Protein Crystallogenesis – From the soluble to the crystalline state

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This workshop will cover the basic steps of protein crystallogenesis and will be divided in two parts:

1. **Individual samples**
   In this part we will do an initial screen with your protein sample(s) to look for suitable crystallization conditions. You will be able to test 384 conditions with up to 3 different protein variations (e.g. different concentrations, different ligands …).
   You will learn how to setup initial screens in a 96-well format by using a crystallization robot and the crystallization method of the sitting drop. The plates will be stored in an imager system that allows automated photographic documentation of the crystal growth.

2. **Model protein: Lysozyme**
   We will work with the model protein lysozyme to get known to the more manual fields of crystallogenesis. Lysozyme is a cheap and especially a very fast crystallizing protein.
   First you will learn how to set up 24-well refinement plates by using the method of the hanging drop. On the next day(s) you will be able to take a look at over-night grown crystals. We will discuss the differences in crystal growth at different conditions. Afterwards we will catch the crystals in a small nylon-loop, cryoprotect and freeze them in liquid nitrogen.
   At the end we will mount the frozen crystals to our Xray-beamline to take some test diffraction images.

Necessary items:
approx. 50 µL, min. 10 mg/mL (depends on the MW of your sample) of each of your protein variation (if you want to do an initial screen; of course you can also join if you don't have an own sample)

Time:
Someday in (the first half of) December. 3 days should be fine, maybe 2 days in a row and another day a few days later.

Max number of participants:
3-4, because of limited space/microscopes.

Let me know if you will join the course till November 28th. Then we can discuss dates & times. Of course you can ask questions regarding your protein sample in advance.