Bernardo P. de Almeida

I am a Computational Biologist interested in building computational models that can read the human genome and interpret its variation.

Born 14 Dec 1994 E-mail: bernardo.almeida94@gmail.com
Portuguese citizenship Website: **https://bernardo-de-almeida.github.io**

EDUCATION

2015 – 2017 **Master in Oncobiology**
University of Algarve, Portugal [Classification: **19**/20; thesis: **20**/20]

2012 – 2015 **Bachelor in Biomedical Sciences**
University of Algarve, Portugal [Class.: **17**/20; thesis: **20**/20]

2009 – 2012 **High School in Science and Technologies area**
Escola Secundária da Cidadela, Cascais, Portugal [Class.: **18**/20]

RESEARCH EXPERIENCE

2018 – Present **PhD in Computational Biology**
University of Vienna and Medical University of Vienna, Austria
Research Institute of Molecular Pathology (IMP), Vienna, Austria
Project: "**Decoding the cis-regulatory information of enhancer sequences**"
Supervisor: Dr Alexander Stark

2016 – 2018 **Master's thesis + Researcher**
Instituto de Medicina Molecular, Lisboa, Portugal
Project: "Discovery of novel mechanisms of centrosome amplification and their therapeutic value in cancer"
Supervisor: Dr Nuno Barbosa Morais (collab. Dr Mónica Bettencourt Dias)

2016 **Visiting Worker**
Gaffney Group, Wellcome Trust Sanger Institute, Cambridge, UK
Project: "Map of histone Quantitative Trait Loci (QTLs) in iPSCs"
Supervisor: Dr Ângela Gonçalves & Dr Daniel Gaffney

2016 **Research fellow**
Centre for Biomedical Research, University of Algarve, Portugal
Project: "Cis-regulation of somatic mutations in breast and ovarian cancers"
Supervisor: Professor Ana Teresa Maia

2015 **BSc's final project + Laboratory traineeship**
Centre for Biomedical Research, University of Algarve, Portugal
Project: "Identification of new genetic risk markers for breast cancer"
Supervisor: Professor Ana Teresa Maia

AWARDS

2022 **Life Science Research Award Austria 2022 - category Basic Science**
Austrian Society for Molecular Biosciences and Biotechnology (ÖGMBT)

2018 **Best Master Student of the Sciences and Technologies field**
University of Algarve, Portugal

2017 **2nd prize of the "Best Master Thesis" awards**
Instituto de Medicina Molecular, Lisbon, Portugal
Prize: Scholarship to spend 1 week at The Francis Crick Institute, London, UK

2012 **Award of Excellence for best student** (High School)
Escola Secundária da Cidadela, Cascais, Portugal

PUBLICATIONS and PREPRINTS (*equal contributions, §co-corresponding authors)

Selected:

14. F. Reiter*, **B.P. de Almeida***, A. Stark. "Enhancers display constrained sequence flexibility and context-specific modulation of motif function". **Genome Research** 2023; 33:346-358

13. **B.P. de Almeida**, F. Reiter, M. Pagani, A. Stark. "DeepSTARR predicts enhancer activity from DNA sequence and enables the *de novo* design of synthetic enhancers". **Nature Genetics** 2022; 54:613–624
. *Featured commentary*: Lin Tang. "Predicting and designing enhancers". Nature Methods 2022
. Awarded the Life Science Research Award Austria 2022, by ÖGMBT

12. **B.P. de Almeida**, A.F. Vieira, J. Paredes, M. Bettencourt-Dias, N.L. Barbosa-Morais. "Pan-cancer association of a centrosome amplification gene expression signature with genomic alterations and clinical outcome". **PLoS Computational Biology** 2019; 15(3):e1006832

11. **B.P. de Almeida***, J.D. Apolonio*, A. Binnie, P. Castelo-Branco. "Roadmap of DNA methylation in breast cancer identifies novel prognostic biomarkers". **BMC Cancer** 2019; 19:219

Others:

10. N. Moreno-Marin, G. Marteil, N.C. Fresmann, **B.P. de Almeida**, K. Dores, R. Fragoso, J. Cardoso, J.B. Pereira-Leal, J.T. Barata, S. Godinho, N.L. Barbosa-Morais, M. Bettencourt-Dias. "High prevalence and dependence of centrosome clustering in mesenchymal tumors and leukemia". **bioRxiv** 2023

9. J.M. Xavier, R. Magno, R. Russell, **B.P. de Almeida**, A. Jacinta-Fernandes, A. Duarte, M. Dunning, S. Samarajiwa, M. O'Reilly, C.L. Rocha, N. Rosli, B.A.J. Ponder, A.T. Maia. "Mapping of cis-regulatory variants by differential allelic expression analysis identifies candidate risk variants and target genes of 27 breast cancer risk loci". **medRxiv** 2022

8. L. Klaus, **B.P. de Almeida**, A. Vlasova, F. Nemčko, A. Schleiffer, K. Bergauer, L. Hofbauer, M. Rath, A. Stark. "Identification and characterization of repressive domains in Drosophila transcription factors". **The EMBO Journal** 2022, e112100

7. L. Correia, R. Magno, J.M. Xavier, **B.P. de Almeida**, F. Esteves, I. Duarte, M. Eldridge, C. Sun, A. Bosma, L. Mittempergher, A. Marreiros, R. Bernards, C. Caldas, S.F. Chin§, A.T. Maia§. "Allelic expression imbalance of PIK3CA mutations is frequent in breast cancer and prognostically significant". **npj Breast Cancer** 2022; 8:71

6. J. Conde*, R.A. Pumroy*, C. Baker*, T. Rodrigues*, A. Guerreiro, B.B. Sousa, M.C. Marques, **B.P. de Almeida**, … , V.Y. Moiseenkova-Bell§, G.J.L. Bernardes§. "Allosteric Antagonist Modulation of TRPV2 by Piperlongumine Impairs Glioblastoma Progression". **ACS Central Science** 2021; 7(5):868–881

5. I. Gomes, **B.P. de Almeida**, S. Daîmaso, A. Mansinho, I. Correia, S. Henriques, R. Cruz-Duarte, G. Vilhais, P. Félix, P. Alves, P. Corredeira, N.L. Barbosa-Morais, L. Costa, S. Casimiro. "Expression of receptor activator of NFkB (RANK) drives stemness and resistance to therapy in ER+HER2- breast cancer". **Oncotarget** 2020; 11(19):1714-1728

4. T. Rodrigues, **B.P. de Almeida**, N.L. Barbosa-Morais, G.J.L. Bernardes. "Dissecting celastrol with machine learning to unveil dark pharmacology". **Chemical Communications** 2019; 55:6369-6372

3. C. Baker, T. Rodrigues, **B.P. de Almeida**, N.L. Barbosa-Morais, G.J.L. Bernardes. "Natural product–drug conjugates for modulation of TRPV1-expressing tumors". **Bioorganic & Medicinal Chemistry** 2019; 27(12):2531-2536

2. S. Braun, M. Enculescu, S.T. Setty, M. Cortés-López, **B.P. de Almeida**, F.X.R. Sutandy, L. Schulz, A. Busch, M. Seiler, S. Ebersberger, N.L. Barbosa-Morais, S. Legewie, J. König, K. Zarnack. "Decoding a cancer-relevant splicing decision in the RON proto-oncogene using high-throughput mutagenesis". **Nature Communications** 2018; 9:3315

1. G. Marteil, A. Guerrero, A.F. Vieira, **B.P. de Almeida**, P. Machado, S. Mendonça, M. Mesquita, B. Villarreal, I. Fonseca, M.E. Francia, K. Dores, N.P. Martins, S.S. Jana, E. Tranfield, N.L. Barbosa-Morais, J. Paredes, D. Pellman, S.A. Godinho, M. Bettencourt-Dias. "Over-elongation of centrioles in cancer promotes centriole amplification and chromosome missegregation". **Nature Communications** 2018; 9:1258

