Appendix C: MembStruk Methods

The MembStruk method is designed to use only the basic information gained from the electron density map of frog rhodopsin (1). From this information about the placement of the seven transmembrane (TM) regions, Membstruk can develop a 3D structure of a G-Protein Coupled Receptor (GPCR). The current methodology for MembStruk is show in Figure 1.

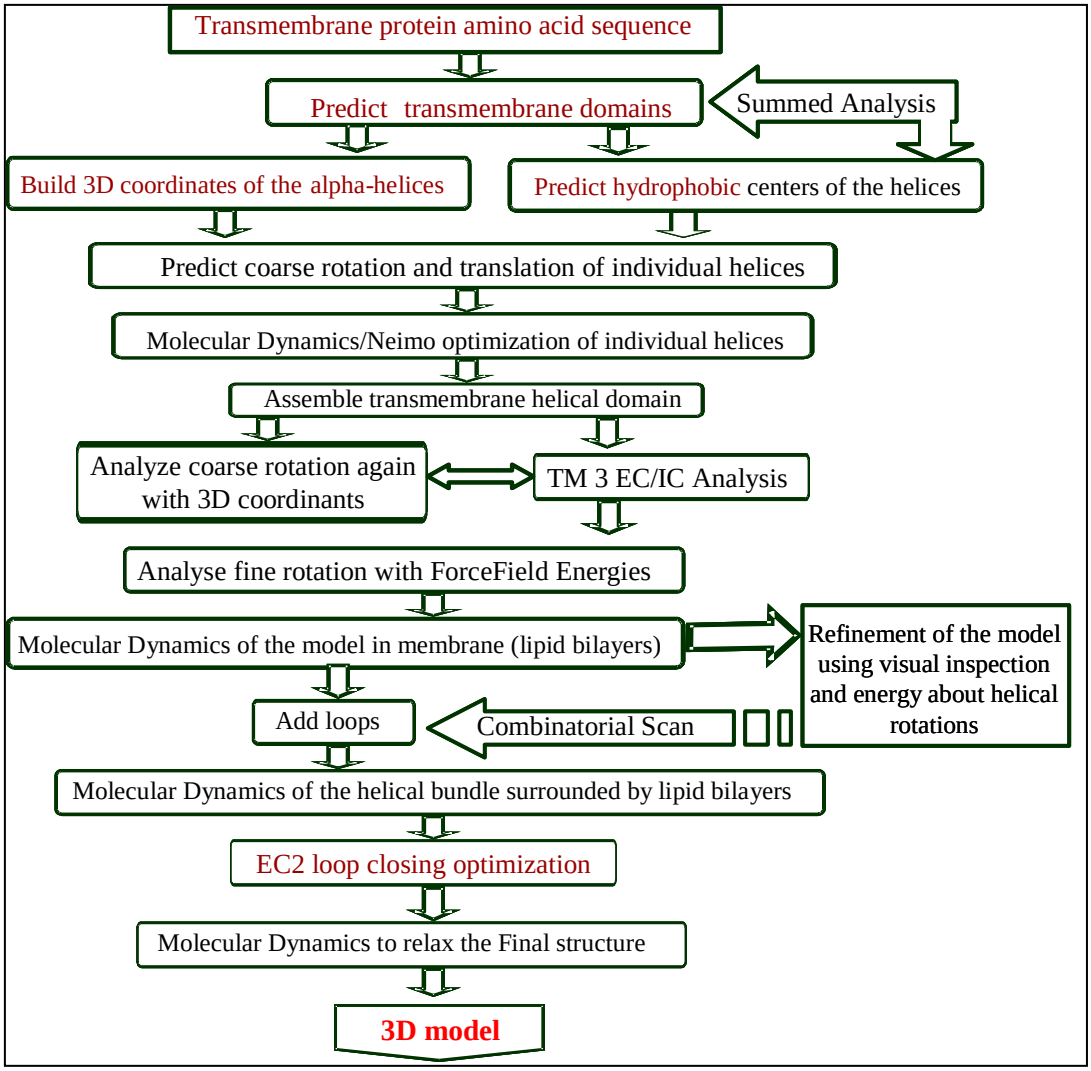

Figure 1 - Flow chart for MembStruk Methodology

The sections in red were developed and coded initially by Rene Trabanino, while the black sections were developed and coded by Spencer Hall. Each section was written as a stand-alone program that would interact with the others to reach the end goal of producing a final 3D model.

