Cholesterol differentially modulates the activity of opioid and muscarinic receptors via common non-canonical binding site

Nikolai Chetverikov, Alena Janoušková-Randáková, Dominik Nelic, and Jan Jakubík*

Institute of Physiology CAS, Prague, Czech Republic

*, corresponding author, e-mail jan.jakubik@fgu.cas.cz, phone +420 2 4106 2620, Laboratory of Neurochemistry, Institute of Physiology CAS, Videnska 1083, 142 00 Praha, Czech Republic

Short title

Cholesterol modulation of opioid and muscarinic receptors

One sentence summary

This study identifies a shared non-canonical cholesterol-binding site at TM6 in muscarinic and opioid receptors, with significant implications for drug development targeting tissue-specific GPCR modulation.

Funding sources

This work was supported by project National Institute for Neurological Research (Programme EXCELES, ID Project No. LX22NPO5107)—Funded by the European Union—Next Generation EU and Czech Academy of Sciences institutional support [RVO:67985823]. Access to computing and storage facilities owned by parties and projects contributing to the Czech National Grid Infrastructure MetaCentrum provided under the programme "Projects of Large Research, Development, and Innovations Infrastructures" (CESNET LM2015042) is appreciated.

Abbreviations

CHO – Chinese ovary; GPCR – G-protein coupled receptor; GTPγS - guanosine 5'-O-[γ-thio]triphosphate; TM – transmembrane α-helix

Abstract

G protein-coupled receptors (GPCRs) are membrane proteins that represent the largest and most therapeutically targeted receptor class, accounting for 30% of currently marketed drugs. Two binding motifs for membrane cholesterol, the cholesterol recognition amino acid consensus (CRAC) domain and the cholesterol consensus motif (CCM), have been postulated. Using a simulation of the molecular dynamics of cholesterol association with the receptor, we predicted the binding of membrane cholesterol to non-canonical sites, distinct from CRAC and CCM, at muscarinic and opioid receptors. We identified a binding site common to muscarinic and opioid receptors at TM6, with arginine 6.35 as the major residue. Membrane cholesterol depletion mimics the effects of $R^{6.35}$ mutations, confirming its role in receptor modulation. Targeting cholesterol-binding sites offers novel pharmacotherapeutic strategies, including tissue-specific sterol-based modulation.

Keywords

cell signalling; cholesterol; receptors/seven transmembrane domain

Introduction

G protein-coupled receptors (GPCRs) are receptors that mediate diverse physiological functions. Over 800 members of the GPCR superfamily comprise the largest and most therapeutically targeted receptor class representing 30% of currently marketed drugs[1]. Numerous studies have shown that cholesterol interacts with GPCRs at specific sites, directly allosterically modulating ligand binding and affecting their activation and pharmacology[2].

Cholesterol has been found co-crystallised with many GPCRs[3]. Two binding motifs for membrane cholesterol were postulated. First, the so-called 'cholesterol recognition amino acid consensus (CRAC) domain common for all membrane proteins that contain a (–L/V-(X)1–5-Y-(X)1–5-R/K-) pattern was described[4]. Subsequently a (K/R)-X1−5-(Y/F)-X1−5-(L/V) reversed pattern (CARC) was found in the nicotinic acetylcholine receptor[5]. The so-called 'cholesterol consensus motif' (CCM) was identified in the structure of the β_2-adrenergic receptor (3D4S) and predicted for a plethora of other GPCRs[6]. While certain motifs like the Cholesterol Recognition Amino-acid Consensus (CRAC) sequence are known to facilitate cholesterol interactions with some GPCRs, not all GPCRs possess these motifs. However, cholesterol still modulates their function, indicating that specific interactions beyond traditional motifs are at play[7, 8]. A current extensive study of cryo-EM and X-ray structures has shown that almost all cholesterol binding to GPCRs occurs in predictable locations that, however, lack perceivable cholesterol-binding motifs[9]. Cholesterol can enhance the conformational stability of GPCRs, either by promoting active or inactive states, which is crucial for their signalling functions. This stabilization is often achieved through direct interactions with specific residues rather than relying solely on conserved motifs[3, 7]. The high plasticity of cholesterol interaction sites and the lack of universal motifs highlight the importance of detailed, residue-level analysis to understand how cholesterol influences GPCR function. This is supported by studies that use molecular dynamics simulations and structural bioinformatics to elucidate cholesterol-GPCR interactions at a finer scale[3, 8].

