

**W0372**

**On Understanding Solution Conditions that Maximize Protein Complex Formation.** P.S. Horanyi, B. Dillard, Z.-J. Liu, J.P. Rose, B.C. Wang, Dept. of Biochemistry and Molecular Biology, Univ. of Georgia, Athens, GA 30602.

Structure determination of protein complexes represents an increasing area of interest in structural biology. However, protein complexes are much more difficult to crystallize than single proteins, since the purified protein complex, when set-up in crystallization trials, routinely yields crystals of the individual proteins alone. This is due, in part, to the lack of understanding the solution conditions that promote stable interactions of the proteins in complex over interactions that promote self aggregation of the individual protein components.

Using the Amplified Luminescence Proximity Homogeneous Assay (ALPHA), we have developed a method to assess protein-protein interactions in solution that can be used to identify conditions that promote protein complex formation.

Initial tests using the T7 RNA polymerase - T7 lysozyme complex showed that we can differentiate between solution conditions that promote single complex formation (which may lead to crystallization of the complex) and those conditions that promote non-specific complex formation (that will not lead to crystallization due to the presence of multiple complex types in solution).

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