

High Output Crystallization in the new Crystal Former

Nabanita De, Ph.D.

nde@microlytic.com











High Output Crystallization

Definition: Crystallization screening experiments in which the number of crystallization events is generally large relative to conventional protein crystallization experiments, minimizing challenges in optimization, data management and analysis.

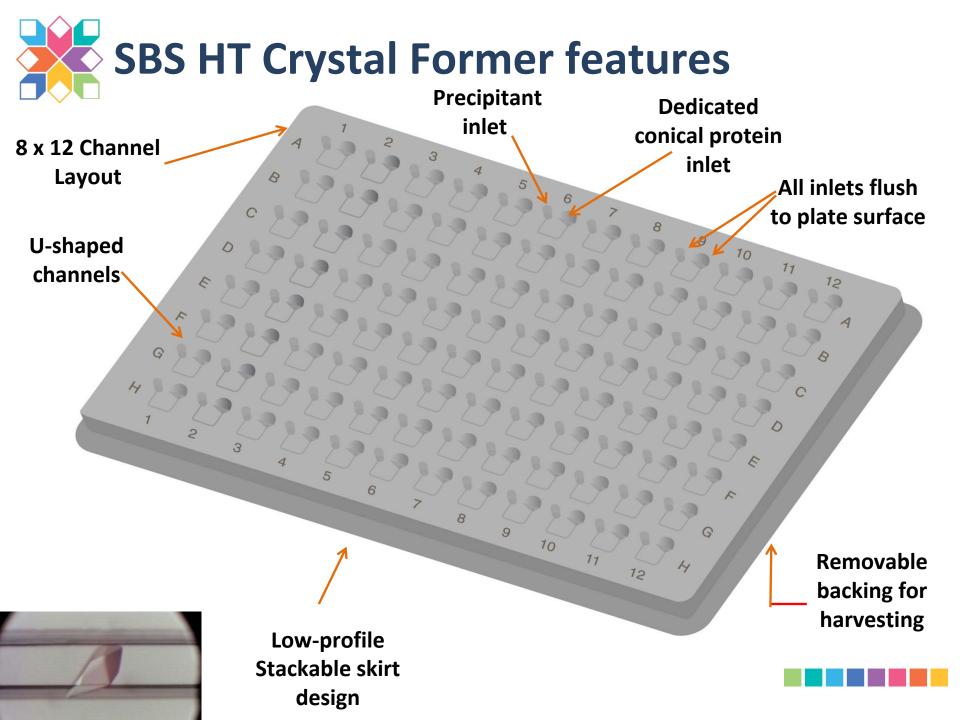
As distinguished from high throughput: high throughput screening refers only to the total number of possible crystallization experiments. Simple automation of vapor diffusion has not resulted in high output.

Challenge: to design new and improved methods for screening and optimization for the production of useful crystals.



Desirable Features of High Output Crystallization Systems

- Increased likelihood of crystallization success
- Low sample consumption
- Systematic and highly informative
 - Even in the absence of crystals
 - Easy to interpret
- Non-redundant
- Automatable
- Integrated with current workflows and robotics

