

Figure S1. Five models were predicted using the I-TASSER tool.

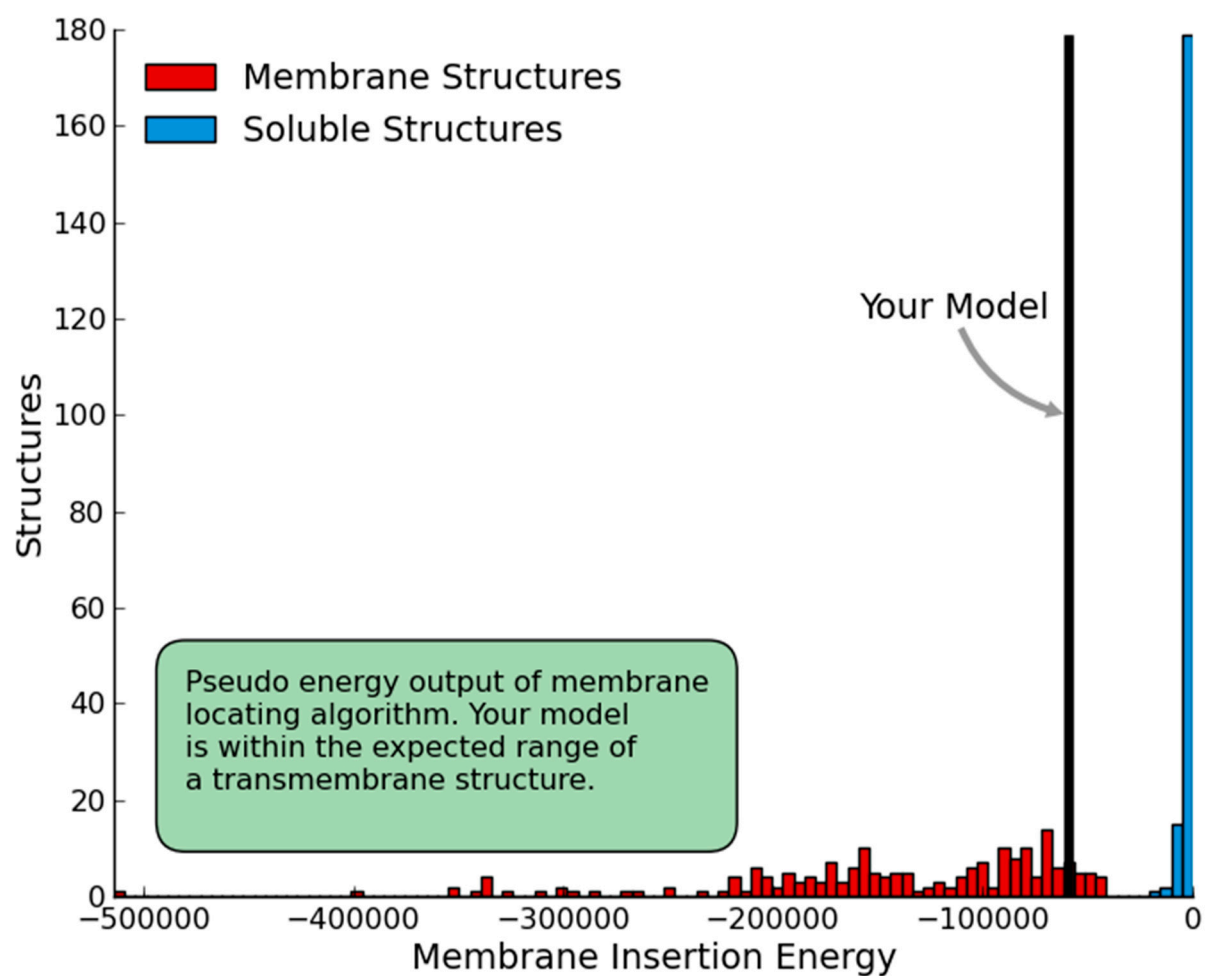


Figure S2. Energy minimization using OPLS-AA was performed on the initial structure obtained from I-TASSER to correct any bond-clashes and refine the stereochemistry of the predicted best protein model.