



ANA R. CORREIA

Work Experience

SCIENTIST | [AMGEN INC.](#)

Thousand Oaks, CA, USA | Apr 2018 - Sept 2022

- Integrated multidisciplinary teams focused on leveraging and structuring data for ML/AI applications.
- Project development and management.
- Protein engineering, development of purification and analytical characterization workflows for established and novel antibody-like formats (including bi- and multivalent biologics).
- Mentoring, cross-training and supervision of junior scientists in purification, data analysis, and high throughput sample tracking systems.

POSTDOC | [CALTECH](#) [Hoelz Lab](#)

PASADENA, CA, USA | Nov 2013 - Mar 2018

- Expression, purification, assembly and characterization of large macromolecular complexes.
- Structural determination of protein complex by X-ray crystallography.
- Expression and characterization of synthetic antibodies, for further use in crystallization assays.

POSTDOC | [CNB-CSIC](#) [Caston Lab](#)

Madrid, SPAIN | Aug 2011 - Oct 2013

- Production of virus in mammalian and fish cell lines. Purification of virus and viral like particles and subsequent biochemical and structural characterization (negative-stain and Cryo-EM).
- Viral ribonucleoprotein complexes extraction and characterization.

VISITNG RESEARCHER | [BONN UNIVERSITY](#) [Voos Lab](#)

Bonn, GERMANY | Feb 2010 - Jul 2010

- In vivo (yeast cells) and ex vivo (isolated mitochondria) characterization of a mitochondrial protein biogenesis.

CO-FOUNDER | [EUROINGREDIENTES](#)

Lisbon, PORTUGAL | 2000 - 2005

- Co-founder, responsible for business development and establishing new suppliers.

Education

PHD STUDENT | [ITQB-NOVA](#) [Gomes Lab](#)

Lisbon, PORTUGAL | 2006 - 2010

- Conformational and functional characterization of a mitochondrial protein using different biophysical techniques namely: fluorescence spectroscopy, differential scanning calorimetry, calorimetry, circular dichroism and NMR.

INTERN AND VISITNG PHD STUDENT | [NIMR-MRC](#)

London, UK | 2005 - 2009

- Research training on molecular biology and NMR.

BACHELOR'S DEGREE, BIOCHEMISTRY, 2005 | [University of Lisbon \(FCUL\)](#)

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PROFILE

Experienced protein biochemist with a passion for solving biological puzzles and transforming raw data into meaningful insights.

SKILLS

Data analysis and visualization.

Python, statistical methods and machine learning.

Project development and management (R&D).

Protein Engineering.

Biologics purification and analytical characterization.

Structural biology and structural-functional analysis of protein complexes.

Basic understanding of R, SQL and Apache Spark for ML.

LANGUAGES

English

Spanish

Portuguese (native)

HOBBIES & INTERESTS

Hiking, scuba diving, ocean conservancy, MTB and traveling

Additional Training & Certifications

- **MicroMasters Programs MITx – Statistics and Data Science** – Expected end date Dec 2024
- Python 3 Programming by University of Michigan on Coursera (2022).
- Applied Machine Learning in Python by University of Michigan on Coursera (2023).
- Machine Learning Specialization by Stanford University & DeepLearning.AI on Coursera (2023).
- Deep Learning Specialization by DeepLearning.AI on Coursera (2023).
- Data Science Specialization by Johns Hopkins University on Coursera (8 courses from the specialization including R programming, 2021).
- Bioinformatics I, II by University of Toronto on Coursera (2023).
- Algorithms for DNA sequencing by Johns Hopkins University on Coursera (2023).
- The Power of Statistics by Google on Coursera (2023).
- SQL for Data Science by University of California, Davis on Coursera (2023).
- Apache Spark for Data Engineering and Machine Learning by IBM on edX (2023)

Actively developing and expanding my skills in computational biology and data science.

Publications (8 as a first author, *)

- [Utility of physiologically based pharmacokinetic modeling to predict inter-antibody variability in monoclonal antibody pharmacokinetics in mice. \(2023\) *mAbs*, 15\(1\): 2263926.](#)
- [Development of in silico models to predict viscosity and mouse clearance using a comprehensive analytical data set collected on 83 scaffold-consistent monoclonal antibodies \(2023\) *mAbs*, 15\(1\):2256745.](#)
- [Architecture of the cytoplasmic face of the nuclear pore \(2022\) *Science*, 376 \(6598\):1174-1192.](#)
- [Enhancing the Prefusion Conformational Stability of SARS-CoV-2 Spike Protein Through Structure-Guided Design \(2021\) *Front. Immunol.*, 12, article 660198.](#)
- [Rational selection of building blocks for the assembly of bispecific antibodies \(2020\) *mAbs*, 13 \(1\), e1870058.](#)
- [Structural and functional analysis of mRNA export regulation by the nuclear pore complex \(2018\) *Nat. Commun.*, 9 \(1\):2319-2338. *](#)
- [A new MR-SAD algorithm for the automatic building of protein models from low-resolution X-ray data and a poor starting model \(2018\) *IUCrJ*, 5 \(Pt 2\):166-171.](#)
- [Nuclear pores. Architecture of the nuclear pore complex coat \(2015\) *Science*, 347, 1148-52. *](#)
- [Probing the kinetic stabilities of Friedreich's Ataxia clinical variants using a solid phase GroEL chaperonin capture platform \(2014\) *Biomolecules*, 4 \(4\): 956-79. *](#)
- [Revertants, low temperature, and correctors reveal the mechanism of F508del-CTFR rescue by VX-809 and suggest multiple agents for full correction \(2013\) *Chem. Biol.*, 20 \(7\):943-55.](#)
- [Iron binding activity in yeast frataxin entails a trade off with stability in the a1/b1 acidic ridge region \(2010\) *Biochem. J.*, 426\(2\):197-203. *](#)
- [No evidence of direct binding between ursodeoxycholic acid and the p53 DNA-binding domain \(2010\) *Biosci Rep.*, 30\(5\):359-64. *](#)
- [The conserved Trp-155 in human frataxin as a hotspot for oxidative stress related chemical modifications \(2009\) *BBRC*, 390\(3\):1007-11. *](#)
- [Dynamics, stability and iron-binding activity of frataxin clinical mutants \(2008\) *FEBS J.*, 275, 3680-3690. *](#)
- [Conformational stability of human frataxin and effect of Friedreich's ataxia related mutations on Protein Folding \(2006\) *Biochem. J.*, 398, 605-611. *](#)

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