Helms, V. 2002. Attraction within the membrane. Forces behind transmembrane protein folding and supramolecular complex assembly. EMBO Reports 3, 1133-1138. [REVIEW]

Stevens, T. J. and I. T. Arkin. 2001. Substitution rates in a-helical transmembrane proteins. Protein Science 10, 2507-2517.

Hedman, M., H. de Loof, G. von Heijne and A. Elofsson. 2002. Improved detection of homologous membrane proteins by inclusion of information from topology predictions. Protein Science 11, 652-658.

Faulon, J.-L., K. Sale and M. Young. 2003. Exploring the conformational space of membrane protein folds matching distance constraints. Protein Science 12, 1750-1761.

DeGrado, W. F., H. Gratkowski and J. D. Lear. 2003. How do helix-helix interactions help determine the folds of membrane proteins? Perspectives from the study of homo-oligomeric helical bundles. Protein Science 12, 647-665.

Howard, K. P., J. D. Lear and W. F. DeGrado. 2002. Sequence determinants of the energetics of folding of a transmembrane four-helix-bundle protein. Proc. Nat. Acad. Sci. USA 99, 8568-8572.

MacKenzie, K. R., J. H. Prestegard and D. M. Engelman. 1997. A transmembrane helix dimer: structure and implications. Science 276, 131-133.

Fleming, K. G. and D. M. Engelman. 2001. Specificity in transmembrane helix-helix interactions can define a hierarchy of stability for sequence variants. Proc. Nat. Acad. Sci. USA 98, 14340-14344.

Donnelly, D., J. P. Overington, S. V. Ruffle, J. H. A. Nugent and T. L. Blundell. 1993. Modeling a-helical transmembrane domains: the calculation and use of substitution tables for lipid facing residues. Protein Science 2, 55-70.

Haspel, N., C. J. Tsai, H. Wolfson and R. Nussinov. 2003. Reducing the computational complexity of protein folding via fragment folding and assembly. Protein Science 12, 1177-1187.

de Brevern, A. G., H. Valadié, S. Hazout and C. Etchebest. 2002. Extension of a local backbone description using a structural alphabet: a new approach to the sequence-structure relationship. Protein Science 11, 2871-2886.

de Brevern, A. G. and S. Hazout. 2003. 'Hybrid Protein Model' for optimally defining 3D protein structure fragments. Bioinformatics 19, 345-353.

Canutescu, A. A. and R. L. Dunbrack. 2003. Cyclic coordinate descent: a robotics algorithm for protein loop closure. Protein Science 12, 963-972.