

Coupling counterdiffusion and micro-seeding techniques to increase protein crystallization succeed

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INTRODUCTION

Distinct methods have been studied to improve quality and size of protein crystals. Protein crystallization in capillaries by counterdiffusion technique has been used routinely for crystal optimization. On the other hand, seeding techniques has open a possibility to improve protein crystal quality and size by carrying on new crystallization experiments on the metastable region of the phase diagram where only growth can occur.

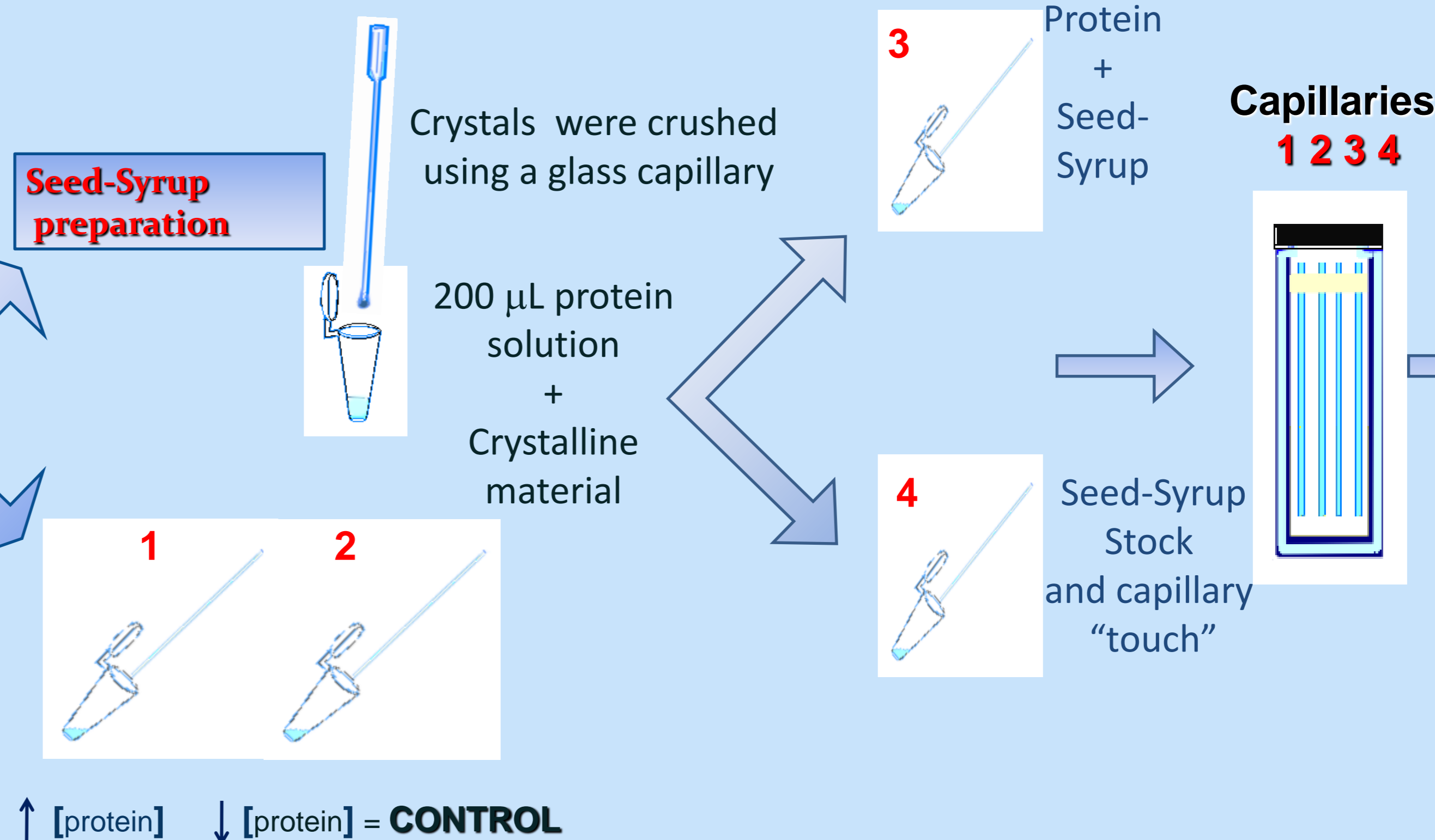
Ideally, seeding should be implemented using batch technique to avoid subsaturation conditions that could dissolve the seed or, high supersaturation conditions as can be obtained in vapour diffusion technique. Counterdiffusion technique allows the introduction of seeds into a system where the mass transport is controlled by diffusion in which supersaturation increase slowly enough to permit the growth of several seeds minimizing cross influence, mixing and convection effects.

