantitative proteomic analysis of the *Saccharomyces cerevisiae* industrial strains CAT-1 and PE-2. *J Proteomics* 151: 114-121, 2017. PM27576599
17. Hawkins AG, Basrur V, da Veiga Leprevost F, Pedersen E, Sperring C, Nesvizhskii AI, Lawlor ER: The Ewing Sarcoma Secretome and Its Response to Activation of Wnt/beta-catenin Signaling. *Mol Cell Proteomics* 17(5): 901-912, 2018. PM29386236/PMC5930412
18. Wippel HH, Inoue AH, Vidal NM, Costa JFD, Marcon BH, Romagnoli BAA, Santos MDM, Carvalho PC, Goldenberg S, Alves LR: Assessing the partners of the RBP9-mRNP complex in *Trypanosoma cruzi* using shotgun proteomics and RNA-seq. *RNA Biol* 15(8): 1106-1118, 2018. PM30146924/PMC6161725
19. Gruening B, Sallou O, Moreno P, Leprevost FV, Ménager H, Søndergaard D, Röst H, Sachsenberg T, O'Connor B, Madeira F, Del Angel VD, Crusoe MR, Varma S, Blankenberg D, Jimenez RC, BioContainers Community, Perez-Riverol Y: Recommendations for the packaging and containerizing of bioinformatics software *F1000 Research* 2: 1, 2018.
20. Clark DJ, Dhanasekaran SM, Petralia F, Pan J, Song X, Hu Y, da Veiga Leprevost F, Reva B, Lih TM, Chang HY, Ma W, Huang C, Ricketts CJ, Chen L, Krek A, Li Y, Rykunov D, Li QK, Chen LS, Ozbek U, Vasaiakar S, Wu Y, Yoo S, Chowdhury S, Wyczalkowski MA, Ji J, Schnaubelt M, Kong A, Sethuraman S, Avtonomov DM, Ao M, Colaprico A, Cao S, Cho KC, Kalayci S, Ma S, Liu W, Ruggles K, Calinawan A, Gümüş ZH, Geizler D, Kawaler E, Teo GC, Wen B, Zhang Y, Keegan S, Li K, Chen F, Edwards N, Pierorazio PM, Chen XS, Pavlovich CP, Hakimi AA, Brominski G, Hsieh JJ, Antczak A, Omelchenko T, Lubinski J, Wiznerowicz M, Linehan WM, Kinsinger CR, Thiagarajan M, Boja ES, Mesri M, Hiltke T, Robles AI, Rodriguez H, Qian J, Fenyö D, Zhang B, Ding L, Schadt E, Chinnaiyan AM, Zhang Z, Omenn GS, Cieslik M, Chan DW, Nesvizhskii AI, Wang P, Zhang H, Clinical Proteomic Tumor Analysis Consortium.: Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. *Cell* 179(4): 964-983.e31, 2019. PM31675502

Non-Peer-Reviewed Journals and Publications

1. Leprevost, FV: Bio::DB::NextProt: a perl module for NeXtProt database information retrieval *PeerJ* 2: 1, 2014.

Abstracts

1. Probst CM, Markini FK, Pavoni DP, Preti H, Biondo CA, Leprevost FV, Baer F, Batista M, Yamamoto F, Goldenberg S, Krieger M: A *Trypanosoma cruzi* differentially expressed gene clone collection (T.cruzi DEG - ORFeome), XXII Annual Meeting of the Brazilian Society of Protozoology / XXXIII Annual Meeting on Basic Research in Chagas Disease, Camxambu, Brazil, Brazilian Society of Protozoology, 2006.
2. Preti H, Pavoni DP, Leprevost FV, Yamamoto F, Marchini F, Rocha J, Batista M, Probst CM, Goldenberg S, Krieger M: Functional characterization of differential expressed protein during t.cruzi metacyclogenesis, XXIII Annual Meeting of the Brazilian Society of Protozoology / XXXIV Annual Meeting on Basic Research in Chagas Disease, Caxambu, Brazil, Brazilian Society of Protozoology, 2007.

