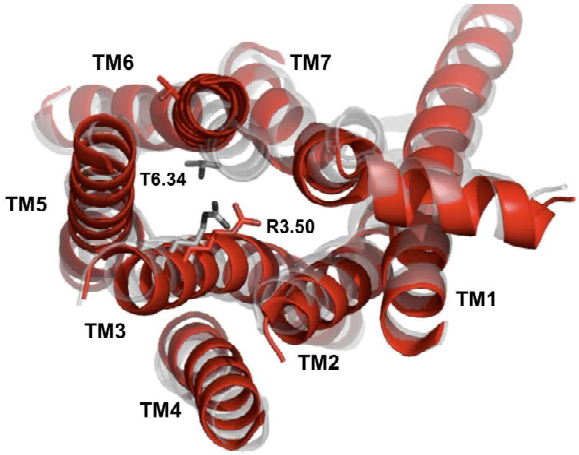
Supporting information – Golebiewska et al.



S1 - Cytoplasmic view of a homology model of the μOR active state (*red*) superimposed on a homology model of the inactive μOR (*grey*). The loop regions have been omitted for clarity. The stick representation shows the polar interaction between $R165^{3.50}$ and $T279^{6.34}$, which has been proposed to be equivalent in the opioid receptors to the 'ionic lock' found in rhodopsin (*40*). For simplicity, only the generic number (see (*41*)) is reported. All images were made using Pymol (*42*).

From this figure, we note that the most tangible difference between these structures consists of the different relative positions of residues $R165^{3.50}$ and $T279^{6.34}$, which are supposed to be involved in ionic-lock breaking upon receptor activation (*40*). Residues here and throughout the text are numbered both according to their position in the mouse μOR sequence, and to the Ballesteros-Weinstein generic two-number (N1.N2) scheme (*41*) reported as a superscript. In this scheme, N1 indicates the TM the residue belongs to, while N2 refers to the residue position in the TM relative to its most conserved residue (position number *50*).