

## Profile

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I am a driven life scientist with a Master's degree in Biochemistry and Biotechnology from the University of Antwerp. I have expertise in molecular biology, bioinformatics, and statistical analysis. Currently, I am pursuing a PhD in computational drug discovery, in collaboration with Eurofins-VillaPharma at UCAM and under the supervision of Prof. Horacio Pérez-Sánchez. The main focus of my PhD is both the development and application of novel computational drug discovery techniques.

## Education

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### **UCAM Universidad Católica San Antonio de Murcia | Murcia, Spain** **2021-Present**

PhD-student at BIO-HPC

- Scope: The discovery and optimization of ligands against protein targets using computational drug discovery techniques
- Key words: *in silico* drug design, molecular docking, virtual screening
- Thesis Director: Prof. Horacio Pérez-Sánchez

### **University of Antwerp | Antwerp, Belgium** **2018-2021**

MSc Biochemistry and Biotechnology

- Major: Systems biology
- Minor: Research
- Key Modules: Datamining, Applied Bioinformatics, Protein technology and Proteomics, Medical Cell Biology, Gene and Genome technology
- Master Thesis (February – June 2021)
  - Title: *FEP viewer: a user-friendly webtool to display free energy perturbation calculations*
  - Summary: Development of an easy-to-use webtool which is able to orderly display previously performed free energy perturbation (FEP) calculations, as well as initiating new FEP calculations.
  - Promotor: Prof. Hans De Winter
  - Laboratory of Medicinal Chemistry (UAMC), University of Antwerp
- FELASA A,B,C accreditation

### **University of Antwerp | Antwerp, Belgium** **2015-2019**

BSc Biochemistry and Biotechnology

- Key Modules: Bioinformatics, (Bio)Statistics, Organic Chemistry, Molecular Biology, Genetics, Cellular Biology, Immunology, Integrated Metabolism
- Internship associated with Bachelor Thesis (March-April 2019)
  - Title: *Systematic meta-analysis of resistance markers for Isoniazid of Mycobacterium tuberculosis*
  - Promotor: Prof. Kris Laukens, Supervisor: Emmanuel Rivière

- Adrem Datalab, University of Antwerp
- The results from this internship contributed to a published paper, which resulted in co-authorship: <https://doi.org/10.1016/j.cmi.2020.07.004>

## Experience

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### Internships

**Laboratory of Medicinal Chemistry (UAMC) | University of Antwerp** **August 2020**

*Voluntary Internship*

Development of a pharmacophore-based conformational sampling tool for small molecules under the supervision of Prof. Hans De Winter.

**Biomina | University of Antwerp** **July 2020**

*Voluntary Internship*

Development of a Python script which is able to visualize molecular structures in the world Minecraft, a popular 3D game. After providing a SMILES-string as input, the script can build the corresponding molecule in the 3D environment of a Minecraft world as either a 2D or 3D molecular structure. This project was performed in association with Biomina, under the supervision of Prof. Kris Laukens.

**Biomina | University of Antwerp** **July 2019**

*Voluntary Internship*

Development of several Python scripts in order to largely automate the workflow of utilizing their in-house developed TCRex tool. This webtool can be used to predict TCR-epitope binding for human T-cell receptors. This project was completed at Biomina, under the supervision of Prof. Kris Laukens.

**Evonik | Antwerp, Belgium** **July 2018**

*Student Job*

Laboratory Assistant at the environmental lab of Evonik Antwerp.

### Teaching

**Physics and Chemistry | Grado en Veterinaria | UCAM** **Sep-Dec 2024**

Taught Physics and Chemistry to 1st-year Bachelor of Veterinary Sciences students (4.5 ECTS), delivering 60 hours of instruction, including theory lectures and supervised laboratory sessions, while also grading practical reports and providing feedback to students.

