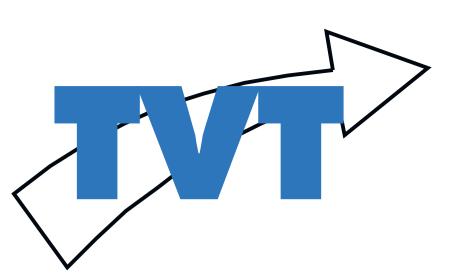


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Preparative Protein Crystallization from Impure Sources: **Incorporation of Impurities into the Crystals**

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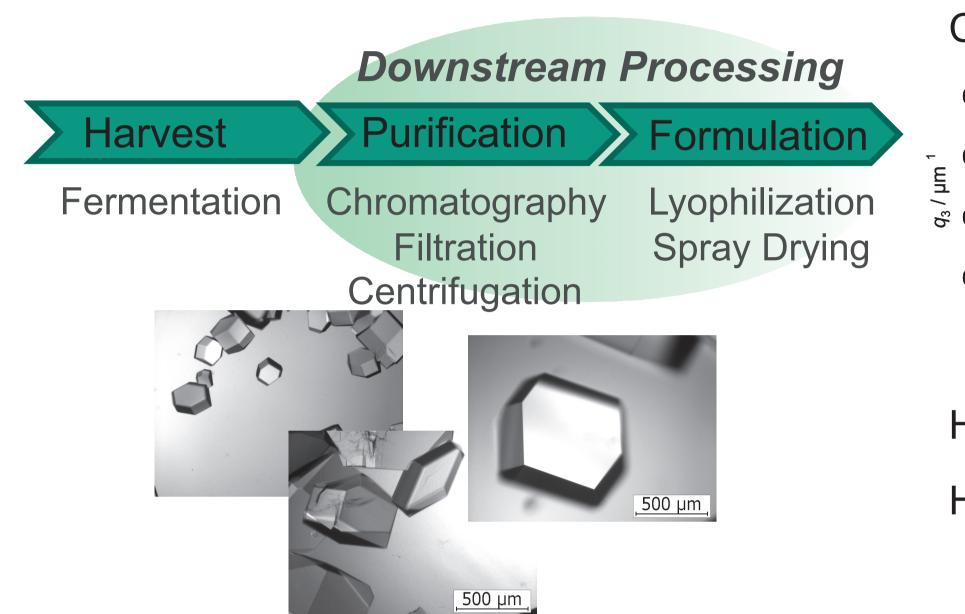
Introduction

Objectives

Research Question

Motivation

Crystallization as an alternative to Conventional Processes



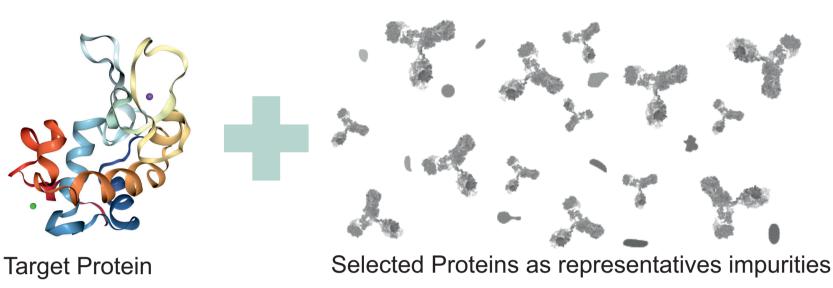
Reproducible and Controlled Protein Crystallization

Controlled crystal size distribution

0.12 0.12 unseeded $M^{v} = 4 \text{ g min}^{-1}$ $\dot{M} = 4 \text{ g min}^{-1}$ M_{seed} = 0.9 g 0.08 $S_{\text{seed}} = 2.1$ Seed B 0.08 0.04 0.00 100 crystal size d / µm

High process yield **Further research is** still required High crystal purity 11

Process Yield and Crystal Purity in a Multicomponent Protein Mixture...

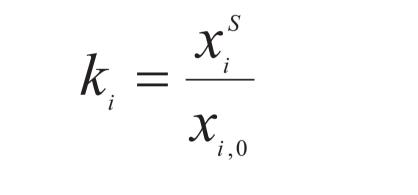


...How extensive is the incorporation of impurities into the protein crystals?

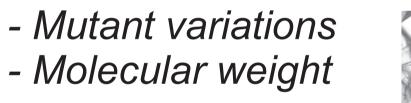
...Can the incorporation of impurities be avoided?

Research Proposal

Systematic Studies of the **Distribution Coefficient**



I. Experimental Studies for Different Model Systems Binary protein mixtures having different similarity degree e.g.





II. Solution Composition and System Conditions Impurity content in the feed, pH and temperature

III. Process Operation

i: impurity, S: solid phase

Vacuum Evaporative Crystallization Evaporation rate, stirring speed

Expected Results

Model Substances <u>System II</u> System I System III **Target Protein Alcohol Dyhidrogenase (LbADH-WT)** Lysozyme (LSZ) Lysozyme (LSZ) **Bovine Serum** β -Lactoglobulin (β -lgB) Alcohol Dyhidrogenase (LbADH-Mutant) Impurity Albumin (BSA) Analytics - Multiwavelength UV absorption spectra - Complementary measuring method Protein via HPLC concentration: 1,5 0.5 200 220 260 280 300 Wellenlänge [nm] 10 Time [min]

Methodology

Experimental Approach

Identification of Process Conditions



