SFS18003 F Soltermann grant report

I was delighted and relieved to receive an SFOU grant of 350 Fr. in December 2018 to cover travel costs for an urgent return to the UK to work on the research for a paper. I highly appreciate that the SFOU offers a unique opportunity to Swiss students to apply for funding for conventional and most importantly unconventional projects, which would not fit into any other funding scheme.

My grant application is a special kind of Christmas story, or a real natural science research story: During a meeting in Oxford on the evening of 20th December, it was supposed to be the last meeting before the long Christmas break, my professor revealed to me that one of his collaborators copied and implemented my idea and that they were close to publishing it. It was a big shock at that moment. However, I quickly realized that the best way to get us out of trouble would be to just submit a better paper, with better quality and more rigorous research. It was then an easy decision to cancel the Christmas holidays and to move my return flight forward from January 6th to December 26th. I did not get the 1.5 weeks of sun in Valais, but at least 3 days of good food prepared by my lovely mum. During this time, it was mentally a big relief to know that the SFOU will probably cover the large amount of additional travel costs arising from the flight cancellation/rebooking. Fortunately, the SFOU really did so, and I can now happily write this report.

Regarding the paper, we were lucky enough that we managed to advance much more than our competitors. Over the past 5 months, we achieved the high-quality standards we wanted and will soon be able to provide the scientific community with a new, well bench-marked microscopy method for single-molecule protein interaction analysis. Following discussions with the highly renowned journal “Nature Methods” we are confident to submit our work by early July 2019. Back in 2018, the basic principles of the technique were published in Science (Young et al, Science, 2018, 360 (6387), p423-7). We showed that the mass of single biomolecules can be determined from their interaction with light, i.e. light scattering is proportional to mass of biomolecules. Being able to observe single biomolecules in solution and directly determining their mass is a great achievement. But even greater would be to quantitatively count these molecules. Here an example to illustrate the significance: I am a pharmaceutical company and would like to know how well a drug candidate binds to the target. This is often an antibody binding to its antigen but could be any other biomolecule interaction. If I mix these two proteins in vitro and the antibody drug candidate is functional, I would expect to observe three species (antibody-antigen complex, free antibody and free antigen), with three distinctive masses. The more antibody-antigen complex I observe, relative to the free species, the stronger the interaction of my antibody with my target, i.e. the better my drug candidate. In our paper we show that we can indeed quantitatively count these single biomolecules and quantify binding affinities. Furthermore, we provide data to explain advantages and limitations and highlight the future suitability for high throughput measurements of binding affinities, giving it the potential to become a powerful tool for both academic and industrial research.