In this work we present the proof of this concept producing optimized crystals of several model proteins by the combination of counterdiffusion and micro-seeding techniques.

Crystalline material

Spherules, amorphous aggregates, needle or micro-crystals aggregates.

Obtained by different techniques (Bath, vapour diffusion, counterdiffusion)



EXPERIMENTAL

RESULTS

TABLE 1. Crystallization conditions for initial protein micro-seeds preparation and the final condition to study micro-seeding.

Protein	Protein concentration and seed preparation conditions	Micro-seeding conditions
Glucosa Isomerase	20 mg/ml, Batch experiment using 100 mM Hepes pH 7.0 and 0.9 M Ammonium sulfate.	30 mg/mL 10 mg/mL 10 mg/mL + seeds 10 mg/mL + dipped in seeds
Ribonuclease-A	240 mg/mL, Counterdiffusion technique, precipitating solution C21**: 6 M Na-Formate.	240 mg/mL 50 mg/mL 50 mg/mL + seeds 50 mg/mL + dipped in seeds
Catalase	36 mg/mL, Vapor diffusion technique using the crystallization mushroom. Precipitating solution 10% w/v PEG-4000.	40 mg/mL 7 mg/mL 7 mg/mL + seeds 7 mg/mL + dipped in seeds
Myoglobin	80 mg/mL, Counterdiffusion technique, precipitating solution C1**: 30% PEG 4K, 0.2 M Mg Chloride, 0.1 M Tris-HCl pH 8.50	80 mg/mL 5 mg/mL 5 mg/mL + seeds 5 mg/mL + dipped in seeds
α -Lactalbumin	72 mg/mL, Hanging drop technique. Precipitating solution C23**: 0.82 M K-Phosphate, 0.82 M Na-Phosphate, 0.1 M Na-Hepes pH 7.50.	30 mg/mL 5 mg/mL 5 mg/mL + seeds 5 mg/mL + dipped in seeds
Thaumatococcus	30 mg/mL, D5 from Jena Bioscience Membrane screen 3; 1.5 M Lithium Sulfate, 100 mM HEPES Sodium Salt, pH 7.5	90 mg/mL 10 mg/mL 10 mg/mL + seeds 10 mg/mL + dipped in seeds
Xylanase	36 mg/mL, No.45 from Molecular Dimensions Structure Screen 1; 4.0M Sodium Formate	56 mg/mL 36 mg/mL 36 mg/mL + seeds 36 mg/mL + dipped in seeds
Trypsin	30 mg/mL, D6 from Jena Bioscience Membrane screen 3; 2.0M Sodium Chloride, 100mM Sodium Formate	90 mg/mL 30 mg/mL 30 mg/mL + seeds 30 mg/mL + dipped in seeds
Concanavalin	5 mg/mL, B8 from (Molecular Dimensions) JCSG plus screen; 10% w/v PEG 8000, 100mM Tris-HCl, pH 7.0, 200mM Magnesium Chloride	15 mg/mL 5 mg/mL 5 mg/mL + seeds 5 mg/mL + dipped in seeds

**Counterdiffusion Screening Kit® ref. GCB-CSK-24. See the last part appendix the composition of the 24 conditions.

One of the goals of this study was to increase the number of hits during the screening in capillaries by counterdiffusion using the minimum Kit (24 conditions) using micro-seeding technique. Our results show that both protocols, mixing the seed with the protein solution and touching the seed syrup, increase the number of hits when compare with the low concentration protein solution (90%). In three cases (33%) the number of hits using seeds was higher than those obtained with high protein concentration solution and in one case we got crystals only when seeds were included.

