

IX PROTEOMICS WORKSHOP

NOVEMBER, 12TH - 13TH, 2019

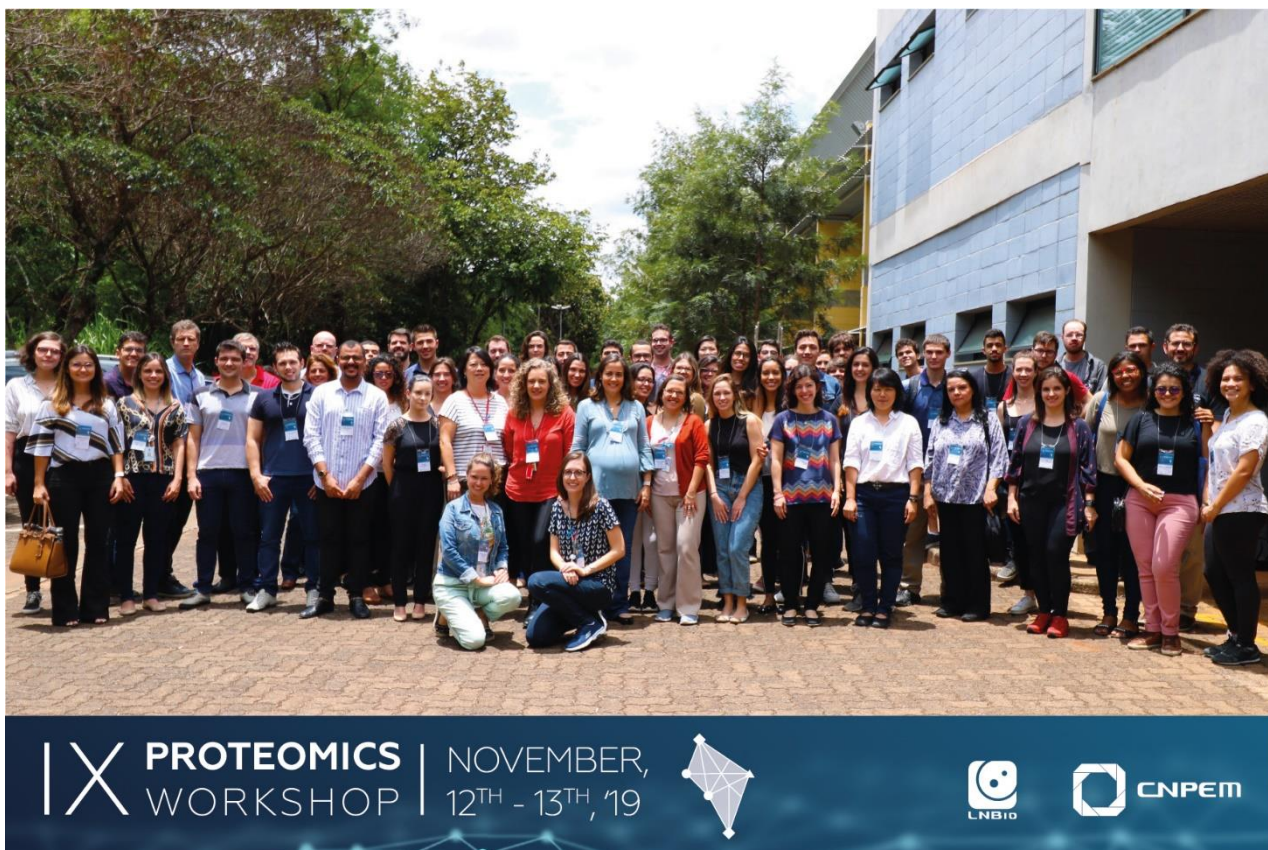


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MINISTRY OF
SCIENCE, TECHNOLOGY,
INNOVATION AND COMMUNICATION





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PRESENTATION

About CNPEM

The Brazilian Center for Research in Energy and Materials (CNPEM) is a non-profit private organization under supervision of the Brazilian Ministry of Science, Technology, Innovation and Communications (MCTIC). Located in Campinas, São Paulo, the Center is comprised of four laboratories, worldwide references in their fields, which are open to the scientific and business communities. The Brazilian Synchrotron Light Laboratory (LNLS) operates the only synchrotron light source in Latin America and is currently assembling Sirius, the new Brazilian electron accelerator. The Brazilian Biorenewables National Laboratory (LNBR) is focused on biotechnological solutions for the sustainable development of advanced biofuels, biochemicals and biomaterials, using biomass and the Brazilian biodiversity. Finally, the Brazilian Nanotechnology National Laboratory (LNNano) conducts scientific research and technologic development into solutions based on nanotechnology. The four Laboratories also have their own research projects and participate in the transversal research agenda coordinated by CNPEM, which articulates scientific facilities and capabilities around strategic themes.

