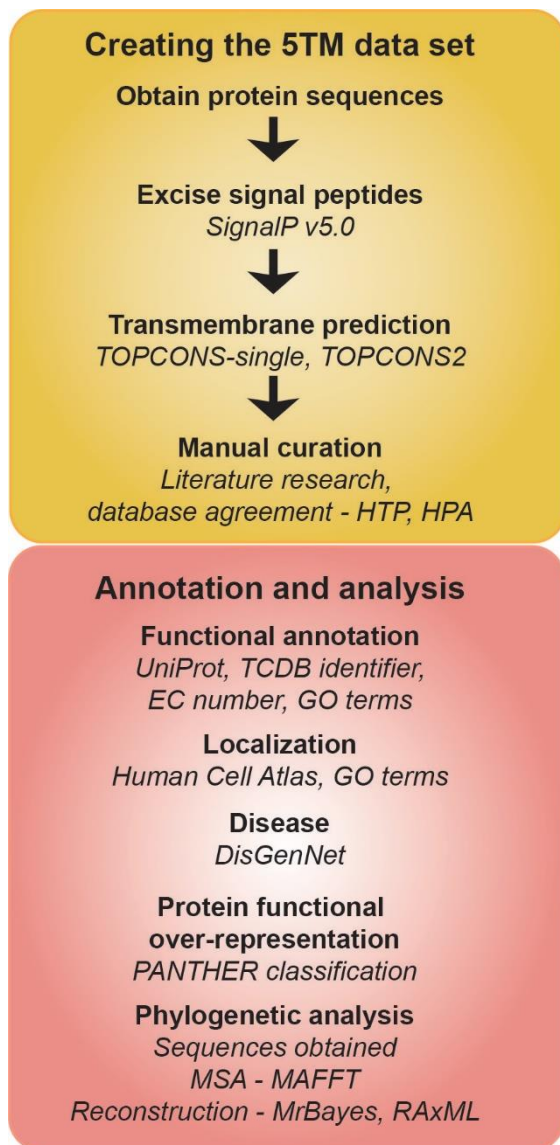Supplementary Figure 1



Supplementary Figure 1. Methods diagram. Creating the 5TM data set included obtaining the protein sequences, preparing the sequences by using SignalP v5.0 to identify the signal peptides and then excise them from the sequences. Transmembrane prediction software applications, including TOPCONS-single and TOPCONS2, were then utilized on the mature sequences. Manual curation followed and included researching literature and comparing results with other databases. The annotation and analysis of the 5TM data set then followed using the identified methods and databases. Abbreviations: HTP, Human Transmembrane Proteome; HPA, Human Protein Atlas; TCDB, Transporter Classification Database; EC, Enzyme Commision; GO, Gene Ontology; PANTHER, Protein Analysis Through Evolutionary Relationships; MSA, Multiple Sequence Alignnment.