



## WILDSCHUT, THIJS

Groups of Alexandre Theocharides/Bernd Wollscheid

Experimental Hematology/Institute for Molecular Systems Biology  
University Hospital Zürich/ETH Zürich  
Schmelzbergstrasse 12, 8091 Zurich/Auguste-Piccard-Hof 1, 8093 Zürich

[thijs.wildschut@usz.ch](mailto:thijs.wildschut@usz.ch)/[mattheus.wildschut@hest.ethz.ch](mailto:mattheus.wildschut@hest.ethz.ch)

[www.haematologie-onkologie.usz.ch/theocharides/](http://www.haematologie-onkologie.usz.ch/theocharides/)  
[www.imsb.ethz.ch/research/wollscheid.html](http://www.imsb.ethz.ch/research/wollscheid.html)



**KEYWORDS** – Hematology, Myeloproliferative Neoplasms, Calreticulin mutations, chaperone, proteomics, drug response profiling

## MAIN FIELDS OF RESEARCH; ABSTRACT

I joined the Theocharides lab in April 2017 as a PhD student in Cancer Biology to start a collaborative project with the lab of Bernd Wollscheid (ETHZ). I have studied Biomedical Sciences in the Netherlands and have a strong personal interest in performing translational cancer research.

In my project, I perform research on the role of Calreticulin mutations in myeloproliferative neoplasms (MPN). MPN are a family of blood diseases that originate from hematopoietic stem cells. By discovering the mechanisms that drive disease, therapeutics targeting these alterations can be developed to improve treatment of patients suffering from MPN. Calreticulin is a protein that normally functions as a chaperone that ensures correct folding of cellular proteins. To find out how mutations in this protein alter the cell and drive pathogenesis of MPN, we take an integrative unbiased approach. In this approach, we combine various techniques to look at the cellular proteome, transcriptome, and Calreticulin interactome, and study how these change upon mutation of Calreticulin using CRISPR/Cas9 technology.

In addition, given our interest in translating biology and mechanisms underlying these diseases, we are currently investigating drug responses of mutated and healthy cells. For this, we employ both targeted approaches, inhibiting the deregulated pathways we found in our screens, and unbiased drug response profiling efforts.

## SPECIAL TECHNIQUES AND EQUIPMENT

Proteomics, CRISPR/Cas9, primary sample handling, drug response profiling, pharmacoscopy, transduction