LNBio

The Brazilian Biosciences National Laboratory (LNBio) is part of the Brazilian Center for Research in Energy and Materials (CNPEM), a social organization qualified by the Ministry of Science, Technology Innovation and Communications (MCTIC). LNBio is dedicated to biotechnology research and innovation, drug discovery and development, and has open facilities for the scientific communities. The Laboratory concentrates world-class expertise, state-of-the-art equipment and qualified researchers with multidisciplinary studies in the fields of structural biology, protein, genetics, metabolomics, bioassays, development of genetically modified organisms, among others



PROTEOMICS WORKSHOP

The IX Proteomics Workshop is promoted by the Brazilian Biosciences National Laboratory (LNBio). The event will be hosted by the Brazilian Center for Research in Energy and Materials (CNPEM) in Campinas-SP, Brazil, on November 12th and 13th, 2019.

The meeting program comprises classes ministered by experts and poster sessions.

IX Proteomics Workshop will offer 2-day courses in advanced themes in Omics Data Analysis. The lecturers will be ministered by 3 Brazilians and 4 foreign invited scientists. This edition will cover Data Integration, Computational and Statistical methods applied for Omics. The topics will be addressed in one-hour theoretical lecture and one-hour practical activity for each speaker.

Why participate?

This meeting represents a training opportunity for current and future users of proteomics and mass spectrometry. Following the example of the previous editions, held in the last eight years, the workshop also promotes the interaction between Brazilian and international researchers and dissemination of knowledge in the scientific community.

ORGANIZING COMMITTEE

Adriana Franco Paes Leme

Bianca Alves Pauletti

Carolina Carnielli

Maria Livia Gonçalves

Cristiane Duarte

Murilo Oliveira



PARTNERSHIPS





PROGRAM

November 12th, 2019

8:00-9:00	Reception and Registration
9:00-9:30	Welcome – Kleber Franchini and Adriana Paes Leme,
9:30-10:30	Lydia Y. Liu, University of Toronto Proteomics Data Integration in Cancer: The Value of Multimodality
10:30-10:40	Viviane Nascimento, Waters
10:40-11:40	Lydia Y. Liu, Hands-on
11:40-12:10	Coffee break and Poster session
12:10-1:10	Dexter Pratt, UC San Diego School of Medicine, San Diego Investigation of Proteomic Datasets using Biological Network Analysis Tools in the Cytoscape Ecosystem
1:10-2:30	Lunch
2:30-3:30	Dexter Pratt, Hands-on
3:30-3:40	Felipe Lugão, NovaAnalítica/Thermo Scientific
3:40-4:40	Nina Hirata, Institute of Mathematics and Statistics, University of São Paulo, SP Machine Learning and Computational Thinking
4:40-5:10	Coffee break and Poster session
5:10-6:10	Nina Hirata, Hands-on
6:10-6:30	Discussion
6:30-8:30	Welcome Reception

**November 13th, 2019**

8:00-9:00	João Carlos Setubal, Chemistry Institute, University of São Paulo, SP Mining of thermostable enzymes from compost metagenomic data
9:00-9:10	Diego Assis, Bruker timsTOF fleX with ESI and MALDI for Proteomics and SpatialOMx
9:10-10:10	João Carlos Setubal, Hands-on
10:10-10:40	Coffee break and Poster session
10:40-11:40	Mariana Boroni, National Cancer Institute, RJ Identifying new therapeutic strategies for Colorectal cancer in the Big Data Era
11:40-12:40	Mariana Boroni, Hands-on
1:00-2:00	Lunch
2:00-3:00	Daniel Clarke, Icahn School of Medicine at Mount Sinai, New York Integrating Bioinformatics Tools for Knowledge Exploration Workflows
3:10-3:20	Maurício Marques, Agilent
3:20-4:20	Daniel Clarke, Hands-on
4:20-4:50	Coffee break and Poster session
4:50-5:50	Igor Jurisica, University Health Network, Toronto, Ontario Data-driven (precision) medicine: from data to models to insights and treatments
5:50-6:50	Igor Jurisica, Hands-on
6:50-7:00	Final Remarks



