RESUME (CURRICULUM-VITAE)
November 2025

GENERAL IDENTIFICATION

NAME: Elton J. R. Vasconcelos, PhD
PROFESSIONAL ADDRESS: Leeds Omics, FMH/FBS, University of Leeds, LS2 9JT, UK.
Email: e.vasconcelos@leeds.ac.uk
ORCID: http://orcid.org/0000-0001-5130-6622
ResearcherID: www.researcherid.com/rid/O-5593-2014
Github: https://github.com/eltonjrv
FBS U of Leeds: https://biologicalsciences.leeds.ac.uk/biological-sciences/staff/1300/elton-vasconcelos

OCCUPATION

Senior Bioinformatics Research Officer at Leeds Omics (https://omics.leeds.ac.uk) from Jun/2023 to present.
Bioinformatics Research Officer at Leeds Omics (https://omics.leeds.ac.uk) from Feb/2019 to May/2023.

EDUCATION

PhD studies: Cell and Molecular Biology at the University of Sao Paulo (Brazil), School of Medicine of Ribeirao Preto, Department of Cell and Molecular Biology and Pathogenic Bioagents, obtained in Aug 2011. Thesis title: *"in silico* Identification and Functional Characterization of Potential Regulatory Sites within Untranslated Regions of *Leishmania* spp. Genomes".

ACADEMIC WORKING EXPERIENCE

I - Postdoctoral researcher, bioinformatician working on microbiome analyses applied to Veterinary Medicine at the College of Veterinary Medicine, Western University of Health Sciences, Pomona, CA, USA. Full time (Jan 2017 – Jan 2019). Member of both Pedro Diniz and Brian Oakley labs.

II – Postdoc Fellowship: PD-FAPESP (Sao Paulo Research Foundation program, personal fellowship for post-doctoral training), full time (Feb 2015 – Jan 2017). Dept. of Biochemistry, Institute of Chemistry, University of Sao Paulo, Verjovski-Almeida Lab. Sao Paulo, SP, Brazil.
Project: Identification and characterization of regulatory long non-coding RNAs on the *Schistosoma mansoni* genome through NGS strategies and systems approach.
Supervisor: Dr. Sergio Verjovski-Almeida

III – Postdoc Fellowship: PDE-CNPq (Brazilian National Council for Scientific and Technological Development program, personal fellowship for post-doctoral training abroad), full time (Jan 2013 – Dec 2014). Center for Infectious Disease Research/Seattle Biomedical Research Institute, Myler Lab – Bioinformatics Core. Seattle, WA, USA.
Project: *in silico* Identification and characterization of novel non-coding elements in the *Leishmania* spp. genomes.
Supervisor: Dr. Peter Myler

IV - PhD Fellowship: Sao Paulo Research Foundation (FAPESP) – full time, (Sep 2006 – Aug 2011). University of Sao Paulo, School of Medicine of Ribeirao Preto, Department of Cell and Molecular Biology, Dr. Angela Cruz Lab. Ribeirao Preto, SP, Brazil.
Project: *in silico i*dentification and functional characterization of potential regulatory sites within the untranslated regions of *Leishmania spp.* genomes.
Advisor: Dr. Angela Kaysel Cruz

