In the Human Protein Atlas (HPA) more than 70% of the human genes are soon portrayed using antibodies. To make this possible, more than 35000 different human protein fragments have been immunized to produce polyclonal antibodies which are then strictly scrutinized prior to their use in the protein expression and localization studies of the atlas. All genes have been initiated in the production pipeline and a strong effort on iterations, of those genes where either antigen production has failed or the antibodies did not pass the thorough HPA validation regime, is in progress. It is our experience that re-immunization of the same immunogen or selection of another fragment of a particular gene is by far the most efficient iteration strategies to gain gene coverage. So far, around 75000 fragments have been selected based on uniqueness relative to proteins from other genes. However, optimization of the protocols for cloning as well as protein expression has been essential for the successful production of immunogens for many of the more challenging genes/proteins and will continue to be so as we approach full coverage and the most demanding genes remain.

The goal to have a first draft of the human proteome portrayed with antibody proteomics based on at least one primary antibody is approaching. For 62% of the proteome an in-house produced antibody is represented in the HPA database, and only 21% remain in antibody generation. Along with this much effort is put into generating paired antibodies to validate the results of the first.

A strict strategy has been set up in order to keep up the antibody production and yet prioritize the production of primary antibodies for the first draft. At several key points of the production the samples are strictly prioritized to give precedence to samples more likely to generate new data on a human protein not yet portrayed in the Human Protein Atlas.

References: