

# Filip (Persson) Ljung | Research Scientist

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## Education

<b>PhD (Teknologie Doktor)</b> <i>Biophysical Chemistry,</i>	Faculty of Engineering <b>Lund University</b> 2012–2018
<b>Master of Science in Engineering</b> <i>Biotechnology,</i>	Faculty of Engineering <b>Lund University</b> 2008–2012

## Experience

<b>Statens Serum Institut</b> <i>Research Scientist</i>	<b>Copenhagen</b> Since 2023
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Conducting early-life disease biomarker discovery using untargeted metabolomics (LC-MS) profiling of biobanked blood samples.

- Identified potential biomarkers for pediatric brain neoplasms.
- Developed software tools for enhanced quality control of metabolomics data.
- Optimized data processing pipelines for high-throughput metabolomics data.

<b>HØIBERG</b> <i>Patent Attorney</i>	<b>Copenhagen</b> 2021–2022
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Drafted and prosecuted patent applications in the Life Science sector, including peptides, antibodies and biosensors.

<b>Lunds Universitet</b> <i>Post Doc</i>	<b>Lund</b> 2018–2021
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Investigated the role of shape in protein function through de novo design of self-assembling proteins for targeted drug delivery.

- Developed computational pipelines for rapid 3D pattern-matching and molecular surface computation.
- Implemented machine learning techniques for 3D superposition of molecular shape data.

<b>Lunds Tekniska Högskola</b> <i>PhD Student</i>	<b>Lund</b> 2012–2018
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Conducted molecular dynamics (MD) simulations to study protein-water interactions.

- Tested and validated models interpreting data from Nuclear Magnetic Resonance (NMR) and scattering experiments.
- Co-teacher in courses in thermodynamics, molecular driving forces, and biophysical chemistry.

## Publications

**9 in total:** 7 first author, H-index of 7.

## Publication list

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- [1] Bertil Halle and Filip Persson. Analysis of protein dynamics simulations by a stochastic point process approach. *Journal of Chemical Theory and Computation*, 9(6):2838–2848, 2013.
- [2] Filip Ljung and Ingemar André. Zeal: Protein structure alignment based on shape similarity. *Bioinformatics*, 37(18):2874–2881, 2021.
- [3] Filip Persson. *Protein-water interactions studied by molecular dynamics simulations*. Doctoral thesis (compilation), Biophysical Chemistry, 2018.
- [4] Filip Persson and Bertil Halle. Transient access to the protein interior: Simulation versus nmr. *Journal of the American Chemical Society*, 135(23):8735–8748, 2013.
- [5] Filip Persson and Bertil Halle. How amide hydrogens exchange in native proteins. *Proceedings of the National Academy of Sciences*, 112(33):10383–10388, 2015.
- [6] Filip Persson and Bertil Halle. Compressibility of the protein-water interface. *The Journal of Chemical Physics*, 148(21), 2018.
- [7] Filip Persson, Pär Söderhjelm, and Bertil Halle. The geometry of protein hydration. *The Journal of Chemical Physics*, 148(21), 2018.
- [8] Filip Persson, Pär Söderhjelm, and Bertil Halle. How proteins modify water dynamics. *The Journal of Chemical Physics*, 148(21), 2018.
- [9] Filip Persson, Pär Söderhjelm, and Bertil Halle. The spatial range of protein hydration. *The Journal of Chemical Physics*, 148(21), 2018.