

The present version is able to predict topologies from eukaryotic and prokaryotic proteins. It calculates:

1) The hydrophobicity profile according with the trapezoid algorithm.

2) The transmembrane segments: TopPred finds all the peaks above an upper cutoff that qualify as certain transmembrane segments, as well as those peaks above a lower cutoff that qualify as putative ones. In the current version, three different algorithms can be used to search the transmembrane domains, as well as its classification into integral, peripheral or non-membrane protein.

3) The possible topologies: TopPred generates the topologies including all certain ones, and either including or excluding the putative transmembrane segments, calculating different distribution parameters for each topology.

A more detailed description of calculations and parameters can be found in:

- Claros & von Heijne (1994) *Comput. Applic. Biosci.* 10:685-686 [about the software]
- von Heijne (1992) *J. Mol. Biol.* 255:487-494 [about (1) and (2)]
- Sipos & von Heijne (1993) *Eur. J. Biochem.* 213:1333-1340 [about (3)]