

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. 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.

We have gathered detailed information for more than 150 human translocating proteins by manual curation of related publications. We have developed a database that contains relevant localization-, structure- 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 (<http://comppi.linkgroup.hu>), from where interaction data of more than 13,000 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 an artificial intelligence algorithm. Further properties (such as information on biological processes from GO [www.geneontology.org]) are annotated to the proteins, which enables the algorithm to predict translocation with an accuracy rate around 80%. 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. We will investigate translocating proteins by dynamic network simulations on a disease-specific cell model to find possible connections between translocating proteins and the pathogenesis of the disease. Our results may lead to the discovery of new drug target candidates.

Veres, D. V. et al. ComPPI: a cellular compartment-specific database for protein-protein interaction network analysis. *Nucleic Acids Res.* 43, D485–D493 (2015).

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