GES .- Engelman,D.M., Steitz,T.A., Goldman,A. (1986) Ann. Rev. Biophys. Biophys. Chem. 15, 321-530.
The most recommended for studies about hydrophobic proteins. All predictions and limits in this software have been calculated with this scale.

GvH1.- von Heijne,G. (1992) J. Mol. Biol. 225, 487-94
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PA.- Persson, B., Argos, P. (1994) J. Mol. Biol. 237, 182-192
This scale, which is double, takes into account the propensity for a residue to be localised in the core or in the boundaries of a transmembrane domain. Prediction of the transmembrane segments is done following a method which differs slightly from the trapezoid method.

AMPHI.- Jähnig, F. (1990) Trends Biochem. Sci. 15, 93-95
This is an algorithm that uses the KD scale to search amphiphilic α-helices and ß-sheets.