OMPdb: A database of β-barrel outer membrane proteins from Gram-negative bacteria

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The β-barrel outer membrane proteins of gram-negative bacteria are implicated in a variety of functions important for the survival of the bacteria. Such functions are passive nutrient uptake, active transport of larger molecules, protein secretion as well as the adhesion to host cells through which the bacteria express their virulence activity. These proteins differ from typical membrane proteins (such as those found in the inner membrane), in their membrane spanning regions, which are formed by amphipathic β-strands instead of α-helices. Their biological importance as well as the inadequate annotation found in the public databases, urges the need for intensive studies and careful data collection regarding these proteins. For constructing the database, multiple resources freely accessible over the Internet were combined and a detailed literature search was performed. The database in total contains entries for more than 27000 β-barrel outer membrane proteins, originating from 680 different Gram-negative bacteria, classified in 78 families based mainly on structural and functional characteristics. Information included in the database, consists of sequence data and annotations for the structural features (such as the transmembrane segments) of proteins, references to literature and links to other publicly available databases. Such features are not offered in any other database currently available worldwide. Furthermore, along with the database, a collection of profile Hidden Markov Models (pHMMs) was also compiled, that were shown to be characteristic of β-barrel outer membrane proteins. Some of these profiles originate from the PFAM database, although we additionally created manually more than 30 profiles that were not previously available elsewhere, describing new and previously uncharacterized families. This collection of profiles, when combined properly with our previously developed prediction methods (PRED-TMBB, MCMBB and ConBBPRED), constitutes an accurate and useful search tool for the detection of new β-barrel outer membrane proteins in fully sequenced genomes.