3. Yamamoto F, Leprevost FV, Preti H, Umaki ACS, Rampazzo RCP, Probst CM, Pavoni DP, Krieger M: Characterization of genes differentially expressed during trypanosoma cruzi metacyclogenesis, XXXV Annual Meeting on Basic Research in Chagas Disease / XXIV Annual Meeting of the Brazilian Society of Protozoology, Águas de Lindóia, Brazilian Society of Protozoology, 2008.
4. Leprevost FV, Yamamoto F, Preti H, Umaki ACS, Rampazzo RCP, Dallabona AC, Marchini F, Probst CM, Krieger M, Pavoni DP: Characterization of genes of unknown function with a higher expression in trypanosoma cruzi metacyclic trypomastigotes, XXXV Annual Meeting on Basic Research in Chagas Disease / XXIV Annual Meeting of the Brazilian Society of Protozoology, Águas de Lindóia, Brazil, Brazilian Society of Protozoology, 2008.
5. Leprevost FV, Rampazzo RCP, Marchini F, Pavoni DP, Krieger MA, Probst CM: Systemic analysis of gene expression modulation after nutritional stress in trypanosoma cruzi, XXVII Annual Meeting of the Brazilian Society of Protozoology / XXXVIII Annual Meeting on Basic Research in Chagas Disease, Foz do Iguaçu, Brazilian Society of Protozoology, 2011.
6. Vidal N, Preti H, Afornali A, Francisco EL, Leprevost FV, Batista M, Pavoni DP, Marchini F, Probst CM, Krieger MA: Trypanosoma cruzi ORFeome project v.1.0, XXVII Annual Meeting of the Brazilian Society of Protozoology / XXXVIII Annual Meeting on Basic Research in Chagas Disease, Foz do Iguaçu, Brazilian Society of Protozoology, 2011.
7. Lima DB, Perez-Riverol Y, Leprevost FV, Nogueira FCS, Barbosa VC, Domont GB, Franca FMG, Carvalho PC: Effectively addressing massively complex proteomic search spaces, First Meeting of the Brazilian Proteomics Society, Rio de Janeiro, Brazilian Proteomics Society, 2012.
8. Leprevost FV, Lima DB, Carvalho PC: PepExplorer: a computational pipeline for analyzing proteomes of non-canonical organisms, First Meeting of the Brazilian Proteomics Society, Rio de Janeiro, Brazilian Proteomics Society, 2012.
9. Leprevost FV, Aflitos SA, Gruning B, Roest H, Barsnes H, Jimenez R, Hermjakob H, Nesvizhskii AI, Perez-Riverol Y: BioDocker: An open source and community-driven framework for software standardization in proteomics, 64th American Society for Mass Spectrometry (ASMS), San Antonio, Texas, American Society for Mass Spectrometry, 2016.
10. Kong A, Avtonomov DM, Leprevost FV, Mellacheruvu D, Nesvizhskii AI: Illuminating the "dark matter" of shotgun proteomics using MSFragger, 65th American Society for Mass Spectrometry (ASMS), Indianapolis, IN, American Society for Mass Spectrometry, 2017.
11. Teo GC, Mellacheruvu D, Bludau I, Urs S, Conlon K, Leprevost FV, Aebersold R, Basur V, Simeone DM, Nesvizhskii AI: LibMatic: a DIA-Umpire based pipeline to generate spectral libraries for targeted re-extraction in DIA, 65th American Society for Mass Spectrometry (ASMS), Indianapolis, IN, American Society for Mass Spectrometry, 2017.
12. Mellacheruvu D, Wright Z, Leprevost FV, Gingras A, Nesvizhskii AI: REPRINT: a resource for evaluation of protein interaction networks, 65th American Society for Mass Spectrometry (ASMS), Indianapolis, IN, American Society for Mass Spectrometry, 2017.
13. Kong A, Leprevost FV, Avtonomov DM, Mellacheruvu D, Nesvizhskii AI: False discovery rates are underestimated by the target-decoy strategy due to unaccounted for chemical and biological modifications, American Society for Mass Spectrometry (ASMS), Indianapolis, IN, American Society for Mass Spectrometry, 2017.
14. Leprevost FV, Shanmugam AK, Nesvizhskii AI: Philosopher: a data processing toolkit for shotgun proteomics, American Society for Mass Spectrometry (ASMS), Indianapolis, IN, American Society for Mass Spectrometry, 2017.
15. Leprevost FV, Kong AT, Avtonomov DV, Chang H, Teo GC, Geiszler DJ, Nesvizhskii AI: Comprehensive Computational Pipeline for Conventional MS/MS Data Processing and Open Search-Based PTM Characterization, 17th Annual World Congress of the Human Proteome Organization (HUPO), Orlando, Proceedings of the Human Proteome Organization, 2018.
16. Kong A, Geiszler D, Avtonomov DM, Leprevost FV, Chang H, Nesvizhskii AI: Characterizing and comparing modification profiles in large-scale shotgun proteomics using PTM-Shepherd, 66th American Society for Mass Spectrometry (ASMS), San Diego, CA, American Society for Mass Spectrometry, 2018.
17. Chang H, Kong AT, Leprevost FV, Avtonomov DM, Nesvizhskii AI: Crystal-C: A computational tool for refinement of open search results, 66th American Society for Mass Spectrometry (ASMS), San Diego, CA, American Society for Mass Spectrometry, 2018.
18. Avtonomov DM, Kong A, Leprevost FV, Chang H, Nesvizhskii AI: MSFragger-based computational framework for conventional MS/MS database searching and open search-based PTM characterization, 66th American Society for Mass Spectrometry (ASMS), San Diego, CA, American Society for Mass Spectrometry, 2018.

