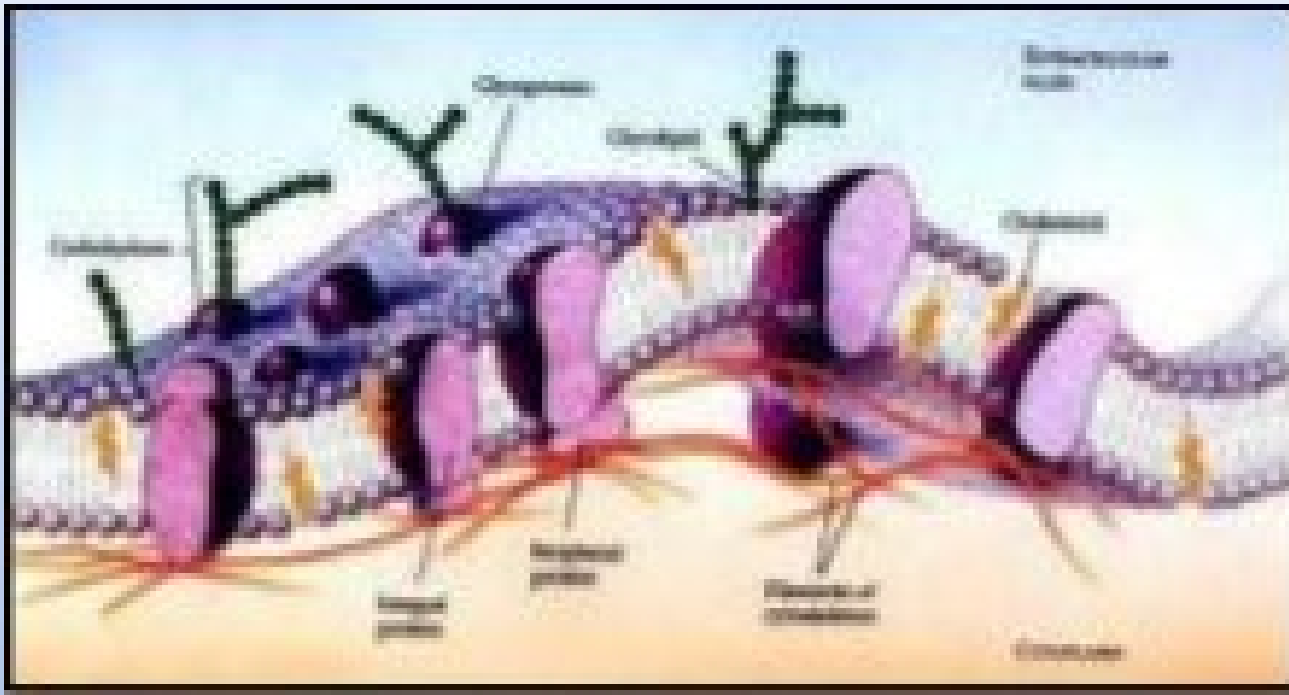


Transmembrane Protein

Transmembrane Protein

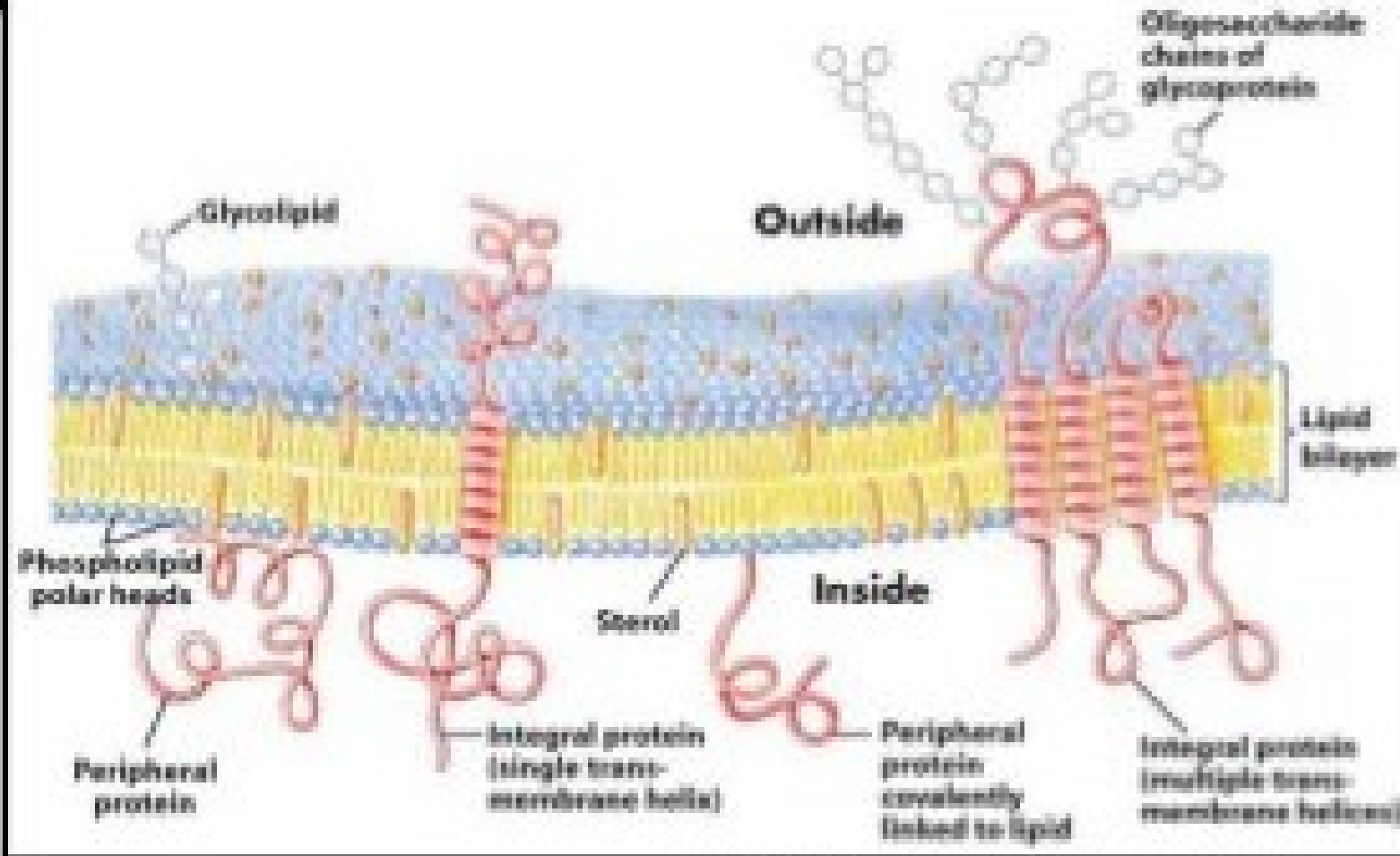
- Every protein assumes a specific shape and performs a specific function.
- Of these proteins that are found embedded in cellular membranes, called as membrane proteins, are of particular importance because they form targets for over 60% of drugs on the market.
- Membrane proteins are crucial for many biological functions and have become attractive targets for pharmacological agents.
- It is seen that 20% - 30% of all the proteins in any organism are membrane proteins.