SELECTED PUBLISHED WORK

- MOTTRAM TJ, HARPER KL, **VASCONCELOS EJR**, WHITEHOUSE A. Pseudouridine prevalence in Kaposi's sarcoma-associated herpesvirus transcriptome reveals an essential mechanism for viral replication. *Proc Natl Acad Sci* U S A. **2025.** PMID: 40961145
- BLANDY A, HOPES T, **VASCONCELOS EJR**, TURNER A, FATKHULLIN B, AGAPIOU M, FONTANA J, ASPDEN JL. Translational activity of 80S monosomes varies dramatically across different tissues. *Nucleic Acids Research.* **2025**. PMID: 40331628.
- STEWART DI, **VASCONCELOS EJR**, BURKE IT, BAKER A. Metagenomes from microbial populations beneath a chromium waste tip give insight into the mechanism of Cr (VI) reduction. *Science of Total Environment.* **2024**. PMID: 38657818.
- ATKINSON R, GEORGIOU M, YANG C, SZYMANSKA K, LAHAT A, **VASCONCELOS EJR**, et al. PRPF8-mediated dysregulation of hBrr2 helicase disrupts human spliceosome kinetics and 5´-splice-site selection causing tissue-specific defects. *Nature Communications*. **2024**. PMID: 38605034
- MURPHY JC, HARRINGTON EM, SCHUMANN S, **VASCONCELOS EJR**, MOTTRAM TJ, HARPER KL, ASPDEN JL, WHITEHOUSE A. Kaposi's sarcoma-associated herpesvirus induces specialised ribosomes to efficiently translate viral lytic mRNAs. *Nature Communications.* **2023**. PMID: 36653366
- MARAN SR, FLECK K, MONTEIRO-TELES NM, ISEBE T, WALRAD P, JEFFERS V, CESTARI I, **VASCONCELOS EJR**, MORETTI N. Protein acetylation in the critical biological processes in protozoan parasites. *Trends Parasitol.* **2021.** PMID: 33994102
- MOREA EGO, **VASCONCELOS EJR**, DE SANTIS ALVES C, GIORGIO S, MYLER PJ, LANGONI H, AZZALIN CM, CANO MIN. Exploring TERRA during Leishmania major developmental cycle and continuous in vitro passages. *Int J Biol Macromol,* **2021**. PMID: 33548324
- DRECHSLER Y[§], **VASCONCELOS EJR**[§], GRIGGS LM, DINIZ PPPV. CRFK and Primary Macrophages Transcriptomes in Response to Feline Coronavirus Infection Differ Significantly. *Frontier in Genetics*, **2020**. PMID: 33343631. [§] Co-1st and co-corresponding authorship.
- RUY PC, MONTEIRO-TELES NM, MAGALHÃES RD, FREITAS-CASTRO F, DIAS L, AQUINO DEFINA TP, **ROSAS DE VASCONCELOS EJ**, MYLER PJ, KAYSEL CRUZ A. Comparative transcriptomics in *Leishmania braziliensis*: disclosing differential gene expression of coding and putative noncoding RNAs across developmental stages. *RNA Biology*, **2019**. PMID: 30689499
- **VASCONCELOS, EJR;** BILLETER, SA; JETT, LA; MEINERSMANN, RJ; BARR, MC; DINIZ, PPVP; OAKLEY, BB. Assessing cat flea microbiomes in northern and southern California by 16S rRNA Next Generation Sequencing. *Vector-Borne and Zoonotic Diseases*, **2018**. PMID: 29893631
- **VASCONCELOS EJR***, MESEL VC, SILVA LF, PIRES DS, LAVEZZO GM, PEREIRA ASA, AMARAL MS, VERJOVSKI-ALMEIDA S. Atlas of *Schistosoma mansoni* long non-coding RNAs and their expression correlation to protein-coding genes. *Database,* **2018.** PMID: 29992321. * Corresponding author
- **VASCONCELOS, E. J. R**.; SILVA, L. F.; PIRES, D. S.; LAVEZZO, G.; PEREIRA, A. S.; AMARAL, M. S.; VERJOVSKI-ALMEIDA, S. . The *Schistosoma mansoni* genome encodes thousands of long non-coding RNAs predicted to be functional at different parasite life-cycle stages. *Scientific Reports,* **2017**. PMID: 28874839
- LAMBERTZ, U. ; OVANDO, M. O. ; **VASCONCELOS, E. J. R.** ; UNRAU, P. J. ; MYLER, P. J. ; REINER, N. E. . Small RNAs Derived From tRNAs and rRNAs Are Highly Enriched in Exosomes From Both Old and New World *Leishmania* Providing Evidence For Conserved Exosomal RNA Packaging. *BMC Genomics*, v. 16, p. 151, **2015.** PMID: 25764986
- **VASCONCELOS, E. J. R.** ; NUNES, V. S. ; SILVA, M. S. ; SEGATTO, M. ; MYLER, P. J. ; CANO, M. I. N. . The Putative *Leishmania* Telomerase RNA (LeishTER) Undergoes Trans-Splicing and Contains a Conserved Template Sequence. *PLoS One*, **2014.** PMID: 25391020
- JENSEN, B. C. ; RAMASAMY, G. ; **VASCONCELOS, E. J. R.** ; INGOLIA, N. T. ; MYLER, P. J. ; PARSONS, M. . Extensive stage-regulation of translation revealed by ribosome profiling of *Trypanosoma brucei*. *BMC Genomics*, v. 15, p. 911, **2014.** PMID: 25331479

