

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

Portuguese citizenship

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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 Molecular Biosciences 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, <u>Wellcome Trust Sanger Institute, Cambridge, UK</u> 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: “ <u>Cis-regulation of somatic mutations</u> 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 <u>genetic risk markers</u> 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: <u>Scholarship to spend 1 week at The Francis Crick Institute, London, UK</u>
2012	Award of Excellence for best student (High School) Escola Secundária da Cidadela, Cascais, Portugal

13. F. Reiter*, **B.P. de Almeida***, A. Stark. "Enhancers display constrained sequence flexibility and context-specific modulation of motif function". **bioRxiv** (doi: 10.1101/2022.08.31.506061)
12. L. Klaus, **B.P. de Almeida**, A. Vlasova, F. Nemčko, A. Schleiffer, K. Bergauer, M. Rath, A. Stark. "Identification and characterization of repressive domains in Drosophila transcription factors". **bioRxiv** (doi: 10.1101/2022.08.26.505062)
11. 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** (doi: 10.1101/2022.03.08.22271889)
10. L. Correia, R. Magno, J.M. Xavier, **B.P. de Almeida**, F. Esteves, I. Duarte, M. Eldridge, C. Sun, A. Bosma, L. Mitterpergher, A. Marreiros, R. Bernardes, 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 (doi: 10.1038/s41523-022-00435-9)
9. **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 (doi: 10.1038/s41588-022-01048-5)
. Featured commentary: Lin Tang. "Predicting and designing enhancers". *Nature Methods* 2022
. Awarded the Life Science Research Award Austria 2022, by ÖGMBT
8. 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 (doi: 10.1021/acscentsci.1c00070)
7. I. Gomes, **B.P. de Almeida**, S. Dâmaso, 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 (doi: 10.18632/oncotarget.27576)
6. 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 (doi: 10.1039/c9cc03116b)
5. **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 (doi: 10.1371/journal.pcbi.1006832)
4. **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 (doi: 10.1186/s12885-019-5403-0)
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 (doi: 10.1016/j.bmc.2019.03.025)

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 (doi: 10.1038/s41467-018-05748-7)
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 (doi: 10.1038/s41467-018-03641-x)

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).

INVITED TALKS

DeepSTARR predicts enhancer activity from DNA sequence and enables the de novo design of enhancers (https://www.youtube.com/watch?v=vq32mqptMdQ&ab_channel=ISCB)
MLCSB - ISCBacademy Webinar 9 Dec 2021

Decoding transcriptional regulation using massively parallel reporter assays and Twist Oligo Pools (https://www.youtube.com/watch?v=qUaR34X2a3I&ab_channel=TwistBioscience)
Twist Bioscience Webinar, Virtual 14 Apr 2021

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

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)

SUPERVISION

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

Mar – Sept 2017

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 Abstract (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

. 21^a 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

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
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LANGUAGES

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