Membrane Proteins



- A membrane protein is a protein molecule that is attached to, or associated with the membrane of a cell or an organelle.
- More than half of all proteins interact with membranes.

Membrane Structure



Membrane Proteins

Biological membranes consists of a phospholipid bilayer and a variety of proteins that accomplish vital biological functions.

Structural proteins are attached to microfilaments in the cytoskeleton which ensures stability of the cell.

Cell adhesion molecules allow cells to identify each other and interact.

Membrane enzymes produce a variety of substances essential for cell function.

Membrane receptor proteins serve as connection between the cell's internal and external environments.

Transport proteins play an important role in the maintenance of concentration of ions.

Transmembrane Protein Prediction

Transmembrane protein plays important role in the life activity of the cells.

Transmembrane α -helix bundle is a common structural feature of membrane proteins

Bent helices are required for appropriate helix-helix and protein-protein interaction in membrane protein complexes.

Determination of kink in a helix is a computationally intensive task.

Thus the functions of transmembrane proteins are attributed by kinks (bends) in helices.

Therefore, knowledge of kink and its prediction from amino acid sequences is of great help in understanding the function of proteins.

Hence it is a computationally intensive task which is useful in drug design and development

The best current prediction methods appear to correctly predict all membrane helices for about 50%–70% of all proteins, and to falsely predict membrane helices for about 10% of all globular proteins.

TMHMM Server v. 2.0

Prediction of transmembrane helices in proteins

→ ↻ ⚠ Not secure | cbs.dtu.dk/services/TMHMM/

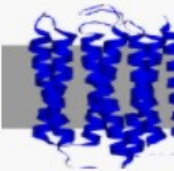


DTU Bioinformatics
Department of Bio and Health Informatics

Services are gradually being migrated to <https://services.healthtech.dtu.dk/>.
Please try out the new site.

TMHMM Server v. 2.0

Prediction of transmembrane helices in proteins



[Instructions](#)

SUBMISSION

Submission of a local file in [FASTA](#) format (HTML 3.0 or higher)

No file chosen

or by pasting sequence(s) in [FASTA](#) format:

Output format:

Extensive, with graphics

Extensive, no graphics

One line per protein

Other options:

Use old model (version 1)

Restrictions:

At most 10,000 sequences and 4,000,000 amino acids per submission; each sequence not more than 8,000 amino acids.

Confidentiality:

Sequences are kept confidential and will be deleted after processing.

TMpred

Prediction of Transmembrane Regions and Orientation

embnet.vital-it.ch/software/TMPRED_form.html

ExPASy
Bioinformatics Resource Portal

TMpred

Prediction of Transmembrane Regions and Orientation

The TMpred program makes a prediction of membrane-spanning regions and their orientation. The algorithm is based on the statistical analysis of TMbase, a database of naturally occurring transmembrane proteins. The prediction is made using a combination of several weight-matrices for scoring.

- **K. Hofmann & W. Stoffel (1993)**
TMbase - A database of membrane spanning proteins segments
Biol. Chem. Hoppe-Seyler 374,166

For further information see the [TMbase](#) documentation.

- Usage: Paste your sequence in one of the supported **formats** into the sequence field below and press the "Run TMpred" button.
Make sure that the format button (next to the sequence field) shows the correct format
Choose the minimal and maximal length of the hydrophobic part of the transmembrane helix

Output format	<input type="text" value="html"/>	minimum	<input type="text" value="17"/>	maximum	<input type="text" value="33"/>
Query title (optional)	<input type="text"/>				
Input sequence format	<input type="text" value="Plain Text"/>				
Query sequence: or ID or AC or GI (see above for valid formats)	<input type="text"/>				
<input type="button" value="Run TMpred"/> <input type="button" value="Clear Input"/>					

Thank you!