The transmembrane β-barrel (TMBB) is one of the two major structural motifs found in membrane-spanning proteins. TMBBs are found exclusively in the outer membranes of Gram-negative bacteria, mitochondria, and chloroplasts. Because TMBBs perform a vast array of functions (e.g. signal transduction and cellular adhesion) and are surface-exposed, they present an exploitable vulnerability in drug-resistant pathogenic Gram-negative bacteria. Technical deficiencies have impeded progress in the structural study of TMBBs, which is unfortunate given the magnitude of their biological significance. Although structural proteomics projects are currently underway to help solve the structures of unknown membrane proteins, the computational prediction of TMBBs has improved rapidly to compensate for the limits of empirical methods. To this end, our lab has developed one of the most accurate TMBB prediction programs available, which was used to build a database of TMBB predictions called TMBB-DB. This is a comprehensive database featuring TMBB prediction data from the proteomes of over 500 species of bacteria with nearly 1.9 million total sequences. Combining the TMBB prediction data with signal peptide prediction data generated using SignalP we predicted that more than 3% of the sequences encoded TMBBs, which on average is more than double the number of known or predicted TMBBs already annotated in the proteomes. Users will have access to an in-depth analysis of each sequence and be allowed to analyze sequences not included in the database using the same prediction tools. This database can be useful in directing the efforts of structural proteomics projects, antimicrobial drug therapy design, or vaccine development.

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