



SDC 1: This is a multiple sequence alignment of the individual subunits from several potential structural templates (GLIC, ELIC, AChBP and GluCl) and LGIC sequences, based on the ClustalW method. GLIC is from *Gloeobacter violaceus*, ELIC is from *Erwinia Chrysanthemii*, 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*. M_GABA refers to mouse GABA α 2 and α 1 sequences. h_GABA refers to the respective human GABA α 2 and α 1 sequences. h_5HT3 refers to the human serotonin receptor. h_GlyRA1 is the human glycine alpha one receptor. torp_AChR refers to the torpedo acetylcholine alpha, gamma and beta receptor subunits. Note that certain homologous amino acid positions are highlighted in blue, with lighter blue suggesting moderate homology and darker blue higher homology. Note the three homologous positions outlined in gray; these are the positions that, when mutated, modulate anesthetic activity.