**Poster Sessions**

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**Growth of high-quality and large crystals of HIV protease for neutron crystallography**

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The biological structure and function of proteins are dominated by hydrogen atoms. Neutron protein crystallography provides a powerful complement to X-ray analysis by enabling the visualization of hydrogen atoms, which allo...require a weak flux of available neutron beam. Although recent advances in protein expression and purification techniques permit large amounts of proteins to crystallize, the bottleneck of protein crystallography is that unusual large crystals (> 1 mm³) are required to compensate...crystallization, the two-liquid system and stirring technique as well as counterdiffusion (CD) technique has proved to be very suitable to grow protein crystals. Since it starts far from the equilibrium, the result of a CD experiment evolves along the length of the growth chamber in time. This means that it is possible to obtain sequentially amorphous precipitation, microcrystals and crystals of the highest quality in a single experiment [2]. Here we present the results of the crystallization screening carried out for several proteins by means of capillary CD technique, using the new version of the Granada Crystallization Box, provided by Triana S&T [3, 4]. Because of the use of short and thin capillaries (0.1 mm diameter), the required volume for experiment is reduced to less than 300 nL. The effect of pH (4 to 9) and precipitants (three different polyethylene glycols, from low to high molecular weight, a mixture of them and ammonium sulphate) related to the isoelectric point (pI) will be discussed in terms of crystallizability and also X-ray diffraction crystal quality using a home lab source.

**Keywords:** protein crystal growth, HIV, neutron crystallography

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**X-ray crystallographic study of the C-terminal domain of Tic110 protein from Cyanidioschyzon merolae**

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Tic110 (translocan of the inner envelope membrane) is an intergal membrane protein containing a short N-terminal membrane anchor and a hydrophobic region (~98 kDa) that extends into the plastid stroma. Here, the crystallization and preliminary analysis of the C-terminal domain (659-1007) of Tic110 protein hydrophilic region from *Cyanidioschyzon merolae* Tic110 (cmTic110C) are reported. The cmTic110C has been crystallized at 293 K using PEG 400 as precipitant. These crystals belong to the hexagonal space group P6₃22 (or P6₃22), with unit-cell parameters a = b = 123.2, c = 246.4 Å. A 99.3% complete native data set from a frozen crystal has been collected to 4.5 Å resolution at 100 K with an overall Rmerge of 7.9%.

The presence of two subunit of cmTic110C per asymmetric unit gives a crystal volume per protein weight (Vm) of 3.46 Å³ Da⁻¹ and a solvent content of 64.5%.

**Keywords:** crystallization of proteins, crystallization methods, counterdiffusion

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**Snapshots in the reaction pathway of bilin reductase**

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Protein crystallization has gained a new strategic and commercial relevance in the post-genomic era due to its pivotal role in Structural Genomics: producing high-quality crystals has always been the rate-limiting step in protein structure determination. Novel crystallization screens and strategies [1] have been developed to make the search for initial crystallization conditions more manageable. Among them, counterdiffusion (CD) technique has proved to be very suitable to grow protein crystals. Since it starts far from the equilibrium, the result of a CD experiment evolves along the length of the growth chamber in time. This means that it is possible to obtain sequentially amorphous precipitation, microcrystals and crystals of the highest quality in a single experiment [2]. Here we present the results of the crystallization screening carried out for several proteins by means of capillary CD technique, using the new version of the Granada Crystallization Box, provided by Triana S&T [3, 4]. Because of the use of short and thin capillaries (0.1 mm diameter), the required volume for experiment is reduced to less than 300 nL. The effect of pH (4 to 9) and precipitants (three different polyethylene glycols, from low to high molecular weight, a mixture of them and ammonium sulphate) related to the isoelectric point (pI) will be discussed in terms of crystallizability and also X-ray diffraction crystal quality using a home lab source.

**References:**


**Keywords:** crystallization of proteins, crystallization methods, counterdiffusion