

Translocatome: a novel tool for the functional analysis of protein translocation between cellular organelles

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Localization of proteins in subcellular compartments has a key role in cellular regulation and function. In eukaryotic cells, organelles are well distinguished cellular components with different microenvironments and specific molecular interactions. Translocation is considered as a process when functionally active proteins change their subcellular localization in a regulated manner. Although, how individual transcription factors translocate from the cytoplasm to the nucleus resulting in an alteration in cellular behaviour is well known, systematic analysis of this phenomenon is still missing.

During our research, we have gathered detailed information for more than 100 human translocating proteins by manual curation of related articles. We have developed a database that contains relevant localization, structural and regulation related properties of the proteins. We have named this database Translocatome, which is planned to be accessible through a user-friendly web application.

The Translocatome server communicates with our in-house developed ComPPI database, from where interaction data for more than 13000 proteins have been imported. This data is used to create a protein-protein interaction (PPI) network, that enables us to predict the probability of protein translocation with a computational algorithm. Further properties (such as information on biological processes from GO [www.geneontology.org]) are annotated to the proteins for more precise predictions. Utilizing this data the algorithm is able to adjust translocation probability scores to the proteins based on the identified differences between a positive (translocating) and a negative (not translocating) training set. The predictions can be validated by manual curation or using experimental techniques.

Translocatome is a novel tool for the systematic analysis of the protein translocation process that helps to understand the role of this phenomenon in the development of certain diseases. Glioblastoma Multiforme (GBM) is a disease with an exceptionally bad prognosis, where certain protein translocations have a key role in pathogenesis. We attempt to further investigate the translocating proteins by dynamic network simulations on a GBM-specific cell model and to find possible connections between the proteins and the malignancy of the disease. With the help of our results new drug targets could be discovered.

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