While canonical cholesterol-binding motifs like CRAC and CCM have been extensively studied, non-canonical binding sites remain poorly understood. This study identifies and characterizes a shared non-canonical site at TM6 in muscarinic and opioid receptors. In our previous study, we have shown that membrane cholesterol prevents persistent activation of muscarinic receptors by wash-resistant xanomeline by interaction with $R^{6.35}$ and $L/I^{6.46}$(Ballesteros and Weinstein numbering[10] in the TM6[11]. The identified cholesterol-binding site does not correspond to any known cholesterol-binding motif. Similarly to M_2 and M_4 muscarinic receptors, a substantial number of $G_{i/o}$-coupled class A GPCRs possess a basic residue in position 6.35 and hydrophobic L/I/V in position 6.46 next to a conserved proline kink (Supplementary Information, Figure S1). We speculate that membrane cholesterol also binds to $R^{6.35}$ at opioid receptors. In the presented study we docked cholesterol to M_2 and M_4 muscarinic receptors and δ-, κ- and μ-opioid receptors by simulation of molecular dynamics of association of cholesterol with receptors[12]. We identified two common cholesterol-binding sites including the one containing $R^{6.35}$. Then we show that depletion of membrane cholesterol has similar effects on functional responses of tested receptors as mutations of $R^{6.35}$ aimed at disruption of cholesterol binding to this residue, confirming a common non-canonical binding site at $R^{6.35}$. Variation in interactions of receptors with the membrane represents a possibility to achieve pharmacological selectivity based on variation in membrane composition among tissues, affording tissue-specific selectivity.

Results

Coarse-grained molecular dynamics

The coarse-grained MD (cgMD) was used to simulate the association of cholesterol to identify potential cholesterol-binding sites at muscarinic and opioid receptors[13]. The cgMD of a 20 nm x 20 nm patch of membrane containing 30% of cholesterol molecules and one receptor was simulated. Throughout cgMD cholesterol molecules associated with the receptor and remained bound to it for hundreds of nanoseconds (Supplementary Information SI Figure 2 to 4). To verify the approach, structures of the β_2-adrenergic receptor (3D4S) and A_{2A}-adenosine receptor (5IU4) were included in the test set. Cholesterol in locations appearing in these crystal structures was observed, validating the method (Supplementary Information Figure S2). Namely, binding to the cholesterol consensus motif (CCM) between TM2 and TM4 of the β_2-adrenergic receptor and TM2-TM3-TM4 extracellular bundle and TM6 extracellular part of the A_{2A}-adenosine receptor was observed. Subsequently, cgMD was run at δ-opioid (4EJ4), κ-opioid (4DJH), μ-opioid (4DKL), M_2-muscarinic (3UON) and M_4-muscarinic (5DSG) receptors in an inactive conformation and δ-opioid (6PT2), κ-opioid (6B73) and μ-opioid (5C1M), M_2-muscarinic (4MQS) and M_4-muscarinic (8FX5) receptors in an active conformation. We have observed up to five concurrently bound molecules of cholesterol to eight unique binding sites (Supplementary Information Figure S3 and S4).

Cholesterol re-docking

Eight unique cholesterol-binding sites on muscarinic and opioid receptors were identified using cgMD simulation of cholesterol association with the receptor, three in the extracellular and five in the intracellular leaflet of the membrane (Figure 1). Cholesterol molecules in the extracellular leaflet interacted with TM1-TM2-TM7 (e1-e2-e7) bundle of helices or groove between TM4-TM5 (e4-e5) or TM6-TM7 (e6/e7) helices. Cholesterol molecules in the intracellular leaflet interacted with the TM1-TM2-TM4 (i1-i2-i4) bundle of helices or groove between TM3-TM4 (i3-i4), TM5-TM6 (i5-i6) or TM6-TM7 (i6-i7) helices or with TM7 (i7) helix. Specifically, cholesterol bound to four sites (e1-e2-e7, e6-e7, i3-i4 and i6-i7) at δ- and κ-opioid receptors, five sites (e1-e2-e7, e6-e7, i5-i6, i6-7 and i7) at the μ-opioid receptor (Supplementary Information Figure S5) and six sites (e1-e2-e7, e4-e5, i3-i4, i5-i6, i6-i7 and i7) at muscarinic receptors (Supplementary Information Figure S6). Individual molecules of cholesterol were back-mapped onto the receptor[14], re-docked[15] and rescored[16]. Re-docking binding energy estimates were above 4 kcal/mol. Two binding sites were common for all studied receptors: e1-e2-e7 and i6-i7. Hydrogen bonding to $R^{6.35}$ was common to all receptors in at least one conformation (Figure 2). Binding to the e1-e2-e7 sites markedly varied among receptors.