19. Leprevost FV, Shanmugam AK, Mellacheruvu D, Chang H, Avtonomov DM, Kong A, Nesvizhskii AI: Philosopher: a complete pipeline for both conventional and open search-based shotgun proteomics data analysis, 66th American Society for Mass Spectrometry (ASMS), San Diego, CA, American Society for Mass Spectrometry, 2018.
20. Yu F, Teo GC, Kong AT, Leprevost FV, Chang HY, Nesvizhskii AI: Comparison of Open Search Tools, 67th American Society for Mass Spectrometry (ASMS), Atlanta, American Society for Mass Spectrometry, 2019.
21. Geiszler DJ, Kong AT, Avtonomov DM, Leprevost FV, Chang HY, Nesvizhskii AI: Exploring the Open Proteome: Proteomics Open Search Analysis with PTM-Shepherd, 67th American Society for Mass Spectrometry (ASMS), Atlanta, American Society for Mass Spectrometry, 2019.
22. Avtonomov D, Kong AT, Leprevost FV, Teo G, Chang HY, Nesvizhskii AI: FragPipe: A Fast Proteomics Pipeline with MSFragger Search Engine at Heart, 67th American Society for Mass Spectrometry (ASMS), Atlanta, American Society for Mass Spectrometry, 2019.
23. Chang HY, Kong AT, Leprevost FV, Yu F, Teo GC, Avtonomov DM, Basrur V, Nesvizhskii AI: Implementation of MSFragger and Philosopher (PeptideProphet) as Proteome Discoverer Nodes, 67th American Society for Mass Spectrometry (ASMS), Atlanta, American Society for Mass Spectrometry, 2019.
24. Teo GC, Yu F, Kong AT, Hui-Yin Chang, Leprevost FV, Avtonomov DM, Nesvizhskii AI: New Features in MSFragger, 67th American Society for Mass Spectrometry (ASMS), Atlanta, American Society for Mass Spectrometry, 2019.
25. Leprevost FV, Shanmugam AK, Mellacheruvu D, Chang HY, Nesvizhskii AI: Updates on Philosopher: a complete toolkit for both conventional and open search-based shotgun proteomics data analysis, 67th American Society for Mass Spectrometry (ASMS), Atlanta, American Society for Mass Spectrometry, 2019.