

## Identifying CRABP-I Interactions in vivo via photo-cross linking

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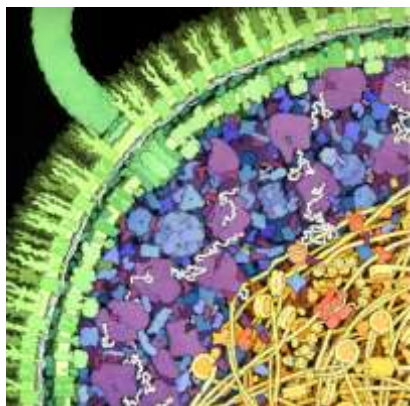


Figure 1. Crowded cellular environment (as envisioned by D. Goodsell).



Figure 2. X-ray structure of CRABP1 (PDB ID 1CBI).

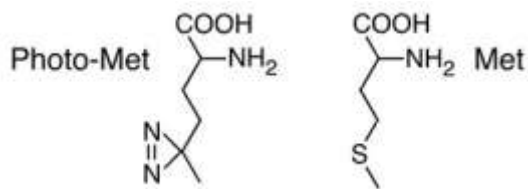


Figure 3. Photo-methionine (left) is structurally similar to methionine (right)

Protein-protein interaction networks in the crowded cellular cytoplasm (Fig. 1) are very complex. For example, interactions with chaperones are essential for proteins while self-association of misfolded species is often linked to diseases such as Alzheimer's.

We use Cellular Retinoic Acid Binding Protein 1 (CRABP1) (Fig. 2) to probe proteostasis networks in *Escherichia coli* which we modeled by FoldEco algorithm. Specifically, this study is aimed at identification of CRABP1 interaction partners in the cell. We use photo cross-linking as experimental approach, where a photo reactive group is incorporated into CRABP1. L-photo methionine (Fig. 3) was chosen due to its structural similarity to endogenous methionine and the presence of two solvent-exposed methionines in CRABP1. Upon activation with UV light the diazirine group of L-photo methionine is able to covalently bind to neighboring species. Once formed, the complexes are isolated and analyzed by Western blotting and mass spectrometry.