

A Prediction Pipeline for Protein Structures

Name of Contact: Ying Xu

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- **Protein Informatics Group has recently developed a computational prediction pipeline for protein structure predictions, which consists of a dozen prediction and analysis tools and a few databases** (<http://compbio.ornl.gov/PROSPECT/PROSPECT-Pipeline/>)
- **Running on a 64-cpu Linux cluster, the Pipeline can make structure predictions for 150-300 proteins a day**
- **Genome-scale structure predictions have been carried out on a number of DOE-relevant microbial genomes, including Synechococcus sp, Prochlorococcus MIT/MED**
- **Our general findings have been over 50% of all predicted ORFs in these genomes have some reliable fold assignments**
- **This research has been supported by DOE/OBER**