SOFTWARES

B.P. de Almeida*, N. Saraiva-Agostinho*, N.L. Barbosa-Morais. "cTRAP: Identification of candidate causal perturbations from differential gene expression data". **R package**, https://bioconductor.org/packages/release/bioc/html/cTRAP.html

PATENTS

"Methods of cancer treatment". Intellectual Patent Office UK, Provisional Patent Application GB 1820975.9. Authors: N.L. Barbosa-Morais, **B.P. de Almeida**, M. Bettencourt-Dias, J. Paredes, A. Vieira (2018).

CO-SUPERVISION

. Monika Heinzl, PhD student
Research Institute of Molecular Pathology (IMP), Vienna, Austria *Oct 2022 –*

. Luís Bento, 6-month internship (Master's student in Biological Engineering)
Instituto de Medicina Molecular, Lisbon, Portugal *Mar – Sept 2017*

COMPUTER SKILLS

Machine learning and deep learning
Next-generation sequencing data analysis
Data visualization & statistical analysis

Software:
RStudio & Jupyter Notebook
Cluster computing
HaploView, MACH 1.0, GATK
Adobe Illustrator and InKscape

Computer languages:
Unix shell (bash/zsh)
R
Python
HTML & CSS

Operating systems:
macOS, Windows,
Linux (Ubuntu)

TEACHING EXPERIENCE

Decoding the genome with deep learning
OLISSIPO Workshop, INESC-ID, Lisbon, Portugal *27 Apr 2023*

INVITED TALKS

DeepSTARR predicts enhancer activity from DNA sequence and enables the de novo design of enhancers
Kipoi seminar series *5 Apr 2023*
MLCSB - ISCBacademy Webinar *(https://tinyurl.com/53drm9k5)* *9 Dec 2021*

Decoding transcriptional regulation using massively parallel reporter assays and Twist Oligo Pools
Twist Bioscience Webinar, Virtual *(https://tinyurl.com/3nuw7wsw)* *14 Apr 2021*

Lecture on "How to do a monograph?"
University of Algarve, Portugal *7 Mar 2016*

ABSTRACTS AND CONFERENCE PROCEEDINGS

3. **B.P. de Almeida**, G. Marteil, M. Bettencourt-Dias, N.L. Barbosa-Morais. "Discovery of novel mechanisms of centrosome amplification and their therapeutic value in cancer". **Porto Biomedical Journal** 2017; 2(5):182 (doi: *10.1016/j.pbj.2017.07.019*)
2. J. Xavier, **B. Almeida**, C. Sun, J. Silva, A. Marreiros, M. Eldridge, R. Bernards, C. Caldas, S.F. Chin, A.T. Maia. "PIK3CA mutant allele differential expression (MADE) associates with breast cancer clinical features". [**abstract**]. In: Proceedings of the 24th Biennial EACR Congress; **European Journal of Cancer** 2016; 14(2_Suppl): Abstract nr 884 (doi: *10.1016/S0959-8049(16)61723-9*)
1. J. Xavier, R. Russell, **B.P. Almeida**, N. Rosli, C. Rocha, S. Samarajiwa, S.F. Chin, C. Caldas, B.A.J. Ponder, A.T. Maia. "Integrative differential allelic expression analysis efficiently reveals the biology underlying risk to breast cancer". [**abstract**]. In: Proceedings of the AACR Special Conference on Advances in Breast Cancer Research; **Molecular Cancer Research** 2016; 14(2_Suppl): Abstract nr A31 (doi: *10.1158/1557-3125.ADVBC15-A31*)

PARTICIPATION IN MEETINGS

(*equal contributions, §co-corresponding authors)

Oral presentations:

DeepSTARR predicts enhancer activity from DNA sequence and enables the *de novo* design of enhancers
B.P. de Almeida, F. Reiter, M. Pagani, A. Stark
. Systems Biology: Global Regulation of Gene Expression, CSHL, USA *9-12 Mar 2022*
. EMBO Workshop Enhanceropathies: Understanding enhancer function to understand human disease *6-9 Oct 2021*

Discovery of novel mechanisms of centrosome amplification and their therapeutic value in cancer
B.P. de Almeida, G. Marteil, M. Bettencourt-Dias, N.L. Barbosa-Morais
. iMed Conference® 9.0, Lisbon, Portugal *(**2nd place** at Innovate Competition)* *25-29 Oct 2017*
. 12th Young European Scientists meeting, Porto, Portugal *14-17 Sept 2017*

Poster Presenter:

Enhancers display constrained sequence flexibility and context-specific modulation of motif function
B.P. de Almeida*, F. Reiter*, A. Stark
. 15th EMBL Conference: Transcription and Chromatin, Heidelberg, Germany *27-30 Aug 2022*

Understanding the contribution of inter-motif spacer sequences to enhancer activity
B.P. de Almeida, F. Reiter, A. Stark
. 11th Visualizing Biological Data meeting (VIZBI), *Virtual* *24-26 Mar 2021*
. 14th EMBL Conference: Transcription and Chromatin, *Virtual* *27-29 Aug 2020*

Pan-cancer analysis of Centrosome Amplification uncovers its association with copy number alterations and poor clinical outcome (***highlighted poster***)
B.P. de Almeida, N.L. Barbosa-Morais
. 3rd ASPIC International Congress, Lisbon, Portugal *10-11 May 2018*

Discovery of novel mechanisms of centrosome amplification and their therapeutic value in cancer
B.P. de Almeida, G. Marteil, A. Guerrero, M. Bettencourt-Dias, N.L. Barbosa-Morais
. 3rd EACR Conference in Cancer Genomics, Cambridge, UK *25-28 June 2017*

PIK3CA mutant allele differential expression (MADE) association analysis with breast cancer
B.P. de Almeida, J.M. Xavier, C. Sun, I.A. Silva, J.J. Silva, A. Marreiros, M. Eldridge, R. Bernards, C. Caldas, S.F. Chin, A.T. Maia
. 2nd ASPIC International Congress, Porto, Portugal *28-29 Apr 2016*

Poster Abstracts (presenter's name underlined)**:**

Distinct enhancer-enhancer cooperative behaviours underlie developmental and housekeeping transcription in Drosophila
V. Loubiere, **B.P. de Almeida**, M. Pagani, A. Stark
. 15th EMBL Conference: Transcription and Chromatin, Heidelberg, Germany *27-30 Aug 2022*

Identification of repressive protein domains and their interacting co-repressors
L. Klaus, A. Vlasova, **B.P. de Almeida**, F. Nemcko, A. Schleiffer, K. Bergauer, M. Rath, A. Stark
. 15th EMBL Conference: Transcription and Chromatin, Heidelberg, Germany *27-30 Aug 2022*

Transcriptional enhancer activity relies on specific TF motif compatibilities (***poster prize***)
F. Reiter*, **B.P. de Almeida***, A. Stark
. EMBO Workshop Enhanceropathies: Understanding enhancer function to understand human disease *6-9 Oct 2021*

cTRAP: identification of candidate causal perturbations from differential expression data
N. Saraiva-Agostinho, **B.P. de Almeida**, N.L. Barbosa-Morais
. 11th Visualizing Biological Data meeting (VIZBI), *Virtual* *24-26 Mar 2021*

Characterization of enhancer-bound proteomes
F. Reiter, **B.P. de Almeida**, R. Imre, K. Mechtler, A. Stark
. 14th EMBL Conference: Transcription and Chromatin, *Virtual* *27-29 Aug 2020*