SPEAKERS

Daniel Clarke, Icahn School of Medicine at Mount Sinai, New York
<http://labs.icahn.mssm.edu/maayanlab/team/>

Title: Integrating Bioinformatics Tools for Knowledge Exploration Workflows

To form novel hypotheses biomedical researchers rely more and more on information stored in public databases and bioinformatics tools that can query these databases. We have integrated several widely used bioinformatics tools and databases developed by the Ma'ayan Laboratory into a directed multi-graph with nodes representing fundamental data objects, for example, gene sets, signatures, disease or drug terms, and edges representing the transformations performed by various tools (for example, enrichment analysis, principal component analysis, or a PubMed search). We then use this graph to direct and facilitate user-driven exploration of the landscape of available knowledge stemming from an initial query or from a given dataset. As a case study, we use this system to investigate the role of under-studied protein kinases in diabetic nephropathy.

Dexter Pratt, UC San Diego School of Medicine, San Diego
<https://home.ndexbio.org/team-members/>

Title: Investigation of Proteomic Datasets using Biological Network Analysis Tools in the Cytoscape Ecosystem

Analyses based on molecular interaction networks and pathway mechanism models have a long history of use in the investigation of high throughput gene expression and proteomic data. The widely used Cytoscape desktop application (cytoscape.org) is one of preeminent tools in this field and is evolving into an ecosystem of both desktop, cloud services and web applications. NDEx, the Network Data Exchange (ndexbio.org), is a central element of the Cytoscape cloud that is a resource for network content and a framework for storing, sharing, publishing and computing with networks. This presentation will review Cytoscape tools relevant to the analysis of proteomic datasets including NDEx, Cytoscape desktop apps, and new web applications. In the following workshop, participants will apply tools described in the presentation to the investigation of an example data set.



Igor Jurisica, University Health Network, Toronto, Ontario
<https://www.uhnresearch.ca/researcher/igor-jurisica>

Title: Data-driven (precision) medicine: from data to models to insights and treatments

To fathom complex disease development processes, we need to systematically integrate diverse types of information and link them using relevant annotations and relationships, leading to meaningful modeling. This ranges from multiple high-throughput datasets, functional annotations and orthology data to expert knowledge about biochemical reactions and biological pathways. Such integrative systems are used to develop new hypotheses and answer complex questions such as what type of system perturbation may result in a desired change in cellular function; what factors cause disease; will patients respond to a given treatment, etc.

Precision medicine needs to be data-driven and corresponding analyses comprehensive and systematic. We will not find new treatments if only testing known targets and studying characterized pathways. Thousands of potentially important proteins remain pathway or interactome “orphans”. Computational biology methods can help fill this gap with accurate predictions, but the biological validation and further experiments are essential. Intertwining computational prediction and modeling with biological experiments will lead to more useful findings faster and more economically.

These computational predictions improved human interactome coverage relevant to both basic and translational research, and importantly, helped us to identify, validate and characterize prognostic signatures. Combined, these results may lead to unraveling mechanism of action for therapeutics, re-positioning existing drugs for novel use and prioritizing multiple candidates based on predicted toxicity, identifying groups of patients that may benefit from treatment and those where a given drug would be ineffective.

Application of graph theory, data mining, machine learning and advanced visualization enables data-driven, precision medicine. Intertwining computational prediction and modeling with biological experiments will lead to more useful findings faster and more economically.



João Carlos Setubal, Chemistry Institute, University of São Paulo, SP
<http://www.iq.usp.br/setubal/>

Title: A transcriptome-based signature of pathological angiogenesis predicts breast cancer patient survival

Compostagem termofílica é uma rica fonte de enzimas relacionadas com degradação de biomassa. No projeto metazoo estudamos a compostagem realizada no Parque Zoológico de São Paulo utilizando sequenciamento de nova geração. Com base no sequenciamento do DNA total (shotgun) de dezenas de amostras, montamos um catálogo com mais de 10 milhões de seqüências codificadoras de proteínas. Esse catálogo foi mineirado em busca de enzimas termoestáveis com bom potencial tecnológico. Através de uma metodologia de aprendizado de máquina chegamos a um subconjunto de 231 enzimas candidatas promissoras. Para quatro dessas candidatas realizamos ensaios experimentais confirmando termoestabilidade e atividade enzimática.

