PromISS Protein Descriptions

Lysozyme: This is the classic model system for protein crystallisation studies. Thus many relevant physiochemical parameters that are relevant to its crystallisation process are known, as well as the nucleation and crystal growth behaviour. Lysozyme is also available in large amounts, in reproducible batches. The protein is extremely soluble, and crystallises rapidly to form large crystals.

Ferritin: Ferritin is a very large hollow sphere of 24 identical subunits. The molecular weight varies between 474.000 daltons (apoferritin), and 780.000 daltons (ferritin), depending on the amount of iron stored within the sphere. The size of ferritin makes it an ideal model system for AFM studies of the crystal growth process. Thus the crystallisation process has been very well characterised. Ferritin crystals grow in the diffusion-controlled regime at high supersaturation. The possibility to use both ferritin and apoferritin, as well as monomeric and dimeric forms of the protein, makes this a useful system for studying impurity incorporation.

Triose phosphate isomerase (TIM): From *Thermotoga maritima* the α/β barrel, or TIM-barrel, is one of the most commonly encountered tertiary folds adopted by proteins displaying little or no sequence homology and performing very different functions. TIM from *Thermotoga maritima* was solved to a resolution of 2.85 Å. TIM is expressed in *E. coli*, and purified by grams. The crystallisation and nucleation are very reproducible, and the protein is stable over time. There is the possibility to make mutations that affect the multimeric form or the flexibility of the active site loop. Thus TIM could be used for studies of diffusional purification and the effect of protein flexibility on crystal quality.

Bovine liver catalase: Bovine liver catalase is a slightly ellipsoidal tetramer of 60 kilodalton subunits. Different crystal forms are known in different crystallisation conditions. Orthorhombic crystals grown in PEG grow up to several millimetres in size, and diffract to 2.2 Ă. The large size of catalase makes this system amenable to AFM measurements.

Arg7p: arg7pcatalyses the fifth step in microbial arginine biosynthesis. It transfers the acetyl group of N-acetylornithine to glutamate thereby forming ornithine while regenerating N-acetylglutamate (NAG). NAG is also produced by the first enzyme of the pathway, N-acetylglutamate synthase (NAGS). Some OATs have been shown to be endowed with NAGS activity and are therefore described as bi-functional. Arg7p was shown to be composed of two distinct subunit peptides α and ß, generated by autoproteolytic cleavage. Arg7p crystal grown by counterdiffusion in gel have been shown to have greatly improved order compared to hanging drop crystals.