Interview: Oliver Rinner – CEO and Founder, Biognosys, Switzerland



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Oliver Rinner, CEO and founder of Biognosys, provides a fascinating account of the company's unique business model and explains how its technical research into proteomics and cell expression is likely to be even more successful despite continuous technological developments.

Biognosys – a proteomics focused company – was initially founded as a spin-off of ETH Zurich, under Prof. Ruedi Aebersold's team (one of the pioneers in the field of proteomics) nearly 10 years ago, with the claim that "the decoding of the proteome will impact the life sciences more than the genome revolution". Why do you think so? And what potential do you foresee in this field?

The main reason is simply because proteins are the most significant functional elements in the body. The human physiology is almost entirely run by proteins in regards to cellular structure, enzymes, and receptors. The purpose behind the creation of Biognosys was to better understand the mode of action of various drugs and biological processes by understanding the changes in the protein levels and activation. Biological systems can be viewed in a number of ways. Genomics can tell if certain genes are mutated or not and their transcripts tell you what genes are expressed and indeed to what extent. However, the transcriptome, however, is not a perfect predictor for protein expression and this is the fundamental basis of our offering, we analyse the proteins directly. If you use our technology you will be able to look at biology in much greater depth which will ultimately change your understanding of your biological systems. We think it is a 'no brainer' to analyse the

proteome directly if the research question addresses proteins, and if that becomes generally accepted there will be a huge potential for our technology.

You stated a few months ago, that "The feedback you get from customers shows there is a shift in the perception of proteomics, away from a highly specialised analytical tool and towards a universally applicable technology for mode of action studies and biomarker development". Can you please comment further on why you have observed this change in perception?

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First, if you look how new analytical technologies become accepted in recent years you can see that scientists tend to be conservative – for good reasons. Those who work in this industry know that you need more than just showing your own data and a few research papers to establish a new technology as standard in the field. It can therefore take a long time to for researchers to change from the methods they used in their studies at university to how studies are conducted at firms like ours. For instance, until 10 years ago the method for investigating the proteome with mass spectrometers was inadequate and only allowed professionals to see the top 200 proteins in a cell. Many biologists don't know how much proteomics has developed since this time so biologists still mostly resort to what they know, which are classical antibody based methods.

However, this is beginning to change as more and more researchers discover that next-generation proteomics provides them with answers that could not be obtained by other means. Another sign for the increasing adoption it that until recently proteomics was mostly featured in technical journals. Now scientists are increasingly using these technologically advanced methods to tackle their biological hypothesises, not for the sake of the technology itself.

Since the company's inception, what have been some of the key developments and achievements that you are the proudest of, and on the contrary, some of the major challenges you have had to overcome?

Biognosys was spun off from the lab of Ruedi Aebersold at the ETH Zurich, who is a pioneer in quantitative proteomics. The latest transformation of the technology, which we and others call next-generation proteomics, is a particularly important one because it solves a major limitation of classical proteomics. In this approach, also known as shotgun proteomics, a mass spectrometer selects a single peptide at a time, and analysed it, before moving on to another peptide. This is a sequential, time consuming process that and leads to irreproducible data. Next-generation proteomics analyses many peptides in parallel, which provides more identifications with a higher

reproducibility. A good analogy is taking a photo of a crowd of people and having a database complete with photographs of all the individuals present. With this you could match all the individuals in a single photograph.

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Technological progress remains important to further increase the analysis depth. The more proteins you see, the more signalling pathways can be monitored, which in turn provides a deeper understanding of the samples. We at Biognosys are not simply buying this technology and offering it to others. We are further improving and developing it and validate it by publishing it in scientific journals. I think the interest in highly-dimensional data has recently revived throughout the life science industry. Although not specific for life sciences, the general trend towards the combination of big data sets with deep learning technologies will further increase the demand for large scale proteomics data.

