



# 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

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

London, UK | 2005 - 2009

- Research training on molecular biology and NMR.

### 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.

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

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raquelvcorreia

## PROFILE

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

## SKILLS

Data analysis and visualization.

Python, knowledge of 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.

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## LANGUAGES

English  
Spanish  
Portuguese (native)

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## HOBBIES & INTERESTS

Hiking, scuba diving, ocean conservancy, MTB and traveling

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## Additional Training & Certifications

- Python 3 Programming by University of Michigan on Coursera. Certificate earned in 2022
- Applied Machine Learning in Python by University of Michigan on Coursera. Certificate earned in 2023
- Applied Text Mining in Python by University of Michigan on Coursera. Certificate earned in 2023
- Machine Learning Specialization by Stanford University & DeepLearning.AI on Coursera. Certificate earned at August 30, 2023
- Deep Learning Specialization by DeepLearning.AI on Coursera. Certificate earned at September 21, 2023
- Data Science Specialization by Johns Hopkins University on Coursera. (8 courses from the specialization including R programming, certificates earned in 2021)
- Bioinformatics I and II by University of Toronto on Coursera. Certificate earned in 2023.
- Algorithms for DNA sequencing by Johns Hopkins University on Coursera. Certificate earned in 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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