



SDC 2: This is the multiple sequence alignment of the sequences and secondary structures of several available structure templates, based on the ***structural*** alignment methods within Modeller. Each structure name is followed by its identification number from the Protein Data Bank at the Research Collaboratory for Structural Biology. GLIC is from *Gloebacter violaceous*, ELIC is from *Erwinia Chrysanthemi*, AChBP is the acetylcholine binding protein from the snail, *Lymnea stagnalis*, which is homologous to the extracellular or ligand binding domain (LBD) within the LGIC's, and GluCl is the glutamate-gated chloride channel from *C. elegans*. Note the relative conservation of secondary structures within the templates of known three-dimensional structure. This is illustrated with the Kabsch and Sander secondary structure identification algorithm signified as orange bars for alpha helices in the transmembrane domain and blue arrows for beta sheet in the extracellular ligand binding domain.