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Brazilian citizenship

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Keywords

Bioinformatics

Computational Proteomics

Artificial Intelligence

Bottom-up & Top-down Proteomics

Structural Biology – XL-MS

Experience

⇒ Research Scientist (Since Sept-2024)

Exact Sciences, Munich, Germany

⇒ Post-doc in Computational Proteomics (Aug-2020 / Jul-2024)

Liu Lab – Leibniz-Forschungsinstitut für Molekulare Pharmakologie (FMP), Berlin, Germany

Research: Development of analysis tools for Cross-linking Mass Spectrometry (XL-MS)

Supervisor: Dr. Fan Liu

⇒ Data Scientist in Proteomics (Jan-2020 / Aug-2020)

Winter Lab – CeMM Research Center for Molecular Medicine of the Austrian Academy of Sciences, Vienna, Austria

Supervisor: Dr. Georg Winter

⇒ Post-doc in Computational Proteomics (Feb-2016 / Nov-2019)

Mass Spectrometry for Biology Unit, CNRS USR 2000 – Institut Pasteur, Paris, France

Research: Computational Mass Spectrometry tailored to Top-down Proteomics

Supervisor: Dr. Julia Chamot-Rooke

Education

⇒ Ph.D. in Bioscience and Biotechnology (Mar-2013 / Jan-2016)

ICC – Carlos Chagas Institute, Oswaldo Cruz Foundation (Fiocruz), Brazil

Research: Computational Proteomics tailored to Cross-linking Mass Spectrometry (XL-MS)

Supervisor: Dr. Paulo Costa Carvalho & Dr. Fabio Cesar Gozzo

⇒ M.Sc. in Computer Science and Systems Engineering (Mar-2011 / Feb-2013)

COPPE – Federal University of Rio de Janeiro (UFRJ), Brazil

Research: Computational Proteomics

Supervisor: Dr. Paulo Costa Carvalho

⇒ B.Sc. in Computer Science (Aug-2006 / Feb-2011)

Federal University of Rio de Janeiro (UFRJ), Brazil

Skills

⇒ Oral and written communication in **English** (C1 level), **French** (B2 level), **German** (B1 level) and **Portuguese** (native)

Scientific production

⇒ **42 publications** in peer-reviewed journals; h-index: 17

⇒ Book chapter: 1

⇒ Patents: 3

⇒ **Five recent significative publications:**

1. M A Clasen*, M Ruwolt*, C Wang, J Ruta, B Bogdanow, L U Kurt, Z Zhang, S Wang, F C Gozzo, T Chen, P C Carvalho#, D B Lima#, F Liu#, “Proteome-scale recombinant standards and a robust high-speed search engine to advance cross-linking MS-based interactomics”, *Nature Methods* 2024

2. M D M Santos, Diogo B Lima, J S G Fischer, M A Clasen, L U Kurt, A C Camillo-Andrade, L C Monteiro, P F Aquino, A G C Neves-Ferreira, R H Valente, M R O Trugilho, G V F Brunoro, T A C B Souza, R M Santos, M Batista, F C Gozzo, R Durán, J R Yates, V C Barbosa, P C Carvalho, “**Simple, efficient, and thorough shotgun proteomic analysis with PatternLab V**”, *Nature Protocols* 2022.
3. D B Lima*, M Dupré*, M D M Santos, P C Carvalho, J Chamot-Rooke, “**DiagnoTop: a computational pipeline for discriminating bacterial pathogens without database search**”, *Journal of the American Society for Mass Spectrometry*, 2021.
4. Diogo B Lima, Y Zhu, F Liu, “**XlinkCyNET: a Cytoscape application for visualization of protein interaction networks based on cross-linking mass spectrometry identifications**”, *Journal of Proteome Research*, 2021.
5. Lima, D.B.*; Melchior, J. T.*; Morris, J.; Barbosa, V. C.; Chamot-Rooke, J.; Gozzo, F. C.; Souza, T. A. C. B.; Fischer, J. S. G.; Carvalho, P. C.; Davidson, W. S., “**Characterization of homodimer interfaces with cross-linking mass spectrometry and isotopically labeled proteins**”, *Nature Protocols* (13): 431-458, 2018.

Reviewer of the following journals

- ⇒ Scientific Reports (Nature Group), Journal of Proteomics; Bioinformatics; Biochimica et Biophysica Acta; Letters in Drug Design & Discovery; International Society for Computational Biology – ECCB; Source Code for Biology and Medicine - BMC

Honors, Awards

- ⇒ Honorable mention award as one of the top 3 PhD theses in biological sciences in Brazil, 2017
- ⇒ One of the best projects presented in the Academic Journey – ICC / Fiocruz/Brazil – 2014 and 2015
- ⇒ Best poster in the M.Sc. category at the 1st Meeting of the Brazilian Proteomics Society, 2012

Teaching experience

- ⇒ Number of supervised or co-supervised theses: Ph.D.: 4; M.Sc.: 2; B.Sc.: 4
- ⇒ Invited Lectures / seminars in Computational Proteomics:
Proteome Analysis by Mass Spectrometry, international course at Institut Pasteur, 2022 & 2018 – Uruguay (lecture)
1st European Top-down Proteomics Symposium, 2019 – France (seminar)
Brazilian Mass Spectrometry Conference – BrMass, 2017 & 2018 – Brazil (seminar)

Projects

- ⇒ **Scout, 2024**
 - MS-cleavable search engine that enables interactomic analysis by identifying tandem mass spectra of cross-linked peptides.
 - <https://github.com/diogobor/Scout>
- ⇒ **XlinkCyNET, 2021**
 - A Cytoscape app for visualization of protein interaction networks based on XL-MS identifications.
 - <https://apps.cytoscape.org/apps/xlinkcynet>
- ⇒ **SIM-XL, 2015**
 - Computational tool that can quickly and seamlessly identify cross-linked peptides using mass spectrometry data.
 - <http://patternlabforproteomics.org/sim-xl>

Hobbies

- ⇒ Hiking, swimming and kickboxing.

References

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