# Cataloguing and annotating flavours of intrinsic disorder in proteins with MobiDB.

*Silvio C.E. Tosatto, Dept. of Biomedical Sciences, University of Padova*
**silvio.tosatto@unipd.it**

Intrinsic disorder (ID) in proteins can be defined in different ways, ranging from missing residues in X-ray crystallography to mobile regions in NMR structures and specific experiments which do not require structure determination (e.g. protease susceptibility). While most definitions broadly converge towards similar IDP definitions, the remaining differences can be confounding especially when training predictors used to annotate thousands of proteins. We have developed the MobiDB database (Potenza et al., NAR database issue 2015; URL: http://mobidb.bio.unipd.it/) to provide a broad and agnostic view on different IDP definitions.

MobiDB is based on UniProt protein sequences using a three tier annotation pyramid. The top level is composed of ca. 700 ID proteins annotated manually by the DisProt database. Indirect sources, such as missing X-ray residues and mobile NMR regions, are extracted for all ca. 110,000 PDB structures to complement the manually curated data. At the lowest curation level, ID predictions are provided with 10 methods for ca. 80,000,000 UniProt sequences. Recent work has been directed at extracting additional statistics on the prevalence of different ID flavours in the database.