Lydia Y. Liu, University of Toronto
<http://kislingerlab.uhnres.utoronto.ca/people.html>

Title: Proteomics Data Integration in Cancer: The Value of Multimodality

“Increasingly translational cancer studies will quantify many types of molecular information in specific model systems or patient samples. These most frequently include the germline and somatic mutation profiles (including point mutations, copy number aberrations and genomic rearrangements), the transcriptome, immune infiltrates, the epigenome and the evolutionary timing of variants at each of these levels. Proteomic data analyses thus need to leverage that data to better understand information flow in cancer cells, develop robust biomarkers and understand the molecular origins of complex phenotypes. We will discuss the broad data-analytic strategies for these large datasets, and the challenges with integrating proteomic data with other datatypes. This will include practical examples of recent work performing such integrative analyses in primary cancer cohorts, and the value of statistical, machine-learning, information-theoretic and network strategies. Overall, we show that data integration across multiple levels of the central dogma improves our understanding of cancer phenotypes. Indeed biomarkers comprising multiple classes of biomolecules systematically outperform those that include only one: despite being an analytic challenge, multi-modality is a key opportunity for the future development of oncoproteomics.”



Mariana Boroni, National Cancer Institute, RJ
<https://www.inca.gov.br/en/node/2375>

Title: Identifying new therapeutic strategies for Colorectal cancer in the Big Data Era.

O câncer colorretal (CCR) é um dos carcinomas de maior incidência e mortalidade no mundo e tem como fatores de risco o baixo consumo de vegetais e alto consumo de carne vermelha e/ou processada, sobrepeso e sedentarismo. O CCR é uma doença altamente heterogênea, apresentando quatro subtipos moleculares, com diferenças na localização anatômica, no microambiente tumoral e nas vias moleculares alteradas. Essa grande heterogeneidade afeta significativamente a resposta a diferentes tratamentos e o prognóstico dos pacientes. Neste sentido, novas estratégias terapêuticas devem ser desenvolvidas considerando-se as alterações moleculares mais relevantes nos subtipos moleculares tumorais. As análises para identificação de alvos terapêuticos se baseiam no conceito de “druggable genome”, isto é, identificação de genes que codificam famílias protéicas específicas que interagem com fármacos, e que estão diretamente relacionados com o estabelecimento da doença. Com base nestas informações, o objetivo do nosso estudo é sugerir o reposicionamento de drogas atualmente utilizadas para o tratamento de outros tipos tumorais, assim como a identificação de novos alvos terapêuticos a partir da análise dos padrões de expressão gênica e do perfil de interação proteína-proteína nos subtipos moleculares de CCR.

Nina Hirata, Institute of Mathematics and Statistics, University of São Paulo, SP
<https://www.ime.usp.br/~nina/>

Title: Machine Learning and Computational Thinking

Machine learning techniques are tools often used to automate certain types of data processing needed for data analysis. They are particularly useful to analyze multidimensional data of complex nature or large amounts of data. In this talk we will start relating computational algorithms to machine learning and discussing how computational thinking is essential for the effective use of computational tools, including machine learning techniques. We will then introduce basic concepts and methods of machine learning. At the end, the discussed concepts and methods will be explored through practical hands-on application examples.

ABSTRACTS



In vivo evaluation of ultrasmall superparamagnetic iron oxide nanoparticle (USPIO)-ibuprofen conjugates

1. Castro, A; 1. Cavaglieri, CR; 1. Chacon-Mikahil, MPT
1. University of Campinas – UNICAMP; School of Physical Education, Laboratory of Exercise Physiology
Funding: FAPESP

Comparative analysis from dentate gyrus from naive Wistar rats and human hippocampus using proteomics and transcriptomics approaches

1.2.Godoi, AB; 1.2.Canto, AM; 1.2.Matos, AHB 2.3.Vieira, AS; 2.4. Rogerio, F; 2.5. Yassuda, CL; 1.2.Lopes-Cendes, I
1.Department of Medical Genetics and Genomic Medicine, School of Medical Sciences University of Campinas - UNICAMP; 2.The Brazilian Institute of Neuroscience and Neurotechnology (BRAINN); 3.Department of Structural Biology, Institute of Biology, University of Campinas - UNICAMP; 4.Department of Pathologic Anatomy School of Medical Sciences, UNICAMP; 5. Department of Neurology, School of Medical Sciences, UNICAMP.

