A number of intrinsically disordered proteins have been shown to associate in a two-state manner, undergoing ‘coupled folding and binding’. IDP systems typically display relatively weak binding affinities (high Kd values for the complex), so under conditions used in biophysical assays the reactions are typically highly reversible. We discuss various approaches that have been used to obtain estimates of the rate constants for association and dissociation, and when they are applicable. We further demonstrate a method for fitting individual association and dissociation kinetic traces in the reversible regime, that is capable of providing estimates of both kinetic and thermodynamic constants, by applying it to a model system.