The following is a breakdown of the persons who wrote programs for MembStruk and were the main developers of those programs. TM2NDS (2) as of 2005 became a part of MembStruk and is the first set of programs to run in the methods.

MembStruk – 105 individual programs consisting of 50711 lines of code

Wely Floriano -	Utilities in handling of pdb and bgf files: 1 C++ program of 84 lines of code, 1 perl script of 142 lines
Peter Freddolino -	Building of the initial template and Building of loops in Modeler: 17 programs of 1501 coded lines written as perl and C-shell scripts, and 1 C++ program
Spencer Hall -	All other programs related to MembStruk: 35 C-Shell scripts of 7514 coded lines, 12 Fortran 77 programs of 14696 lines of code, 2 C++ programs of 10608 lines of code, 1 perl script of 113 lines
Jiyoung Heo -	Interhelical H-bonds: 1 perl script of 66 lines
Barry D. Olafson -	Conversion of Biograf to the linux platform
Rene Trabanino –	TM2NDS programs and the EC2_SIM_LOOPS: 31 programs of 15,781 coded lines in c++
David Zhang -	For tools and utilities in handling bgf files: 1 C++ program of 207 lines of code, 2 perl scripts of 206 lines

Membstruk also uses the following outside programs:
Biograf (3)
Blast (4-5)
Clustal (6)
HBPLUS (7)
Modeller (8-10)
MpSim (11)
Scwrl (12)

References for Appendix MembStruk Methods

1) Schertler, G. F. X. (1998). Structure of rhodopsin. *Eye* 12, 504-510.

2) Trabanino R. J., Hall, S. E., Vaidehi N., Floriano W. B., and Goddard III W. A. (2004). First Principles Predictions of the Structure and Function of G-Protein Coupled Receptors: Validation for Bovine Rhodopsin. *BioPhys. J.* 2004 86, 1904-1921

3) Molecular Simulations Inc., BIOGRAF Manual, (1994).

4) Altschul, S. F., Gish, W., Miller, W., Myers, W. E., and Lipman, D. J. (1990). Basic local alignment search tool. *J. Mol. Biol.* 215, 403–410.

5) Altschul, S. F., Madden, T. L., Schaffer, A. A., Zhang, J., Zhang, Z., Miller, W., and Lipman, D. J. (1997). Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Res.* 25, 3389–3402.

6) Thompson, J. D., Higgins, D. G., and Gibson, T. J.(1994). Clustal-W—improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. *Nucleic Acids Res.* 22, 4673–4680.

7) McDonald, I. K., and Thorton, J. M., (1994). Satisfying Hydrogen Bonding Potential in Proteins. *JMB* 238, 777-793.

8) Sali, A., and Blundell, T. L. (1993). Comparative protein modelling by satisfaction of spacial restraints. *J. Mol. Biol.* 234, 779-815.

9) Fiser, A., Do., R. K., and Sali, A., (2000). Modeling of loops in protein structures. *Protein Science* 9, 1753-1773.

10) Marti-Renom, M. A., Stuart, A., Fiser, A., Sanchez, R., Melo, F., and Sali, A. (2000). Comparative protein structure modeling of genes and genomes. *Annu. Rev. Biomol. Struct.* 29, 291-325

11) Lim, K-T, Brunett, S., Iotov, M., McClurg, R.B., Vaidehi, N., Dasgupta, S., Taylor, S., and Goddard III, W. A. (1997). Molecular dynamics for very large systems on massively parallel computers: The MPSim program. *J Comput. Chem.* 18(4), 501-521.

12) Bower, M., Cohen, F. E., and Dunbrack Jr., R. L. (1997). Prediction of protein side-chain rotamers from a backbone-dependent rotamer library: a new homology modeling tool. *J. Mol. Biol.* 267, 1268-1282