Biological features of estrogen receptor-positive breast cancer with elevated RANK (*TNFRSF11A*) expression
S. Casimiro, I. Gomes, **B.P. de Almeida**, P. Alves, P. Félix, G. Vilhais, A. Mansinho, M.R. Dionísio, N.L. Barbosa-Morais, L. Costa
. 2019 ASCO Annual Meeting, Chicago, USA *31 May – 04 June 2019*

Integrative genomic approach elucidates the risk mechanism for breast cancer associated 5q14.1 locus (***highlighted poster***)
J.M. Xavier, R. Magno, **B.P. de Almeida**, M. Dunning, A. Jacinta-Fernandes, R. Russell, S. Samarajiwa, M. O'Reilly, N. Rosli, C. Nobrega, N.L. Barbosa-Morais, C. Caldas, B.A. Ponder, A.T. Maia
. 3rd ASPIC International Congress, Lisbon, Portugal *10-11 May 2018*

Mapping of cis-regulatory variants helps dissecting the risk mechanism for breast cancer associated 5q14.1 locus
J.M. Xavier, R. Magno, **B.P. de Almeida**, M. Dunning, A. Jacinta-Fernandes, R. Russell, S. Samarajiwa, M. O'Reilly, N. Rosli, C. Nobrega, N.L. Barbosa-Morais, C. Caldas, B.A.J. Ponder, A.T. Maia
. 21ª Reunião da Sociedade Portuguesa de Genética Humana, Portugal *16-18 Nov 2017*

Roadmap of DNA methylation in breast cancer identifies 15 novel potential biomarkers
B.P. de Almeida, J.D. Apolonio, A. Binnie, P. Castelo-Branco
. 2nd CBMR/ProRegem Annual Meeting, University of Algarve, Portugal *8-9 Sept 2017*

Analysis of potential *cis*-regulatory variants at locus 17q22
F. Esteves, J. Xavier, R. Magno, **B.P. de Almeida**, A. Fernandes, C. Rocha, A.T. Maia
. 2nd CBMR/ProRegem Annual Meeting, University of Algarve, Portugal *8-9 Sept 2017*

PIK3CA mutant allele differential expression (MADE) associates with breast cancer clinical features
J.M. Xavier, **B.P. de Almeida**, C. Sun, J. Silva, A. Marreiros, M. Eldridge, R. Bernards, C. Carlos, S.F. Chin, A.T. Maia
. 24th Biennial EACR Congress, Manchester, UK *9-12 July 2016*
Integrative differential allelic expression analysis efficiently reveals the biology underlying risk to breast cancer
J.M. Xavier, R. Russell, **B.P. de Almeida**, N. Rosli, C. Rocha, S. Samarajiwa, S.F. Chin, C. Caldas, B.A.J. Ponder, AT Maia
. 2nd ASPIC International Congress, Porto, Portugal *28-29 April 2016*
. AACR Conference on Advances in Breast Cancer Research, Washington, USA *17-20 Oct 2015*

PARTICIPATION IN COURSES & WORKSHOPS

2020-2021	**Deep Learning Specialization** (online) Coursera, DeepLearning.AI, by Andrew Ng
29-31 May 2019	**Adobe Illustrator workshop** Research Institute of Molecular Pathology (IMP), Vienna, Austria
19-27 Feb 2018	**Introduction to Linear Mixed Effects Models, GLMM with R** Highland Statistics Ltd. & CCIAM, Faculty of Sciences, University of Lisbon, Portugal
29-31 May 2017	**ReTuBi Summer School – From cancer biology to therapy** Instituto de Medicina Molecular, Lisbon, Portugal
22-24 Feb 2017	**Career Development and soft skills for young scientists** Instituto de Medicina Molecular, Lisbon, Portugal
23–24 Sept 2015	**Workshop: R language for Absolute Beginners** University of Algarve, Portugal.

OTHER PROFESSIONAL ACTIVITIES

Jan 15 – Jan 16	**Vice-President of the University of Algarve Academic Association** (AAUAlg), Portugal

LANGUAGES

Portuguese (native), English (fluent), Spanish (fluent), German (basics), French (basics)