

**S010** Proteomic Complex Detection using Sedimentation (ProCoDeS): a method for identification of proteins in complexes.

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Proteomic Complex Detection using Sedimentation (ProCoDeS) was recently proposed as a medium-throughput methodology to give information on proteins in high molecular weight stable complexes (Hartman et al. 2007). It is based on a combination of complex separation e.g. by rate zonal centrifugation, followed by mass spectrometric protein detection and quantitation. The method can indicate that polypeptides sediment as stable protein complexes. Unlike pull-down, yeast two hybrid or similar strategies, the determination of proteins in complexes in ProCoDeS is not based on the direct detection of proteins attached to a bait or target protein. It does not rely on availability of antibody or of expression of a tagged protein fusion, and is potentially applicable to tissues and organisms where these approaches are not feasible.

Co-sedimentation of proteins in a stable protein complex can be observed in ProCoDes data. Co-sedimenting proteins may either be in complexes of similar size, or in the same complex. Using gold standards of known protein complexes, it is possible to estimate the degree of co-sedimentation that can suggest complex membership. The combination of ProCoDes with other independent sources of information is valuable in order to get more accurate predictions about possible protein-protein interaction.