S-nitroproteoma analysis during embryogenesis in Brazilian pine (*Araucaria angustifolia* (Bertol.) Kuntze).

1.Araujo AJB; 2.dos Santos ALW
University of São Paulo
Funding: FAPESP

Search for agrin interaction partners to study their role in the progression of oral cancer.

1.Santana, AG; 1.Granato, DC; 1.Yokoo, S; 1.Neves, LX; 1. Sá, JO; 1.Busso, AL; 1.Oliveira, AK; 1.Câmara, GA; 1.Domingues, RR; 1.Pauletti, B; 2. Sherman, NE; 1.Paes Leme, 1.AF. Paes
1. Mass Spectrometry Laboratory, Brazilian Biociences Laboratory, LNBio, CNPEM 2. Department of Microbiology, University of Virginia
Funding: FAPESP



Proteomic analysis reveals disease progression in the hippocampus of patients with mesial temporal lobe epilepsy

1,2. AM do Canto, 1,2. AB Godoi; 2,3. AS Vieira; 2,5. F Rogério; 2,4. CL Yasuda; 2,4. E Ghizoni; 2,4. H Tedeschi; 6. AB Arul; 6. RAS Robinson; 2,4. F Cendes; 1,2. I Lopes-Cendes;

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Funding: Cepid-BRAINN FAPESP

Validation of target proteins associated with the progression of potentially malignant disorders into oral cancer

1,2. Normando, AGC; 1. Lopes, MA; 1. Santos-Silva, AR; 2. Granato, DC; 2. Leme, AFP
1. Universidade Estadual de Campinas - UNICAMP; 2. Laboratório de Espectrometria de Massas, Laboratório Nacional de Biociências – LNBio/CNPEM

Oral cancer cell-derived extracellular vesicles can modulate an immunosuppressive microenvironment through M2 phenotype polarization

1. Oliveira, AK; 2. Patente, TA; 3. Ramos, RN; 1. Lopes, AB; 1. Camargo, ME; 1. Domingues, RR; 4. Amano, MT; 5. Marengo, EB; 2. Barbuto, JAM; 1. Paes-Leme, AF.
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Funding: FAPESP



Proteomics approach to understand stress response in adaptive evolution experiments in industrial yeast

Jacobus, AP; Gross, J
Institute for Research in Bioenergy – Universidade Estadual Paulista Julio de Mesquita filho
Funding: FAPESP

Proteomic analysis predicts involvement of USP7 in breast cancer cells and Epithelial Mesenchymal Transition

1,2. Silvestrini, VC; 1,2. Thome, CH; 1,2. Lanfredi, GP.; 1. Masson, AP; 1,2. Faça, VM.
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Funding: FAPESP, CNPq, CTC – CEPID.

Cariogenic potential of human and bovine milk and its effect on enamel demineralization

Ricomini-Filho AP; de Assis ACM; Costa-Oliveira BE; Cury JÁ
Piracicaba Dental School - University of Campinas – UNICAMP.
Funding: CNPq

Malignant and non-malignant cells from primary tumor and lymph node show different behavior and prognostic protein signatures in head and neck cancer

1. Busso-Lopes, AF; 2. Rivera, C; 1. Granato, D; 1. Neves, L; 3. de Mello, BP; 3. Villa, LL; 4. González-Arriagada, W; 1. Paes Leme, AF
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Funding: FAPESP



Proteomic analysis of endothelial cells (HUVEC) and uric acid oxidation

Dempsey, B; Mineiro, MF; Silva, ARM; Ronsein, GE; Meotti, FC.

1. Departamento de Bioquímica, Instituto de Química (IQ-USP), Universidade de São Paulo - USP, São Paulo, SP, Brazil.
Fapesp and CNPq

Comparative analysis of the proteome profile of adenoid cystic carcinoma of salivary glands

1.Rodrigues-Fernandes, CI; 2.Zanella, VG; 3.Martins, MD; 1.Vargas, PA; 4.Fonseca,FP
1.Universidade Estadual de Campinas - UNICAMP; 2. Santa Casa de Misericórdia de Porto Alegre; 3.Universidade Federal do Rio Grande do Sul; 4.Universidade Federal de Minas Gerais

Bothrops snake venoms: glycoproteomic analysis and the role of sialic acid in toxin function.