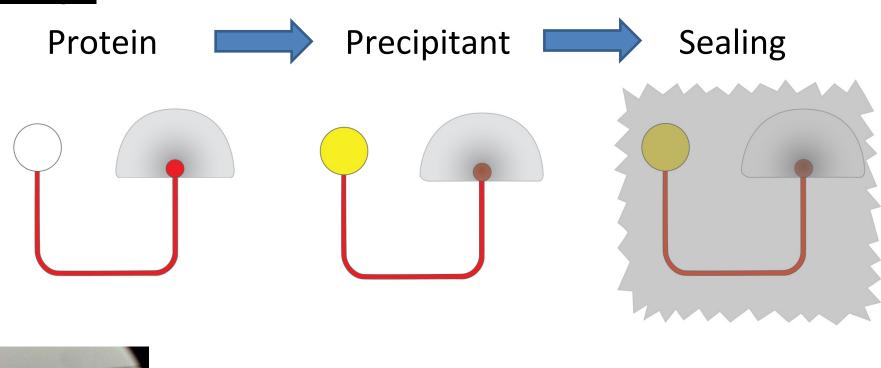




The Crystal Former Design

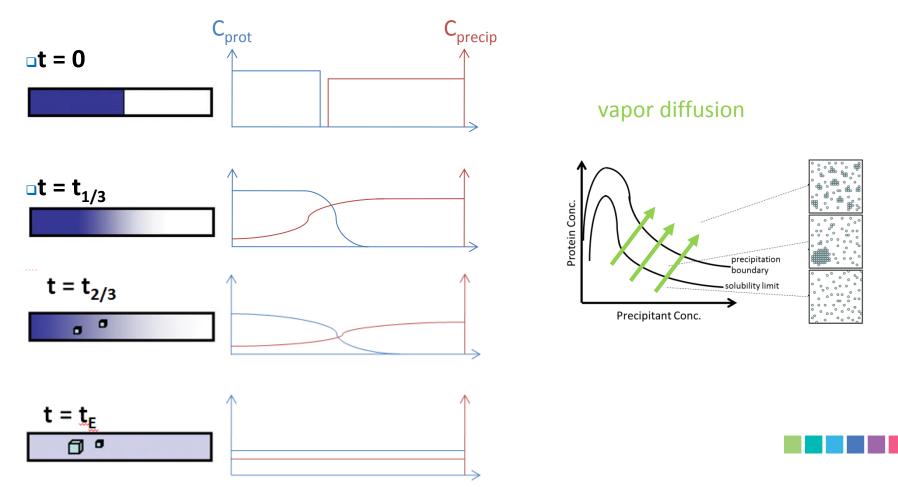


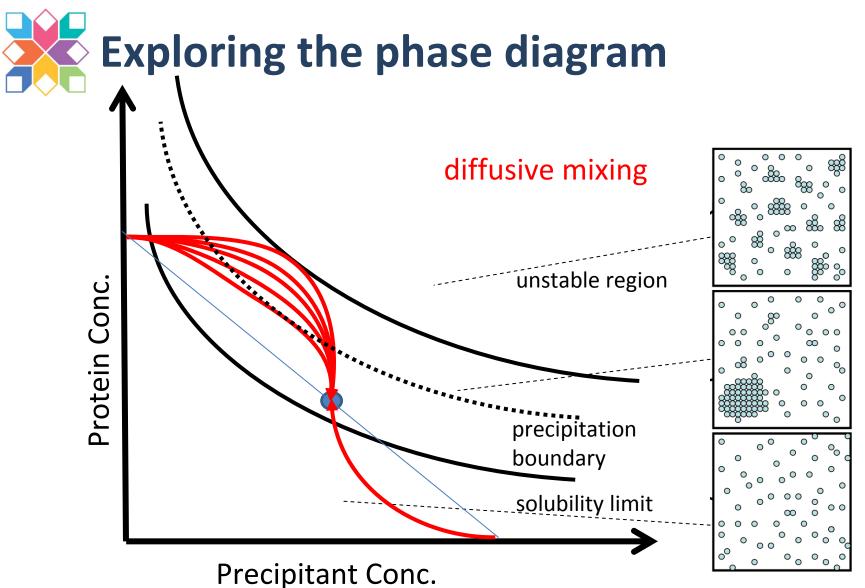
Setup:

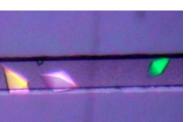


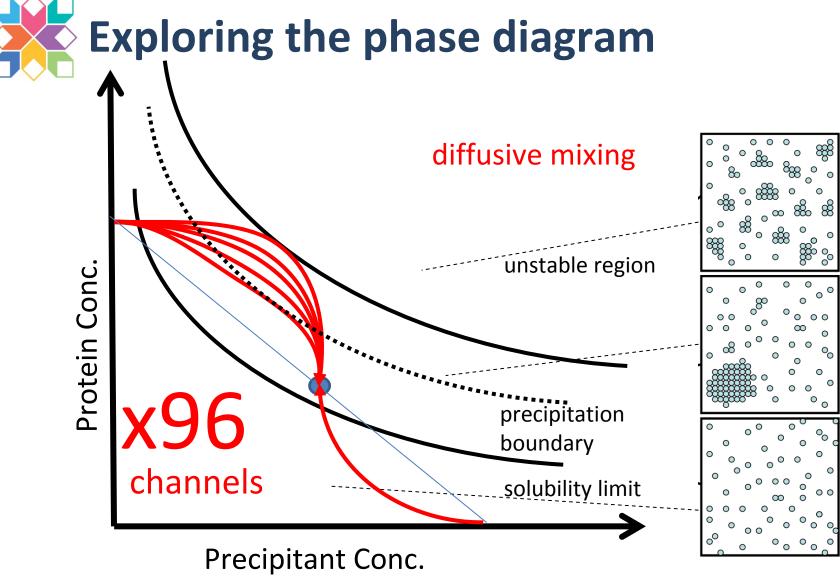
Liquid-Liquid Diffusion

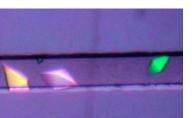
 Concentration profiles of the protein and precipitant are spatiotemporally modulated