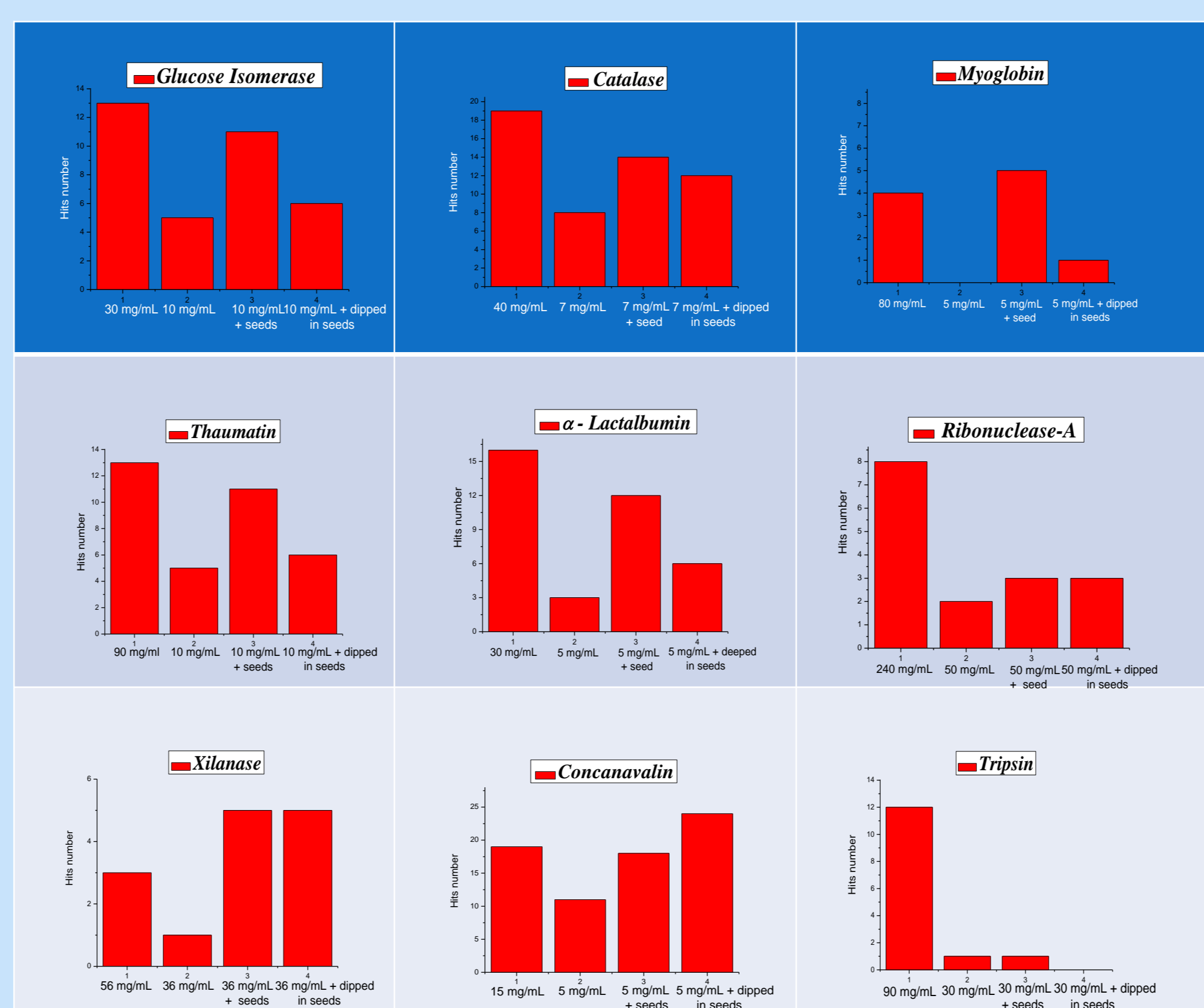


TABLE 2. Number of hits in the protein crystallization study in capillaries by combination of counterdiffusion and micro-seeding techniques using different model proteins.

NOTE: The last capillary correspond to the filled with the proteins solution and after dipped in the Seed-Syrup Stock solution also named as "touch".

