

## Sequence- and structure-based approaches for annotating protein sequences

For the typical proteome, there are no functional annotations for a third or more of its proteins. In this talk, I will discuss several sequence- and structure-based approaches we have been developing for annotating protein sequences in order to gain hints about their functions. I will describe computational approaches my group has developed for predicting sites in protein sequences that interact with small molecules and confer specificity; for identifying protein domains by exploiting sequence context; and for predicting interaction specificities for certain structural classes of transcription factors.