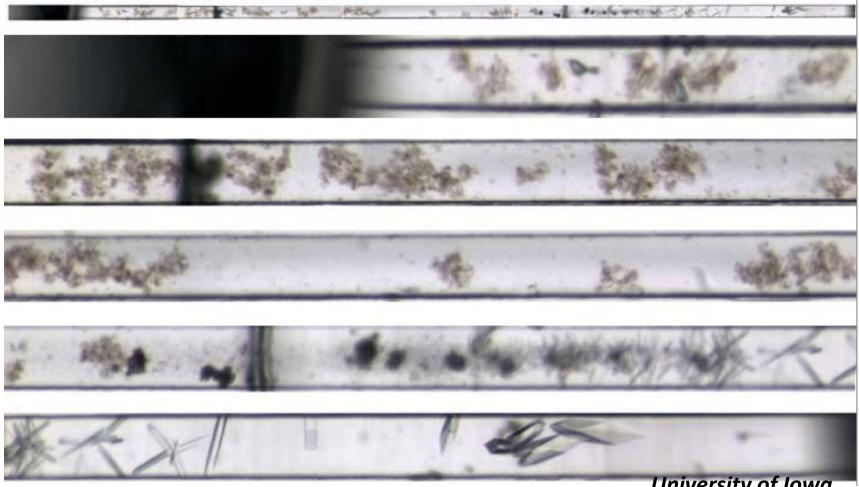






View along the channel (high to low precipitant):







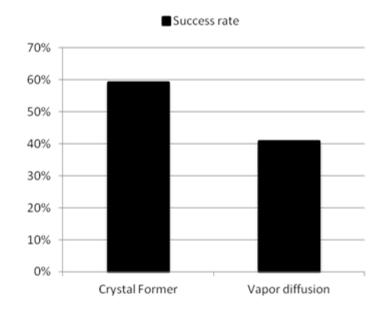
Practical Advantages

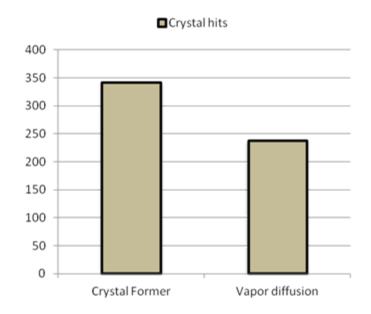
- Significantly increased likelihood of determining crystallization conditions
- <u>Fewer</u> discrete crystallization conditions need be explored
 - Reduces the amount of protein necessary
 - Maximizes the amount of protein behavior information
- Each capillary provides a <u>complete overview</u> of protein behavior across the complete condition gradient
- Can guide follow up experiments
 - Optimize initial hits



Comparative Data Summary

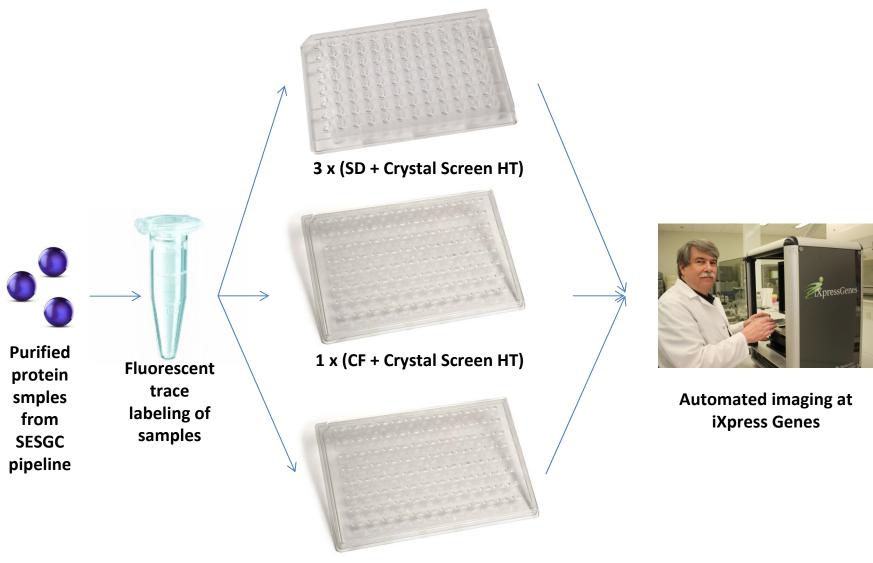
				Not crystallized in
Tested	Crystallized	CF crystallized	VD crystalized	any format
54	36	32	22	18