### Conferences

- Using consensus molecular docking for the discovery of Wee1 inhibitors in the context of cancer, II Symposium on Chemical and Physical Sciences for Young Researchers, 24/03/2022-25/03/2022, Universidad de Murcia
- Optimizing Consensus docking by incorporating predicted binding pose similarity: a Wee1 case study, I Simposio de Estudiantes Hispanohablantes de Bioinformática y Biología Computacional, 02/06/2022-03/06/2022, Online (SEH2Bioinfo)
- Optimizing consensus docking by incorporating predicted binding pose similarity: a Wee1 case study, VIII Jornadas de Investigación y Doctorado, 24/06/2022, UCAM
- Visualizing the Impact of Chemical Substructures on Compound Activity for Improving the Drug Discovery Process, III Symposium on Chemical and Physical Sciences for Young Researchers, 15/06/2023-16/06/2023, Universidad de Murcia

- Awarded a prize for the **best Flash presentation**
- Unpacking the Black Box: Understanding Machine Learning models to Aid the Drug Discovery Process, IX Jornadas de Investigacion y Doctorado, 23/06/2023, UCAM
- Visualizing Molecular Impact: Understanding the Role of Substructures in Drug Activity Prediction, II Congreso Estatal de Estudiantes de Biociencias (CEEBI), 18/07/2023-21/07/2023, Universidad de Granada
  - Also paired with an article in the Spanish magazine “Hidden Nature” (ISSN 2531-0402) titled “[Descodificando la caja negra: Mejorando y guiando el descubrimiento de fármacos usando inteligencia artificial e interpretabilidad de las subestructuras moleculares](#)”.

## **Publications**

- Nelen J, Pérez-Sánchez H, De Winter H, Van Rompaey D. Matched pairs demonstrate robustness against inter-assay variability. *Journal of Cheminformatics* 2025;17:8. <https://doi.org/10.1186/s13321-025-00956-y>.
- Grzelczyk J, Pérez-Sánchez H, Nelen J, Carmena-Bargueño M, Gałązka-Czarnecka I, Budryn G, et al. Interaction of an anticancer oxygenated propenylbenzene derivatives with human topoisomerase II  $\alpha$  and actin: molecular modeling and isothermal titration calorimetry studies. *J Therm Anal Calorim* 2024. <https://doi.org/10.1007/s10973-024-13569-8>.
- Rodríguez-Martínez A, Nelen J, Carmena-Bargueño M, Martínez-Cortés C, Luque I, Pérez-Sánchez H. Enhancing MD simulations: ASGAR’s automated analysis for GROMACS. *Journal of Biomolecular Structure and Dynamics* 2024:1–13. <https://doi.org/10.1080/07391102.2024.2349527>.
- Nelen J, Carmena-Bargueño M, Martínez-Cortés C, Rodríguez-Martínez A, Villalgordo-Soto JM, Pérez-Sánchez H. ESSENCE-Dock: A Consensus-Based Approach to Enhance Virtual Screening Enrichment in Drug Discovery. *J Chem Inf Model* 2024;64:1605–14. <https://doi.org/10.1021/acs.jcim.3c01982>.
- Dakpa G, Kumar KJS, Nelen J, Pérez-Sánchez H, Wang S-Y. Antcin-B, a phytosterol-like compound from *Taiwanofungus camphoratus* inhibits SARS-CoV-2 3-chymotrypsin-like protease (3CLPro) activity in silico and in vitro. *Sci Rep* 2023;13:17106. <https://doi.org/10.1038/s41598-023-44476-x>.
- Rivière E, Whitfield MG, Nelen J, Heupink TH, Van Rie A. Identifying isoniazid resistance markers to guide inclusion of high-dose isoniazid in tuberculosis treatment regimens. *Clinical Microbiology and Infection* 2020;26:1332–7. <https://doi.org/10.1016/j.cmi.2020.07.004>.

## **Additional Skills**

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- **Languages:** Dutch (Native), English (Fluent), Spanish (Novice), French (Notion)
- **Microsoft Office:** Proficient in Word, Excel and PowerPoint
- **Programming Languages:** Python (Advanced), R (Intermediate), Java (Intermediate), HTML (Intermediate), CSS (Intermediate), JavaScript (Intermediate), PHP (Novice)