

# POPS: predicting and enhancing protein solubility

## Basic workflow of POPS

>Protein Sequence  
KHYRGVRQRPWGKFA  
AEIRDPKNGARVWL  
GTFETAEDAALAYDRA  
AFRMRGSRALLNFPL



Solubility Value

### Presenter:

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### Motivation:

Protein solubility is a prerequisite for many biophysical studies and biochemical applications. However, it remains challenging to produce soluble proteins by using heterologous expression systems. In this regard, computational approaches that are able to correctly predict the solubility level of a protein and further enhance the solubility level by modifying the protein sequences are highly valuable.

### Introduction:

Protein solubility is an important issue in structural biology, pharmaceuticals, and industrial applications. For many experiments, such as protein purification and X-ray crystallography, protein solubility is an indispensable factor in determining the success of a study. However, it is often quite challenging to efficiently express proteins in a soluble form. Experimentally enhancing the solubility of proteins usually has a low success rate and requires much trial and error. Therefore, the development of methods to accurately predict the solubility level and provide suggestions to further enhance the solubility of a target protein is very desirable. POPS is a web server that performs the above-mentioned tasks. In addition to predicting the solubility level of the query protein, POPS provides users with valuable suggestions on how to improve the solubility of a query protein by trimming sequences or by adding peptide tags. POPS incorporates 12 different types of peptide tags to modify the protein at both the C' and N' terminals to determine which tags have the best chance to improve protein solubility.

### Estimation of the expected number of attendees:

20+ for each half hour