Assessing crystallization returns



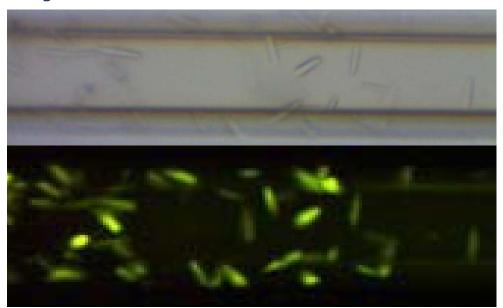
1 x (CF + SuperCOMBI)



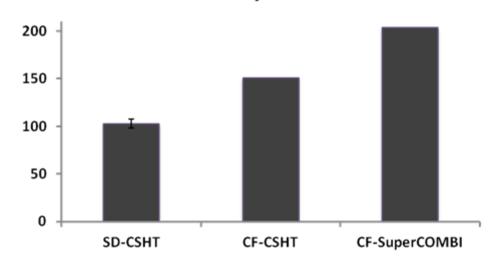
Visual Scoring/Crystallization Outcomes

iXpress Genes

Reported improved
 crystallization rates
 versus vapor diff
 CRYSTAL X2 Imager



No. of crystal hits





Focusing on the laboratory workflow

A.K.A. When your protein doesn't crysallize...

- > Set more vapor diffusion drops with additional crystallization screens for the identical, or highly similar, protein sample
 - Use of the CF = increased likelihood of crystal growth
- Reclone and/or repurify the protein of interest for identical crystallization trials
 - CF offers a minimum of 3-fold cost savings to the most efficient efforts
 - CF saves time

Screening using crystal formers parallel to vapor diffusion method for the same protein sample could increase likelihood of crystal growth significantly, save time and money



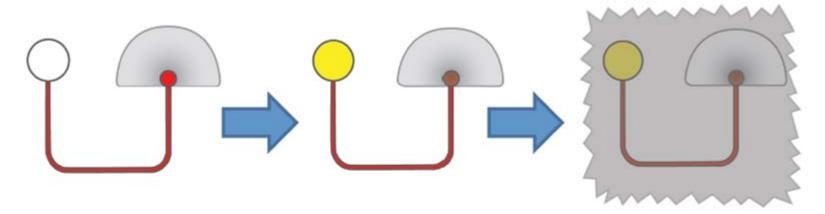
The Crystal Former Compatible Formats

- Mosquito (TTP LabTech)
 - 250-350nL consistent channel filling
- Phoenix/Gryphon (Art Robbins)
 - CrystalMation (Rigaku)
 - 250-350nL consistent channel filling
- Oryx (Douglas Instruments)
 - 250nL consistent channel filling
- Echo ADE (LabCyte)
 - 150-250nL consistent channel filling
- Formulatrix NT8
 - 250-350 nL consistent channel filling
- Hand setup, single or multi-channel pipette



The Crystal Former

Simple crystallization set-up in either manual or automated mode



The equilibration kinetics is a major determinant in the success or failure of a crystallization trial. Microfluidics offers a unique method for exploring the phase diagram and for manipulating the equilibration kinetics. The kinetics in different methods can be strikingly different, even when the same precipitant is used. Therefore, it makes good sense to try different ones, especially when screening, but also in the optimization phase. We use the Crystal Former as part of our overall crystallization strategy. The sample volume requirements are modest and it is easy to use.

~Terese Bergfors, Uppsala University, Sweden



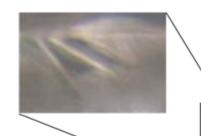
Zhijie Li, Rini Laboratory, University of Toronto



Leu Transporter, P.
Nissen, Aarhus
University



A. Guskov, Nanyang Technological University, Singapore



A.Weger & A. Joachimiak, Argonne National Lab



Thank You!



Lili Liu, University of Saskatchewan



Malarial Drug Target, T. Bergfors,
Uppsala University



Human phosphatase with inhibitor, I. Saez, Institut de Biologie Structurale



Workflow impact

