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UniHI: Unifying Large-Scale Maps of the Human Protein Interactome



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Short Abstract: We present here a web-based database called UniHI (Unified Human Interactome) which aims to integrate available protein interaction maps. It is currently based on 10 interaction maps including over 16000 unique proteins and 150000 distinct interactions in total. UniHI offers researchers a direct entry gate into the human interactome.

Long Abstract:

Protein interactions constitute core processes of the cellular machinery. Comprehensive catalogs of such interactions would facilitate the unveiling of complex biological mechanisms. After initial assemblies of interaction maps for model organisms such as yeast, worm and fly, the mapping of human interactome has moved into the focus. Both computationally and experimentally based maps of protein-protein interactions have recently been constructed. While most of these maps are publicly accessible, a platform for integration of the various maps is still lacking diminishing possible benefits for researchers. We present here a web-based database called UniHI (Unified Human Interactome) which aims to integrate available protein interaction maps. It is currently based on 10 interaction maps including over 16000 unique proteins and 150000 distinct interactions in total. UniHI offers researchers a flexible and direct entry gate into the human interactome.

Protein-protein interactions are central for a vast majority of cellular processes. This pivotal role of protein-protein interactions has evoked the construction of large-scale interaction maps. Whereas the first of such global interaction maps were generated for the model organisms *S. cerevisiae*, *D. melanogaster* and *C. elegans*, the focus recently shifted towards the systematic mapping of human protein-protein interactions [1-8]. To date, most of the approaches to catalog the human interactome are based either on review of literature [1-3], extrapolation from interactions between orthologous proteins [4-6] or application of high-throughput (Y2H)-assays [7-8]. Although the interaction maps constructed are likely to have profound impact on biological research and biomedical applications, their application is currently limited due to their incompleteness and missing integration.

To overcome at least partially these hurdles, we have started to integrate available interaction maps to a combined map termed UniHI (Unified Human Interactome). In its initial version, UniHI is based on the unification of ten large scale interaction maps recently proposed. These maps have been derived from manually curated databases (HPRD [1], BIND [2]), computational approaches based on text-mining (Ramani et al. [3]) or homology assignment (Lehner and Fraser [4], Persico et al (HomoMint) [5], Brown and Jurisica

(OPHID) [6]) and Y2H-assays screens (Stelzl et al. [6], Rual et al.[7]). After unification, the resulting map of the human interactome consists of over 16000 proteins and 150000 interactions.

UniHI will be made publicly accessible via a web-server. It aims to offer researchers a convenient entry gate to the human interactome [9]. UniHI is not restricted to the maps currently included, but has an open structure. Thus, future versions will incorporate further available maps of the human interactome. Already incorporated maps will be regularly updated.

Notably, UniHI is not intended to replace already available interaction maps. All protein interactions included in UniHI are directly linked to the database where they originated from. Thus, UniHI might represent a junction linking hitherto unconnected protein interactions. Such concept provides the user an integrated platform of the human interactome without sacrificing the strengths of the individual databases.

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