<https://www.ncbi.nlm.nih.gov/books/NBK26878/>

* Transmembrane proteins are typically - 𝝰 helices, 𝞫 barrels, amino acid residues with non-polar side chains, single-pass vs multi-pass transmembrane proteins
* Segments containing 20-30 hydrophobic amino acids is long enough to contain a transmembrane 𝝰 helix -- can be determined via a hydropathy plot
* Beta barrel can’t be can’t be predicted via hydropathy plots since 10 or less amino acids are needed to transverse a lipid bilayer and every other chain is hydrophobic - guess can be made but very loosely.
* ccv

<https://www.chem.wisc.edu/deptfiles/genchem/netorial/modules/biomolecules/modules/protein1/prot13.htm>

* This shows which amino acids are hydrophobic and which are polar

**TRAPEZOID RULE? Positive-negative, hydrophobicity -- do research on!**

<https://www.cgl.ucsf.edu/chimera/docs/UsersGuide/midas/hydrophob.html>

* This one shows the hydrophobicity

SAMMY: Check these notes on ToPredII software

<http://nemates.org/uky/520/Lab/lab7/TopPredII.pdf>

This gives step-by-step instructions and references for implementing a more robust program.

SAMMY: The UCSF Chimera Server

<https://www.cgl.ucsf.edu/chimera/>

SAMMY:

Charged residues next to transmembrane regions revisited: “Positive-inside rule” is complemented by the “negative inside depletion/outside enrichment rule” [James Alexander Baker](https://bmcbiol.biomedcentral.com/articles/10.1186/s12915-017-0404-4#auth-1), [Wing-Cheong Wong](https://bmcbiol.biomedcentral.com/articles/10.1186/s12915-017-0404-4#auth-2), [Birgit Eisenhaber](https://bmcbiol.biomedcentral.com/articles/10.1186/s12915-017-0404-4#auth-3), [Jim Warwicker](https://bmcbiol.biomedcentral.com/articles/10.1186/s12915-017-0404-4#auth-4) & [Frank Eisenhaber](https://bmcbiol.biomedcentral.com/articles/10.1186/s12915-017-0404-4#auth-5)

*BMC Biology***volume 15**, Article number: 66 (2017) . Couldn’t find free copy.

SAMMY:

EASILY PROGRAMMABLE - but probably less effective - Maybe this should be our first program also \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

A Simple Method for Displaying the Hydropathic Character of a Protein JACK KYTE AND RUSSELL F. DOOLITTLE, J. Mol. Biol. (1982) 157, 105-132

Free copy at: <https://www.biosyn.com/Images/ArticleImages/pdf/A%20simple.pdf>

A computer program that progressively evaluates the hydrophilicity and hydrophobicity of a protein along its amino acid sequence has been devised. For this purpose, a hydropathy scale has been composed wherein the hydrophilic and hydrophobic properties of each of the 20 amino acid side-chains is taken into consideration. The scale is based on an amalgam of experimental observations derived from the literature. The program uses a moving-segment approach that continuously determines the average hydropathy within a segment of predetermined length as it advances through the sequence. The consecutive scores are plotted from the amino to the carboxy terminus. At the same time, a midpoint line is printed that corresponds to the grand average of the hydropathy of the amino acid compositions found in most of the sequenced proteins. In the case of soluble, globular proteins there is a remarkable correspondence between the interior portions of their sequence and the regions appearing on the hydrophobic side of the midpoint line, as well as the exterior portions and the regions on the hydrophilic side. The correlation was demonstrated by comparisons between the plotted values and known structures determined by crystallography. In the case of membrane-bound proteins, the portions of their sequences that are located within the lipid bilayer are also clearly delineated by large uninterrupted areas on the hydrophobic side of the midpoint line. As such, the membrane-spanning segments of these proteins can be identified by this procedure. Although the method is not unique and embodies principles that have long been appreciated, its simplicity and its graphic nature make it a very useful tool for the evaluation of protein structures.

Another Older literature

<https://www.annualreviews.org/doi/pdf/10.1146/annurev.bb.15.060186.001541>

IDENTIFYING NONPOLAR TRANSBILA YER HELICES IN AMINO ACID SEQUENCES OF MEMBRANE PROTEINS

D. M. Engelman, T. A. Steitz, and A. Goldman Department of Molecular Biophysics and Biochemistry, Yale University, New Haven, Connecticut 06511

Ann. Rev. Biophys. Biophys. Chem. 1986. 15 : 321-53 Copyright © 1986 by Annual Reviews Inc. All rights reserved

Has numbers we can code up.

[Volume 426, Issue 2](https://www.sciencedirect.com/science/journal/00222836/426/2), 23 January 2014, Pages 484-498

# A Simple Atomic-Level Hydrophobicity Scale Reveals Protein Interfacial Structure

Author links open overlay panel[Lauren H.Kapcha](https://www.sciencedirect.com/science/article/pii/S0022283613006232" \l "!)[Peter J.Rossky](https://www.sciencedirect.com/science/article/pii/S0022283613006232" \l "!)

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<https://doi.org/10.1016/j.jmb.2013.09.039>

Hydrophobicity Values

<https://www.cgl.ucsf.edu/chimera/docs/UsersGuide/midas/hydrophob.html>

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4057987/>

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4057987/>

[Biochim Biophys Acta](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4057987/). Author manuscript; available in PMC 2015 Aug 1.

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Published online 2013 Dec 14. doi: [10.1016/j.bbamcr.2013.12.007](https://dx.doi.org/10.1016%2Fj.bbamcr.2013.12.007)

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# Lipids and topological rules governing membrane protein assembly[☆](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4057987/#FN3)

[Mikhail Bogdanov](https://www.ncbi.nlm.nih.gov/pubmed/?term=Bogdanov%20M%5BAuthor%5D&cauthor=true&cauthor_uid=24341994),\* [William Dowhan](https://www.ncbi.nlm.nih.gov/pubmed/?term=Dowhan%20W%5BAuthor%5D&cauthor=true&cauthor_uid=24341994),\*\* and [Heidi Vitrac](https://www.ncbi.nlm.nih.gov/pubmed/?term=Vitrac%20H%5BAuthor%5D&cauthor=true&cauthor_uid=24341994)

* Has nice picture of steps in insertion of membrane proteins