1,2. Costa, CB; 1,2. Andrade-Silva D; 1. Carvalho, DC; 1. Serrano S MT.

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Funding: FAPESP

Determination of the protein composition of extracellular vesicles of plasma from patients with oral cancer and its correlation to prognosis

1.Carnielli, CM; 1.Granato, DC; 1. de Oliveira, AK; 1.Domingues, RR; 1.Pauletti, BA; 1. Yokoo, S; 2. Patroni, FMS; 3,4. Ribeiro, ACP; 3. Brandão, TB; 1. Paes Leme, AF.

1. Laboratório de Espectrometria de Massas, Laboratório Nacional de Biociências – LNBio, Centro Nacional de Pesquisa em Energia e Materiais CNPEM, Campinas, São Paulo, Brazil; 2. Centro de Biologia Molecular e Engenharia Genética, Universidade Estadual de Campinas - UNICAMP, São Paulo, Brazil; 3. Serviço de Odontologia Oncológica, Instituto do Câncer do Estado de São Paulo, ICESP-FM Universidade de São Paulo - USP, São Paulo, Brazil; 4. Universidade Brasil, Fernandópolis, Brazil.

Funding: FAPESP

**Differential MMP-9 expression and activity in prostate cancer compared to benign prostatic tissue**

Quina, D; Kawahara, R; Ortega F; Srougi M; Leite KRM; Palmisano G
Institute of Biomedical Science of Universidade de São Paulo - USP
Funding: FAPESP/CNPq

Evaluation of sub-cytotoxic effects of PA-BJ upon blood outgrowth endothelial cells from human peripheral blood using proteomics approaches.

Daniela Cajado-Carvalho, Débora Andrade Silva, Milene Cristina Menezes, Dilza Trevisan Silva, Solange M. T. Serrano.
Laboratório Especial de Toxinologia Aplicada, Center of Toxins, Immune - Response and Cell Signaling - CeTICS, Instituto Butantan, Brazil.
CNPq, FAPESP

16S rRNA amplicon sequencing combined with salivary proteomics identifies microbiome associated with oral cancer prognosis.

Daniela Granato; Leandro X. Neves; Ariane Lopes; Bianca A. Pauletti; Sami Yokoo; Romênia R. Domingues; Carolina M. Carnielli; Henry Heberle; Gabriella Felix; Douglas Paixão; Guilherme Telles; Fabio Squina; Adriana F. Paes Leme
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Funding: FAPESP

Exploring glycosylation levels of snake venom proteins by mass spectrometry: microheterogeneity determination of glycosylated toxins in Bothrops genus

1. Andrade-Silva, D; 2. Rosa-Fernandes, L; 3. Palmisano, G; 4. Travaglia-Cardoso, SR; 1.Serrano, SMT, 2. Larsen, MR
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Funding: FAPESP; the Villum Center for Bioanalytical Sciences at SDU



Proteomic analysis of *Synechococcus* sp. GFB01 under nutritional stress associated with glucosidase inhibitors production.

1.Gradíssimo, DG; 1.Mourão, MM; 1.Xavier, LP; 2.Valadares, RBS; 1.Santos, AV
1.Laboratory of Enzyme Biotechnology and Biotransformations (LABEB)- ICB-UFPA.
2.Vale Institute of Technology (ITV)
CAPES, PROPESP

Multi-omics analysis revealed systemic effects of HF3 from *Bothrops jararaca* venom in a murine model.

