**Suppl. Fig. 1.** Structures of some $\beta_{1,3}$AR ligands mentioned in the manuscript. The moieties proposed to contact the secondary binding region of $\beta$ARs are marked in green. The labels are in green letters for ligands considered as a full or partial agonist, and in red for ligands considered as an antagonist or inverse agonist.
Suppl. Fig. 2. Alignment of transmembrane domains involved in the secondary binding site for $\beta_{1,3}$ARs.
Suppl. Fig. 3. Phylogenetic tree of the human catecholamine receptors, built by considering all the residues included in the transmembrane domains. Plots done with GPCRDB software.\textsuperscript{108}