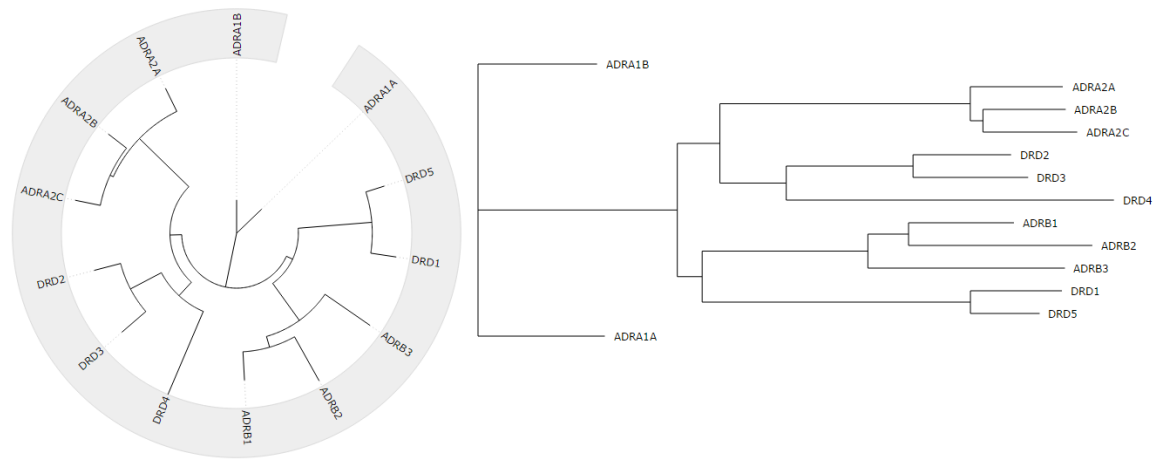


Suppl. Fig. 1. Structures of some β_{1-3} AR ligands mentioned in the manuscript. The moieties proposed to contact the secondary binding region of β ARs are marked in green. The labels are in green letters for ligands considered as a full or partial agonist, and in red for ligands considered as an antagonist or inverse agonist.



Suppl. Fig. 3. Phylogenetic tree of the human catecholamine receptors, built by considering all the residues included in the transmembrane domains. Plots done with GPCRDB software.¹⁰⁸