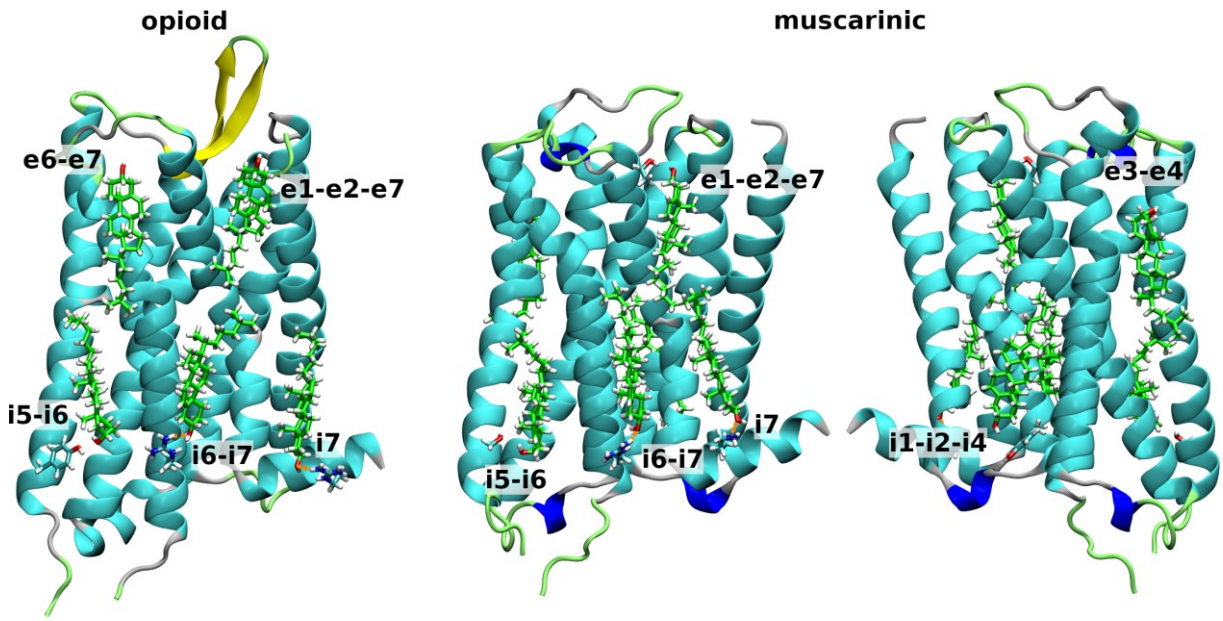

Figure 1 Cholesterol binding to opioid and muscarinic receptors

Molecules of cholesterol that associated with the opioid (left) or muscarinic receptor (middle and right) were back-mapped and re-docked to the receptor. Orientation: extracellular up, TM6 front (left and middle) or TM4 front (right). Cholesterol (green carbons) in the extracellular leaflet interacting with TM1-TM2-TM7 (e1e2-e7) bundle or TM3-TM4 (e3-e4) or TM6-TM7 (e6-e7) groove and in the intracellular leaflet interacting with TM1-TM2-TM4 (i1-i2-i4) bundle or TM5-TM6 (i5-i6) or TM6-TM7 (i6-i7) groove or TM7 (i7) helix is shown.