1.Trevisan-Silva D; 1. Andrade-Silva, D; 1.Nishiyama, Y; 1.Oliveira UC; 1.Menezes, MC; 1. Junqueira-de-Azevedo, ILM; 2.Schilling, O; 1.Serrano, SMT.
1.Laboratório Especial de Toxinologia Aplicada,CeTICS, Instituto Butantan. 2. Institute of Surgical Pathology, University of Freiburg.
CNPq, FAPESP

Detection of limonene and pinene degradation pathway in *Leptospira biflexa* by proteomics analysis

1,2. Nascimento Filho EGN; 2. Vieira ML; 3. Pimenta DC; 4. Dias M; 5.Heinemann MB;
2. Nascimento ALTO.
1.ICB- Universidade de São Paulo - USP, São Paulo, Brazil; 2. Laboratório Especial de Desenvolvimento de Vacinas, Instituto Butantan, São Paulo, Brazil; 3. Laboratório de Bioquímica e Biofísica, Instituto Butantan, São Paulo, Brazil; 4. Laboratório Dempster de Espectrometria de Massas, POLI-University of São Paulo - USP, São Paulo, Brazil; 5. Laboratório de Zoonoses Bacterianas, FMVZ-University of São Paulo - USP, São Paulo, Brazil
Funding: FAPESP, CAPES, CNPq, Fundação Butantan

Oncological safety of intraoral and extraoral photobiomodulation therapy in oral and oropharyngeal squamous cell carcinoma patients

1.Fontes, EK; 2.Faria, KM; 3.Alves, CGB; 4.Ribeiro, ACP; 5.Brandão, TB;
6.Santos-Silva, AR;
Faculdade de Odontologia de Piracicaba Fop, Universidade estadual de Campinas - UNICAMP
Funding: Fapesp



Molecular characterization of the in vivo effects of the hemorrhagic metalloproteinase HF3: analysis of the proteome of mice muscle tissue.

1.Brito-Pereira,EJ; 1.Trevisan-Silva,D; 1.Serrano,SMT
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Funding: CAPES, CNPq and FAPESP

Proteomic analysis of tears in patients with oral potentially malignant lesions and oral squamous cell carcinoma

1.Santos, ES; 2.Leme, AFP
1. University of Campinas - UNICAMP; 2. Brazilian Biosciences National Laboratory
Funding: FAPESP

Proteomic biomarkers of the rectus abdominis muscle of pregnant women with gestational diabetes and pregnancy-specific urinary incontinence

Alves, FCB; Reys, DRA; Oliveira, RG; Costa, SMB; Barbosa, AMP; Rudge, MVC
Botucatu Medical School. Julio de Mesquita Filho Sao Paulo State University - UNESP.
Funding: FAPESP

Oxidation of Uric Acid in Inflammation and the Consequences in Infection and Cardiovascular Disease

Silva R.P; Bonifacio JPP; Carvalho LAC; Chaves-Filho A.B; Santana M; Miyamoto S;
Lotufo PA; Meotti FC.
1.Instituto of Chemistry; 2. Research group in Redox Processes in Inflammation
Funding: FAPESP

Quantitative targeted proteomics by target LC-MS (SRM) to determine the ligands and interaction interface of Cystatin B complex

Câmara, GA; Granato, DC; Carnielli, CM; Pauletti, BA; Domingues, RR; Leme, AFP.
Brazilian Biosciences National Laboratory – LNBio/CNPEM

**Identification of proteins associated with posttranslational modifications in histones altered in melanoma progression and its role in the malignant p**

Guilherme Cavalcante Pessoa¹, Débora Kristina Alves Fernandes¹, Júlia Pinheiro Chagas da Cunha², Miriam Galvonas Jasiulionis¹ ¹Laboratory of Ontogeny and Epigenetics, Department of Pharmacology, Escola Paulista de Medicina, Universidade Federal de São Paulo São Paulo, SP; ²Special Laboratory of Cell Cycle - Center of Toxins, Immune-Response and Cell Signaling - CeTICS, Instituto Butantan, São Paulo, SP.

Funding: FAPESP and CNPQ

Targeted Proteomics in cyst fluid to profile early stage ovarian tumor

Lanfredi, GP; Poersch, A; Masson, AP; Cândido dos Reis, FJ; Faça, VM
Ribeirão Preto Medical School – University of São Paulo - USP

Funding: CNPQ =

Proteomic analysis of post-mortem brain tissues from patients with schizophrenia

1. Reis-de-Oliveira, G; 2. Zuccoli, GS; 3. Fioramonte, M; 4. Almeida, V; 5. Schmitt, A; 6. Falkai, P; 7. Martins-de-Souza, D Lab of Neuroproteomics

Funding: FAPESP

Modeling Premature Cardiac Aging by Induced Pluripotent Stem Cell From a Patient With Hutchinson-Gilford Progeria Syndrome