For a complete list of my publications, please visit the following URL:
https://www.ncbi.nlm.nih.gov/myncbi/1DQPtcY9Fwc/bibliography/public/

BOOK CHAPTER(S)
1. IRIZARRY, K. J. L. & **VASCONCELOS, E. J. R.** Chapter title: Population Genomics of Domestication and Breed Development in Canines in the Context of Cognitive, Social Behavioral, and Disease Traits. Population Genomics: Concepts, Approaches and Applications. Om P. Rajora (ed.). **https://doi.org/10.1007/13836_2018_43**, part of Springer Nature **2018**.

EVALUATOR (i) Czech Academy of Sciences – 2020, Phase I for Biological Sciences B panel;
(ii) UK Government Office for Science Foresight Project, Drivers of Technology Needs, Omics & Bioinformatics – Nov/2022;
(iii) Czech Academy of Sciences (Member of the External Evaluation Commission) – 2025, Phases I and II for Biological Sciences.

REVIEW EDITOR of Frontiers in Genetics (**https://loop.frontiersin.org/people/718252/overview**).
***Ad hoc* PEER-REVIEWER:** Annals of Human Genetics; Archives of Microbiology; BMC Bioinformatics; BMC Microbiology; BMC Neurology; BMC Research Notes; BMC Veterinary Research; Frontiers in Cellular and Infection Microbiology; Frontiers in Molecular Biosciences; Infection, Genetics and Evolution; Journal of Biomedical Informatics; MDPI Animals; MDPI Biology; MDPI IJMS; MDPI Life; MDPI Viruses; PLoS One; RNA Biology; Scientific Data (Nature); Scientific Reports (Nature); Vaccine; Veterinary Microbiology.

LECTURING: - PBL facilitator for 1st and 2nd year students at the CVM/WesternU (2018); - Lecturer on training workshops at the University of Leeds since 2019 ("RNA-Seq Data Analysis" and "R for Omics"); - **Data Carpentry** Instructor on Genomics since Nov/2021

MENTORING: Co-Advisor of Edna Gicela Ortiz Morea (2015-2018), PhD in Genetics at the Sao Paulo State University, Botucatu, SP, Brazil). Supervisor: Dr. Maria I. Cano.

Member of EXAMINATION COMMITTEE for PhD thesis: 1) External examiner of Beatriz Cristina Dias de Oliveira, PhD candidate in Genetics at the Sao Paulo State University, Botucatu, SP, Brazil. Supervisor: Dr. Maria I. Cano. (Jan/2024); 2) External examiner of Tanakamol Mahawan, PhD candidate in Bioinformatics and Computational Biology at the BCSB, ISMIB, University of Liverpool, UK. Supervisor: Dr Eva Caamano-Gutierrez (Jun/2024).

SPECIFIC TRAINING

- Machine Learning with Omics Data. Provided by Bristol Medical School, online training courses. June 19th-20th, 2025 (16 hours);
- Nanopore direct-RNA-Sequencing Data Analysis. Provided by Oxford Nanopore Technologies, Oxford, UK. March 20th-24th, 2023 (40 hours);
- Single Cell Technologies and Analysis. Provided by Wellcome Connecting Science, Wellcome Genome Campus, Hinxton, UK. July 26th-30th, 2021 (40 hours);
- EMBL-EBI Proteomics Bioinformatics course. Provided by EMBL-EBI, Hinxton, UK. July 21st-26th, 2019 (40 hours);
- STAMPS Course (Strategies and Techniques for Analyzing Microbial Population Structures). Provided by Marine Biological Laboratory – University of Chicago, Woods Hole, MA, USA. July 30 – August 9, 2017 (75 hours);
- Microbiome Bioinformatics with QIIME2 (Workshop). Provided by Dr. Greg Caporaso's group (Northern Arizona University). Las Vegas, NV, USA. June 2017 (24 hours);
- Summer Course on Systems Biology of Disease provided by the Institute for Systems Biology, Seattle, WA, USA. July 2014 (40 hours);