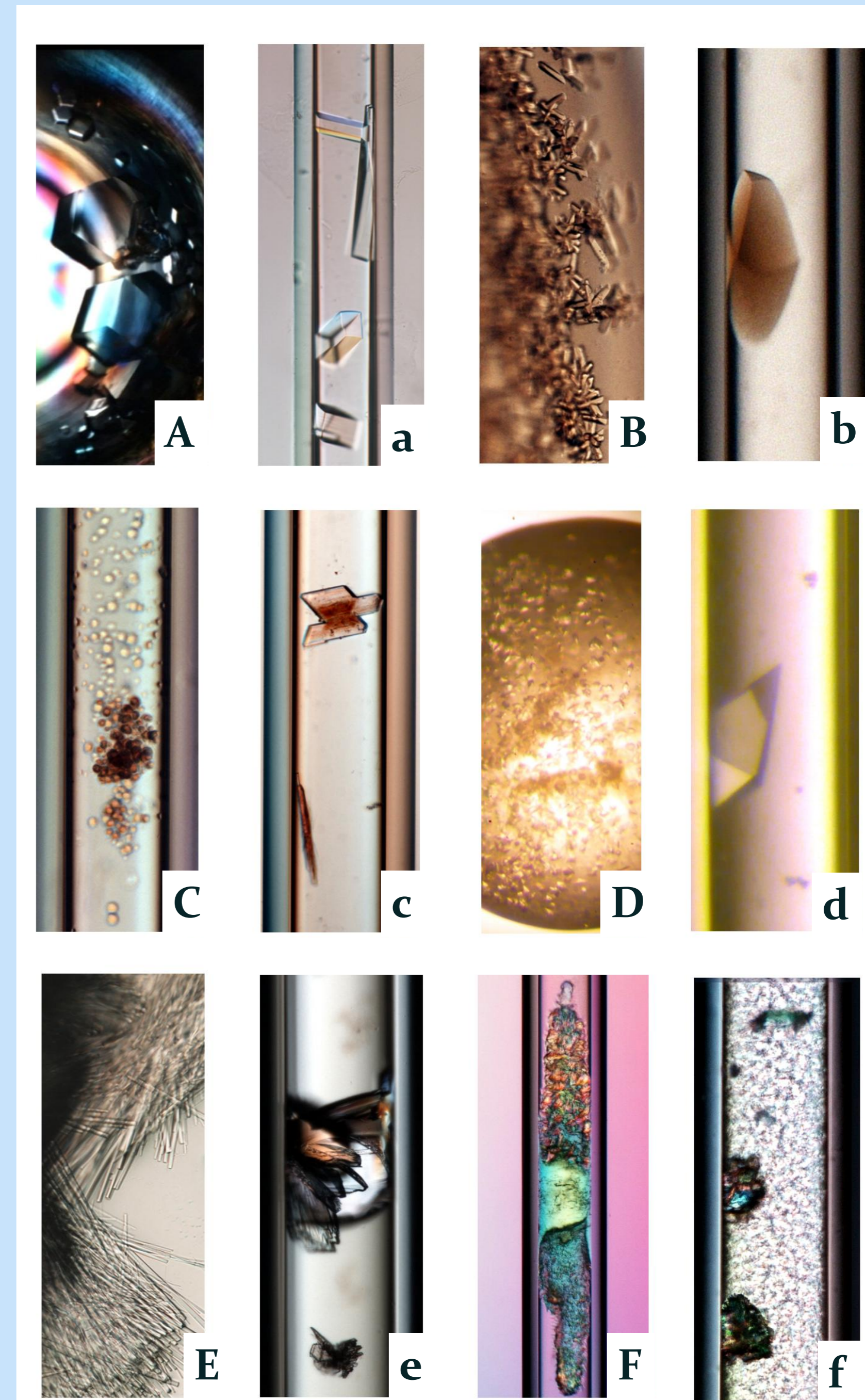


Figure 1. Protein crystals microphotographs. Capital letters show the seeds used, small letter crystals after seeding. A) Glucosa Isomerase crystals obtained by batch 20 mg/mL and 100 mM Hepes pH 7.0 and 0.9 M Ammonium sulfate, a) Glucosa Isomerase crystals after seeding 10 mg/mL condition C2 B) Catalase crystallized at 36 mg/mL by vapor diffusion technique and 10% w/v PEG-4000, b) Catalase at 7 mg/mL condition C8**, C) Myoglobin obtained at 20 mg/mL condition C1**, c) Myoglobin crystallized at 5 mg/mL condition C1**, D) Thaumatococcus 30 mg/mL and precipitated with D5 from Jena Bioscience Membrane screen3; 1.5 M Lithium Sulfate, 100 mM HEPES Sodium Salt, pH 7.5; d) Thaumatococcus 30 mg/mL and obtained in condition C7**, E) α -Lactalbumin crystallized at 72 mg/mL by Hanging drop technique and 0.82 M K- Phosphate, 0.82 M Na-Phosphate, 0.1 M Na-Hepes pH 7.50.; e) α -Lactalbumin crystallized at 5 mg/mL. C13**, F) Ribonuclease-A obtained at 240 mg/mL condition C21**, f) Ribonuclease-A crystallized at 50 mg/mL condition C21**.**

CONCLUSIONS

For the first time, it is reported the crystallization of several model proteins using micro-seeding by the counterdiffusion technique. Overall, most of the protein studied (90%) increase the number of hits in which the nucleation occurs even when the capillary only touches the "seeds syrup".

The most effective protocol was mixing the protein solution with the seed-syrup, which produced an homogeneous distribution of seeds along the capillary.

It is well known that the initial seed may influence definitively the quality of the final crystals. However in this work the use of (in appearance) not so good quality crystals, such as the case of spherulites of Myoglobine, was done on purpose resulting in the growth of faceted crystals.

Seeds from the initial crystalline-precipitate can be used to set-up a minimum counterdiffusion screening experiment, even at low protein concentration, to find new crystallization conditions and to produce crystals of improved visual quality.

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