Gustavo Monnerat, Tais Brunswick, Karina Asensi, Danubia Santos, Raiana Andrade, Fernanda Mesquita, João Paulo Albuquerque, Raphaela Ferreira, João Simões, Mariana Muniz, Camila Wendit, Erika Velasquez, Gilberto Dumont, Fabio Nogueira, Antonio C Campos de Carvalho

National Institute of Cardiology; Federal University of Rio de Janeiro – UFRJ

Metabolomics study of testosterone depletion and replacement in healthy men,

1,2. Guedes, JS; 2. Cahli, GM; 1,2. Carneiro, GRA; 1,2. Almeida, NP; 3. Marques, ACS; 3. Padilha, MC; 2. Domont, GB; 1,2. Nogueira, FCS; 4,5. Pla, I; 4,5. Sahlin, KB; 4,5. Appelqvist, R; 4,5,6. Marko-Varga, G; 7. Giwercman, A; 4,5. Sanchez, A and Malm, J



Search for *Pythium insidiosum* antigens candidates for the diagnosis of pythiosis

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A coregulatory mRNA-miRNA network in a murine model of oxygen-induced retinopathy (OIR)

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Evaluation of Tomosyn pathway modulation in pancreatic beta cell function gain in in vitro hyperglycemia model

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Peptidomics-driven strategy reveals peptides and proteases associated with oral cancer prognosis

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Immobilization of potential biomarkers in ZIF-8 biosensor applied in head and neck cancer prognosis

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High sensitivity determination of serum thyroglobulin by targeted proteomics for accurate diagnostic of thyroid cancer

Viana, L.G;Schuch,R.A;Cardozo,K.H.M;Carvalho,V.M.
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Proteomic effects of interaction between silver nanoparticles and arsenic in *Caenorhabditis elegans*

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Identification of attack and counterattack strategies of sugarcane x *Sporisorium scitamineum* interaction using a cell wall proteomic approach

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Impact of the use of diode laser in the treatment of oral leukoplakia and proteomic profile related to recurrence and malignization.



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In vivo evaluation of ultrasmall superparamagnetic iron oxide nanoparticle (USPIO)-ibuprofen conjugates

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Toma SH, Araki K, Farsky SHP
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Revealing the interaction partners of TcISWI, a putative chromatin remodeler in Trypanosoma cruzi

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Study of neuronal development by quantitative proteomics in cerebral Organoids

1.Martins M; 2. Lívia Goto-Silva; 1. Fábio C. S. Nogueira; 1. Gilberto B. Domont; 1,2.
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The predictive potential of salivary proteomics for characterization of the phases of allogeneic hematopoietic stem cell transplant

1,3. Souza,MM; 2.Paula, FM; 4.Paula, F; 3.Coutinho-Camillo, CM; 4.Lourenco, SV.
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Secretome profiling of astrocytes derived from induced pluripotent stem cells of patients with Progressive Supranuclear Palsy

1,2. de Carvalho Aguiar, P; 1. Griesi, K; 1. Sertie A; 1,2; 1. Pardo, M; 1. Lins, L; 2. Ferraz, HB

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Funding: FAPESP

Identification of Cardiac Amyloidosis Fibrils by Laser Microdissection and Mass Spectrometry-Based Proteomics

Schuch, RA.; Lima, FM; Viana, LG; Cardozo, KH; Carvalho, VM.
Grupo Fleury

Proteômica baseada em Descoberta para Busca de Alvos Terapêuticos e Biomarcadores Potenciais utilizando-se Análise Multivariada

Domingues,RR; Heberle, H; Paes Leme, AF
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ADAM10 and ADAM17 activity in extracellular vesicles

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Metabolomic and Proteomic Investigation of Banisteriopsis caapi and Psychotria viridis Specimens and of Ayahuasca Decoction Using Mass Spectrometry

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Development and optimization of novel mass spectrometry-based (glyco)proteomic methods for biomarker analysis in serum and plasma

1.Viggiani, TV; 2. Palmisano, G
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Plasma protein signature of gestational malaria

1.Santiago, VF; 1,2,4. Rosa-Fernandes, LR; 1.Santana, TV; 3.Javier, OM; 2. Larsen, MR, 4. Marinho, CFR; 1.Palmisano, G.
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Proteomics applied to the study of Castor bean (*Ricinus communis* L.)

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