A Holder for Diffracting Crystals and *Mesophases* Straight from Crystallization Plates

<u>Ariel Mechaly</u>^a, J. Agirre^a, A. Cabo^a, D.M.A. Guérin^b, ^aUnidad de Biofísica (UPV/EHU-CSIC), Bilbao, Spain. ^bUNSur, Bahía Blanca, Argentine. E-mail: gbxguxxd@lg.ehu.es

High throughput crystallization entails miniaturization of the protein+precipitant solution mixture reaching drops of less than 100 nanoliters. Crystals growing in such small volume are difficult to handle and quite often most of crystals grown together in the same drop get injured when scrambling with the loop trying to fish a single one for mounting. This situation is critical when, for example, we just want to check crystals under x-rays to distinguish proteins from salts. Things gets even worse when the crystallization experiment is in mesophase where the growing medium is much more viscous than all solutions used in vapour diffusion methods. In order to avoid crystal handling and mounting we designed and constructed a holder to put the plate directly into the diffractometer. The holder is fixed to a x-y-z standard goniometer head and -when mounted on a MAR345 Image Plate detector- a 96-well plate can rotate about 30 degrees. This attachment can hold standard hanging, sitting and micro batch 96-well plates and was proved to be useful for checking crystals directly inside the growing solution. This holder was also useful for screening precipitant solutions that destabilize monoolein-based cubic phases when setting up for membrane protein crystallization assays using the micro-batch method.

Keywords: mesophase, x-ray diffraction, crystallization plates