

Representing Protein Interactions in the UniProtKB database

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In order to fully understand the role of a protein in a particular cell or tissue, it is important to know the molecules with which it interacts and the functional consequence of those interactions. The UniProtKB database (www.uniprot.org) represents protein interaction data in several ways. The COFACTOR field is used to describe non-protein molecules required for a protein to be catalytically active. The SUBUNIT comment is a free text description of both the quaternary structure of a protein and proteins to which it binds. The fields are created by UniProtKB/Swiss-Prot curators. Additionally, the INTERACTION lines contain a structured representation of high-confidence binary protein interactions. These data are integrated, filtered and exported by the IntAct database (www.ebi.ac.uk/intact) at the EMBL-EBI and represent the work of the IMEx Consortium (www.imexconsortium.org), of which UniProtKB is an actively contributing member. A new graphical viewer enables users to see the interaction partners of a protein and also shows which of those partners interact with each other. The data is displayed in an adjacency graph, which enable a clear visualisation of large numbers of protein interactors in a way that is both easy to understand and readily navigable. The data is also able to be filtered, initially by subcellular location or by interacting partners with a link to disease.