This new generation protein quantification technology is available to researchers worldwide through contract research services or your portfolio of innovative reagent and software products. How exactly is Biognosys planning on further growing and further generating revenues? Tell us more about your overall business model.

That is an important question. When spinning off a new technology from an academic setting, you need to know how to apply it to the market and what returns you can expect. Like any company operating in this way, we had to adapt our business model as the technology and the market evolved.

Many people ask whether we are a product or a service company? As far as I am concerned, that is the wrong question. Ultimately, we enable our clients to perform better biological studies by using next generation proteomics technology. Some of our clients are experts for mass spectrometry themselves and use our software and reagent products to obtain better results. Others are just interest in the data and don’t want to operate a mass spectrometer. For these customers we start we the samples, process them in-house and provide back the interpreted data, effectively using our own products to perform services. In that sense we consider sales of services and products as different sales channels for the same Biognosys technology. We expect that the vendors of mass spectrometers will make their instruments easier to use for a broader user base in the future, and with this the proportion of product sales vs. services may shift, but on the other hand with the increasing use of proteomics data the service marker is expected to grow as well.

One important aspect is the relationship between data generation and data interpretation. The latest technological developments have enabled the acquisition of huge data sets but ultimately researchers want to test their hypotheses and answer their research questions. Converting data into knowledge is often the hardest step in this process as few biologists come from a statistical or data analysis focussed background. We assist with all aspects of reporting in addition to our training platforms. Moving forward, I think data interpretation become the main value driver in the omics fields. By using reference data sets for example, we can offer contextualised information that has been built up over many years.

What are some of the key changes that as CEO you are looking to implement?

Firstly, to continue to push the frontier of the technology. We have already shown that our technology can in principle identify more than 10,000 different proteins. This is a huge landmark but there is more to come. There is the potential to see 15,000-16,000 expressed proteomes in cells. It is not only how many but also the quality, the depth and the throughput (how many samples you can process). In the past perhaps 5 samples were tested against another 5 samples and the process took a very long time. This has now become much easier and we can test thousands of samples without complications. This opens new opportunities, such as applications in clinical research where large sample numbers need to be analysed. We have just begun to address this market.

We are also finding a lot of joy in the marketing and communication side of our business. By this I do not mean creating slogans or promotional material for clients but really educating the field. People ultimately want to know what can be done to advance their research and they not to be able to make the connection between the capabilities of next-generation proteomics and their own questions. For instance, researchers are using RNA-expression to indicate regulation on the protein level. Many of them don’t know yet, that it has become possible to directly quantify protein expression changes using proteomics. If clinicians want to know what is expressed in a particular cell type, they should directly look on the protein level. It is our mission to educate the field about these new possibilities.

Today you work with distributors in India, China, Japan, Korea and Brazil, and you have your own office set up in Boston. What is the rationale behind this internationalization strategy?

From the beginning, we have been an international business. Our biggest market is the US which makes sense not only due to the size of the market but also its peculiar structure with venture

financed pharmaceutical and biotech firms who do not have the capacity for in-house research but a high need for early stage R&D.

We have distributors in Asia for example to have easy market access. China is a difficult market to operate for a company like ours so we have partners there who can meet customers directly. The same is true for India. We also have distributors in various locations who can deal with international logistical problems.

What do you value so much about the Swiss life sciences ecosystem?

I think there are many great places in the world for life sciences, with the US being a prime example. But for a company such as ours, that has a strong focus on developing technologies to a very high-quality level, Switzerland is the perfect environment. First of all, when looking at our background and origins; we were created within ETH from one of the leading universities globally for proteomics. Secondly, it is all about people. Finding the right talents and experts is key, and Switzerland can attract highly qualified specialists from abroad. At Biognosys, we today have over 12 different nationalities.

To conclude, I would like to say that the field of proteomics has come a long way, and it can now be applied to solve important biological questions. It has reached the depth and quality level needed to do functional studies. We strive for a “systems biology” where there would be enough room for genomics, transcriptomics and proteomics.

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