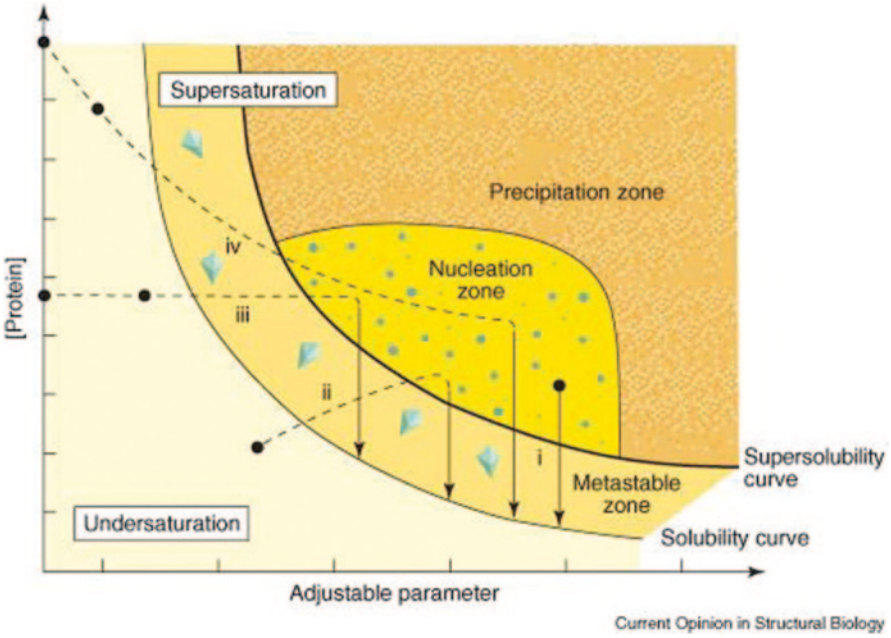

Fig. 2 Schematic illustration of a protein crystallization phase diagram. Adjustable parameters include precipitant or additive concentration, pH and temperature. The four major crystallization methods are represented: (i) microbatch, (ii) vapor diffusion, (iii) dialysis, and (iv) free interface diffusion (*FID*). Each involves a different route to reach the nucleation and metastable zones, assuming the adjustable parameter is precipitant concentration. The *filled black circles* represent the starting conditions. Two alternative starting points are shown for FID and dialysis because the undersaturated protein solution can contain either protein alone or protein mixed with a low concentration of the precipitating agents. The solubility is defined as the concentration of protein in the solute that is in equilibrium with crystals. The supersolubility curve is defined as the line separating conditions under which spontaneous nucleation (or phase separation or precipitation) occurs from those under which the crystallization solution remains clear if left undisturbed (Adapted with permissions from [8])

biological significance [12, 20, 44, 47, 57]. Such consortium-based collaborative efforts utilizing structural genomics have provided fundamental knowledge and understanding for drug discovery, particularly in the area of infectious diseases and other neglected diseases of developing nations [3]. Tuberculosis Structural Genomics Consortium (TBSGC), formed as a part of the PSI is one such consortium dedicated towards solving structures of proteins from the pathogen *Mycobacterium tuberculosis* (*Mtb*) the causative agent of tuberculosis (TB). Novel purification and crystallization means and crystal structures for *Mtb* proteins, as reported by consortium members and nonmembers have provided a meaningful insight into drug discovery and design efforts towards countering TB [2, 10, 11, 15, 16, 32, 38]. Figure 3 describes a typical process flow of structural elucidation for proteins by X-ray crystallography [44]. In the recent past, protein crystallography finds extensive application in drug discovery and design of small molecule inhibitors.