

### 3. Protein crystallization

3. Protein crystallization .....	1
3.1. Overview of protein crystallization experiments .....	3
3.2. Understanding protein crystals .....	7
3.2.1. Properties and assembly of protein crystals.....	9
3.2.2. Crystal stability and intermolecular contacts.....	11
3.2.3. Local nature of crystal contacts .....	12
3.2.4. Crystal packing effects, artifacts, and solvent .....	13
3.2.5. Crystal forms and morphology .....	13
3.3. Protein properties and crystallization.....	14
3.3.1. Protein constructs and affinity tags.....	15
3.3.2. Batch variation and contaminants.....	16
3.3.3. Protein concentration .....	16
3.3.4. Purity, freshness, and conformational state .....	16
3.3.5. Buffers, salts and additives in protein stock .....	17
3.4. Thermodynamics of protein solutions .....	18
3.4.1. Solubility diagrams and supersaturation.....	18
3.4.2. Effect of pH on protein solubility .....	20
3.4.3. Effect of temperature on protein solubility.....	21
3.4.4. Entropic contributions drive crystallization.....	21
3.5. Self-assembly and crystallization kinetics.....	24
3.5.1. Activation and phase separation .....	24
3.5.2. Supersaturated solutions and nucleation.....	24
3.5.3. Crystallization diagrams .....	26
3.5.4. The growth of real crystals .....	28
3.6. Crystallization cocktails.....	31
3.6.1. Salts.....	32
3.6.2. Organic precipitants.....	33
3.6.3. Additives, detergents and cofactors .....	36
3.6.4. Buffers and the effect of pH on protein crystallization.....	38
3.7. Crystallization techniques.....	41
3.7.1. Vapor diffusion techniques .....	42
3.7.1.1. Hanging drop vapor diffusion.....	42
3.7.1.2. Crystallization diagram of a vapor diffusion experiment .....	43
3.7.1.3. Sitting drop vapor diffusion.....	44
3.7.2. Batch crystallization.....	46
3.7.3. Dialysis .....	48
3.7.4. Free-interface diffusion.....	49
3.7.5. Overlap between crystallization techniques.....	54
3.7.6. Control of nucleation by seeding .....	56
3.7.7. Robotics in the crystallization laboratory .....	58
3.8. Protein crystallization strategies .....	60
3.8.1. Against all odds.....	60
3.8.2. Crystallization as a multivariate sampling problem.....	61
3.8.3. Crystallization screen designs.....	62

3.8.4. Random sampling, reagent propensities, and number of experiments .....	63
3.8.5. Two-tiered approaches.....	66
3.8.6. Analyzing the outcome of crystallization trials .....	66
3.8.7. Optimization .....	71
3.9. Soaking and co-crystallization.....	73
3.9.1. Protein-ligand complexes.....	73
3.9.2. Binding constant and site occupation .....	74
3.9.3. Heavy atom soaking.....	77
3.9.4. Harvesting and mounting of crystals .....	80
3.10. Advanced crystallization problems.....	81
3.10.1. Integral membrane proteins .....	81
3.10.1.1. Detergent exchange and crystallization.....	83
3.10.1.2. Lipid cubic phases.....	84
3.10.2. Antibody scaffolding and F <sub>ab</sub> structure.....	85
3.10.3. Protein-DNA complex crystallization.....	88
3.11. Key concepts.....	90
Fundamentals of crystallization .....	90
Physical chemistry of crystallization .....	91
Crystallization techniques.....	92
Crystallization strategies.....	93
Special challenges.....	94
3.12. Thought questions.....	95
3.13. Additional reading .....	95
3.14. References.....	95

In the end, no matter how sophisticated our reasoning and statistics are, one can only increase the *probability* of crystallization success - or increase the degree of belief in it - but *never guarantee* success for any particular protein.

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**C**rystallizing the protein is a crucial step during the course of a protein structure determination, and there is no known method to predict exactly under what conditions a specific protein will form single crystals. The general procedure is to reduce the solubility of the stock protein, in the hope that the protein separates from the solution while self-assembling into diffracting crystals. The reason for the difficulty to control crystallization lies foremost in the complexity of the weak interactions that are necessary between the irregularly shaped and flexible protein molecules in order to self-assemble into a regular, periodic crystal lattice. Viewing a protein crystal as a periodic network of specific interactions emphasizes that each protein's *intrinsic properties*, such as local surface charge distribution, flexibility, and conformational homogeneity, are *key factors pre-determining* the chance for success in protein crystallization.