Accurate prediction from first principles of helical membrane protein structures requires accurate prediction of the transmembrane (TM) regions within the protein. PredicTM is a simple, flexible, and effective method for predicting the TM regions in a protein and replaces similar methods previously used in the MSC.

The PredicTM method begins with a BLAST search using the ExPASy proteomics server. This search is set up to yield all matching sequences that satisfy the E-Value threshold. This differs from the previous method where only a few dozen to a few hundred sequences were used. Additionally, the PredicTM method is relatively tolerant of unrelated sequences, so hand-filtering of sequences by the user is unnecessary.

A multiple sequence alignment of the BLAST results is performed using MAFFT. MAFFT is better at aligning the diverse results from BLAST than the previously used multiple sequence alignment program, ClustalW, without increasing the amount of time of the computation.

Finally, the hydrophobic profile is generated through a series of averaging methods in a way that ignores gaps, one of the significant failings of the previous method.

Results show PredicTM to be an accurate method in predicting the transmembrane regions of both Beta2 Adrenergic and Bovine Rhodopsin. Furthermore, PredicTM can be applied to any helical membrane protein; it is not restricted to GPCRs, as indicated by its performance in the TMH Benchmark.

![D1 - Average of Windows 7-21 - Final Profile](image)