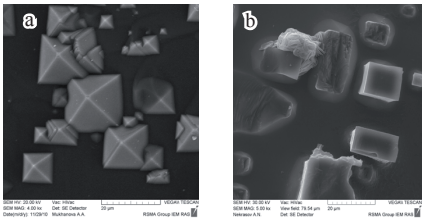
up to $1 \cdot 10^3$ nuclea in cm^3. The aggregates are similar to the natural "diamondite" type and consist of microcrystals sized from 10-20 nm to 50-100 μm. Composition of the experimental growth carbonate melt-carbon solutions is chemically similar to the natural parent medium [2] that determines the physicochemical mechanism of the "carbonate-synthetic" diamond formation and, respectively, peculiarities of the face growth and morphology. By kinetic indication, it is possible to determine regions (1) of spontaneous nucleation and crystallization of diamond ("region of labile carbon oversatutations") and (2) of diamond seeded growth ("region of metastable carbon oversaturation") within the PT region of diamond thermodynamic stability. A boundary between the two regions is positioned of less than 0.5 GPa to the diamond-graphite equilibrium lines creating a narrow region of diamond seeded growth between the boundaries. Within the diamond-seeded growth region, morphological peculiarities of growing faces and crystallization steps and fronts are kinetically-dependent. The crystallization fronts are variable from polycentric and roughly blocked to smooth with nano-dimential growth steps. The interaction of crystallization fronts can impose the effects of the layers overgrowth. All the new growing layers, independently of the seed face (111) with smooth layers or (100) with semi-octahedral hills, have the "octahedral" orientation for growth layers (fig. a). The "cubic" morphology demonstrated in the fig. b is firstly obtained; it is important that the orientation of the growing layers in the case is "cubic". This uncommon result is obtained at highest temperature of 2400°C.



Support: Grants of RF President MK-913.2011.5, RAS Presidium P02, RFBR 10-05-00654 and 11-05-00401.

[1] A.V. Spivak, A. Litvin Yu,.*Diamond Relat. Mater.* **2004**, *13*, 482-487. [2] A. Litvin Yu.*In Ohtani, E., ed. Advances in High-Pressure Mineralogy: Geological Society of America Special Paper* **2007,** *421*, 83-103.

Keywords: carbonate-synthetic diamond, morphology, seeded growth

MS35.P06

Acta Cryst. (2011) A**67,** C457

Synchrotron topography of (Nb,Yb):$RbTiOPO_4$ single crystals and related materials

Joan J. Carvajal,[a] Balaji Ragothamachar,[b] Vishwanath Sarkar,[b] Xavier Mateos,[a] Michael Dudley,[b] Francesc Díaz,[a] Magdalena Aguiló,[a] *[a]Physics and Crystallography of Materials and Nanomaterials (FiCMA-FiCNA) and EMaS, University Rovira i Virgili, Tarragona (Spain). [b]Stony Brook Synchrotron Topography Facility, Department of Materials Science & Engineering, Stony Brook University, Stony Brook, NY (USA).* E-mail: joanjosep.carvajal@urv.cat

Rubidium titanyl phosphate, $RbTiOPO_4$ (RTP) is isostructural with the well-known potassium titanyl phosphate, $KTiOPO_4$ (orthorhombic, $Pna2_1$). Its non-linear optical properties make it suitable as a frequency doubling material when doped with active lanthanide ions such as Yb^{3+} [1]. However, the distribution coefficient of Yb^{3+} in RTP crystals is very low and the codoping with Nb^{5+} is required to increase the concentration of Yb^{3+} in the crystals through a mechanism of electrical compensation of the matrix [2]. Laser action has been demonstrated at ~1 μm for these crystals [3]. The (Nb,Yb):RTP crystals are grown by the top-seeded solution growth (TSSG) technique using self-fluxes to avoid the presence of undesired ions in the solution that can affect the physical properties of the crystals. However, the crystals exhibit a tendency to crack during removal from the furnace after growth. Such cracked crystals are obviously not suitable for optical and spectroscopic applications.

Synchrotron white beam X-ray topography (SWBXT) has been employed to characterize the structural defects in these crystals to investigate the cause of cracks. X-ray topographs recorded from both doped and undoped crystals reveal defect features such as growth striations, growth sector boundaries, dislocations, grain boundaries, and especially, inhomogeneous strain that might be responsible of cracking. The distribution of these defects have been mapped in each type of crystal along the three main crystallographic directions and compared. Defect distribution was also analyzed with respect to the growth conditions in order to gain insights into the growth mechanism and the origin of cracks. Results from these studies will be presented.

[1] J.J. Carvajal, V. Nikolov, R. Solé, Jna. Gavaldà, J. Massons, M. Aguiló, F. Díaz, *Chem. Mater.* **2002**, *14*, 3136-3142. [2] J.J. Carvajal, J.L. García-Muñoz, R. Solé, Jna. Gavaldà, J. Massons, X. Solans, F. Díaz, M. Aguiló, *Chem. Mater.* **2003**, *15*, 2338-2345. [3] X. Mateos, V. Petrov, A. Peña, J.J. Carvajal, M. Aguiló, F. Díaz, P. Segonds, B. Boulanger, *Opt. Lett.* **2007**, *32*, 1929-1931.

Keywords: synchrotron white beam X-ray topography, top-seeded solution growth, RbTiOPO4

MS35.P07

Acta Cryst. (2011) A**67,** C457-C458

The CrystalHarp™ - an advanced high throughput capillary plate for protein crystallization

Mareike Kurz,[a] Beat Blattmann,[a] Christophe Briand,[a] Paul Reardon[b] Andres Käch,[c] and Markus G. Grütter,[a] *[a]Institute of Biochemistry, University of Zürich, Zürich (Switzerland). [b]SWISSCI AG, Neuheim, (Switzerland). [c]Center for Microscopy and Image Analysis, University of Zürich, Winterthurerstrasse, Zürich (Switzerland).* E-mail: m.kurz@bioc.uzh.ch

Counter diffusion crystallization in capillary is an easy, cost-effective and practical procedure for obtaining protein crystals for *in situ* X-ray data analysis. This method is used simultaneously for screening, incorporation of heavy atoms and cryo protection in a single capillary [1], [2].

We present a novel capillary crystallization plate, based on the counter-diffusion method and designed for 48 high throughput-screening experiments. Due to the plate's design only 20 μl of protein is needed to load the plate very quickly. A liquid handling robot can facilitate the pipetting of the individual well conditions. The crystallization plate is compatible with any incubation and imaging systems and allows *in situ* X-ray diffraction measurements. Alternatively, an individual capillary can be removed from the CrystalHarp™ and the crystal can be analysed 360° *in situ* by X-ray diffraction.

For initial plate validation, crystallization experiments with six commercially available soluble proteins, two soluble in-house proteins