

# Resource Summary Report

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## ConBBPRED

RRID:SCR\_006194

Type: Tool

### Proper Citation

ConBBPRED (RRID:SCR\_006194)

### Resource Information

**URL:** <http://bioinformatics.biol.uoa.gr/ConBBPRED/>

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**Description:** A web tool for the Consensus Prediction of TransMembrane Beta-Barrel Proteins. Prediction of the transmembrane strands and topology of beta-barrel outer membrane proteins is of interest in current bioinformatics research. Several methods have been applied so far for this task, utilizing different algorithmic techniques and a number of freely available predictors exist. The methods can be grossly divided to those based on Hidden Markov Models (HMMs), on Neural Networks (NNs) and on Support Vector Machines (SVMs). In this work, we compare the different available methods for topology prediction of beta-barrel outer membrane proteins. We evaluate their performance on a non-redundant dataset of 20 beta-barrel outer membrane proteins of gram-negative bacteria, with structures known at atomic resolution. Also, we describe, for the first time, an effective way to combine the individual predictors, at will, to a single consensus prediction method. We assess the statistical significance of the performance of each prediction scheme and conclude that Hidden Markov Model based methods, HMM-B2TMR, ProfTMB and PRED-TMBB, are currently the best predictors, according to either the per-residue accuracy, the segments overlap measure (SOV) or the total number of proteins with correctly predicted topologies in the test set. Furthermore, we show that the available predictors perform better when only transmembrane beta-barrel domains are used for prediction, rather than the precursor full-length sequences, even though the HMM-based predictors are not influenced significantly. The consensus prediction method performs significantly better than each individual available predictor, since it increases the accuracy up to 4% regarding SOV and up to 15% in correctly predicted topologies.

**Abbreviations:** ConBBPRED

**Resource Type:** analysis service resource, data analysis service, production service resource, service resource

**Defining Citation:** [PMID:15647112](#)

**Keywords:** predict, topology, beta-barrel outer membrane protein, outer membrane protein, protein, consensus prediction, gram-negative bacteria, transmembrane, beta-barrel protein

**Funding:** Greek Ministry of National Education and Religious Affairs

**Availability:** Free, Non-commercial

**Resource Name:** ConBBPRED

**Resource ID:** SCR\_006194

**Alternate IDs:** nlx\_151740

**Record Creation Time:** 20220129T080234+0000

**Record Last Update:** 20260919T195656+0000

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## Ratings and Alerts

No rating or validation information has been found for ConBBPRED.

No alerts have been found for ConBBPRED.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 3 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [nidm-terms](#) .

Hui X, et al. (2021) Computational prediction of secreted proteins in gram-negative bacteria. Computational and structural biotechnology journal, 19, 1806.

Venko K, et al. (2021) Prediction of Transmembrane Regions, Cholesterol, and Ganglioside Binding Sites in Amyloid-Forming Proteins Indicate Potential for Amyloid Pore Formation. Frontiers in molecular neuroscience, 14, 619496.

Bagos PG, et al. (2005) Evaluation of methods for predicting the topology of beta-barrel outer membrane proteins and a consensus prediction method. BMC bioinformatics, 6, 7.