Supplementary Figures

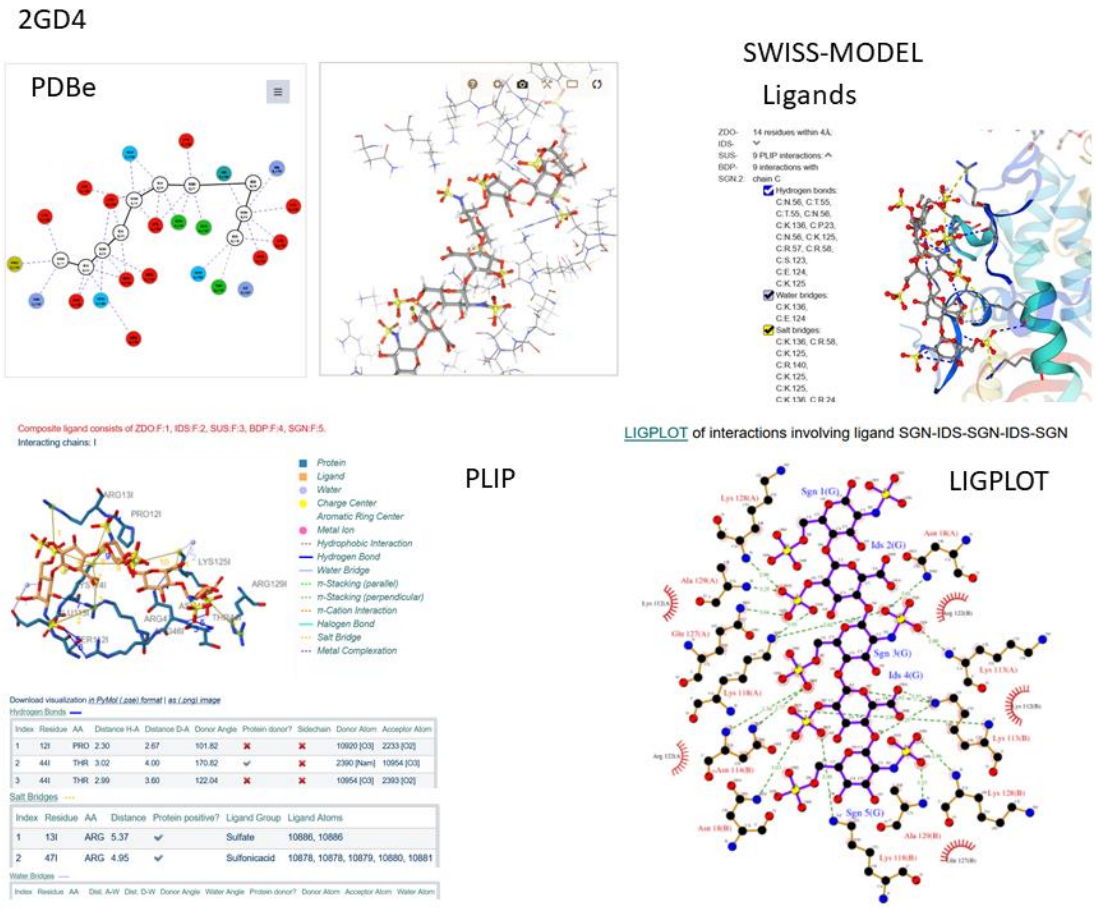

Figure S1. Detailed of the analysis of GAG binding in crystal structure of a ternary FGF1-FGFR2-Heparin complex (PDB 2GD4) available from different souces ; PDBe ; Swiss-Model ; PLIP, LIGPOLT.

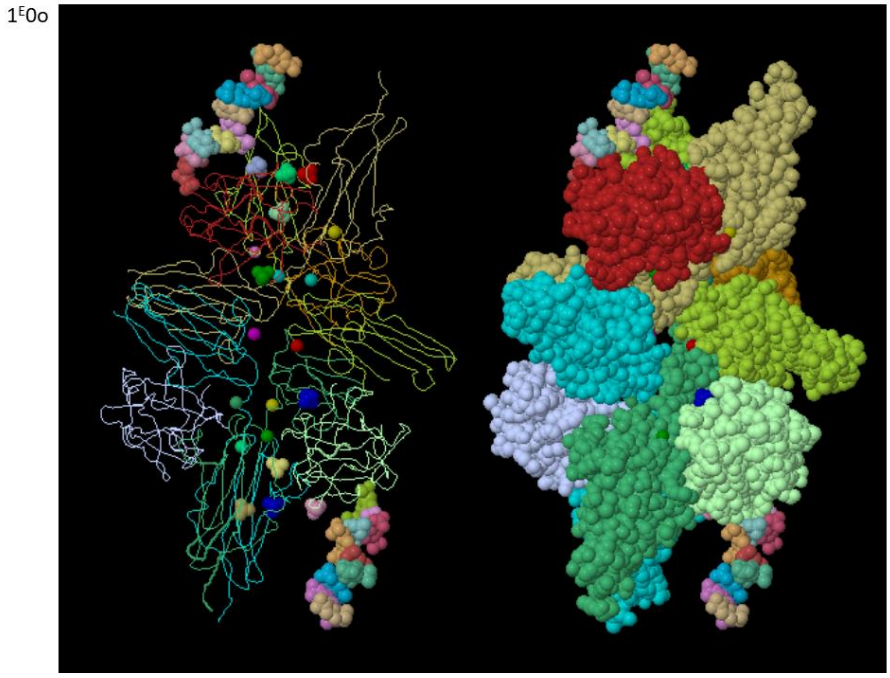

Figure S2. Quaternary organisation in the crystal Structure of the Antithrombin-S195A Factor Xa-Pentasaccharide Complex (PDB 1EO0) computed and displayed by PISA.