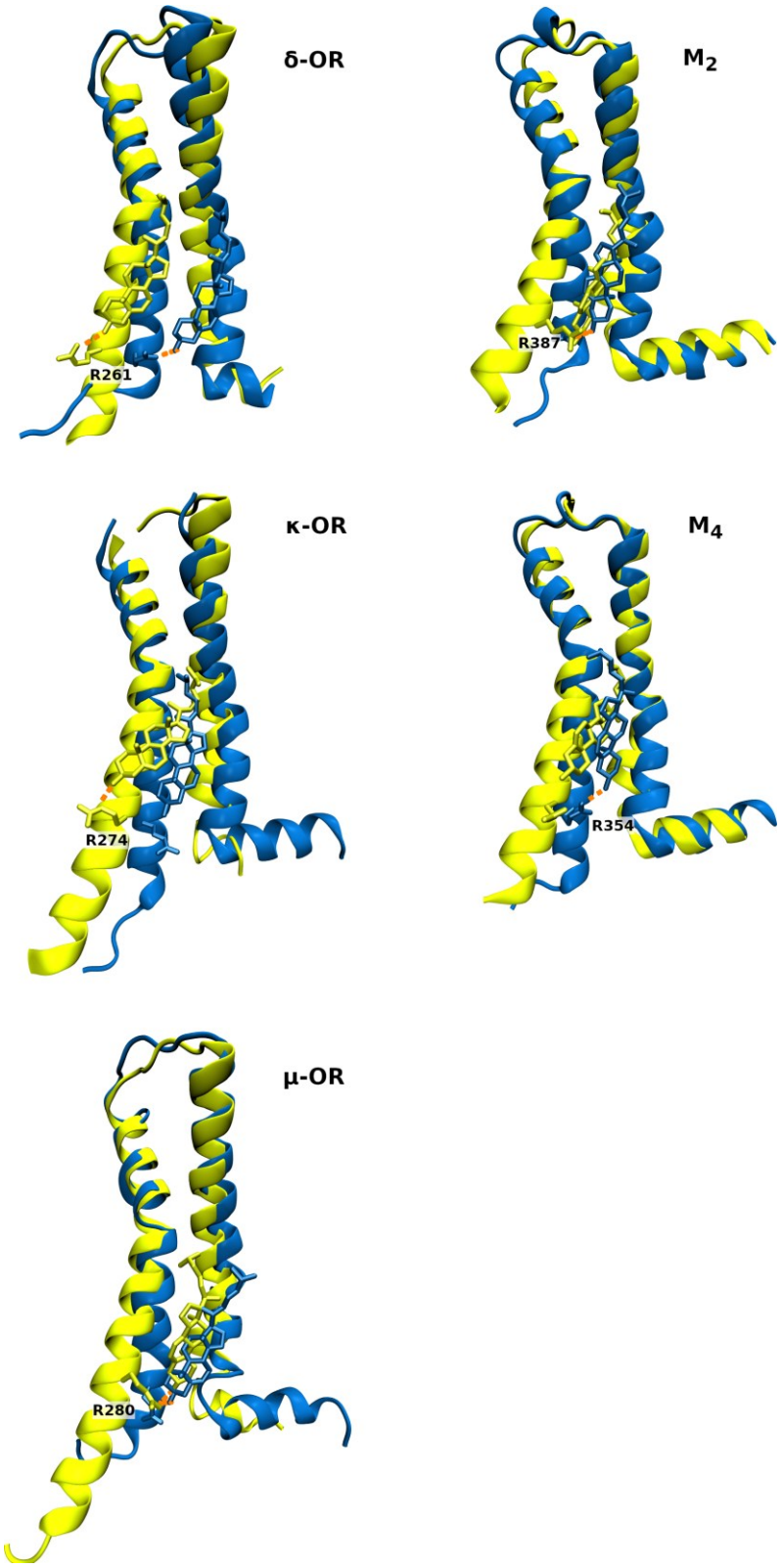

Figure 2 Interaction of cholesterol with $R^{6.35}$ in top docking poses

Interaction of cholesterol with $R^{6.35}$ in top scoring docking pose of opioid (left) and muscarinic receptors (right) in an active (yellow) and an inactive conformation (blue). Orange dashed lines indicate hydrogen bonds.

Conventional molecular dynamics

The complexes of receptors with the top-scoring cholesterol molecule in re-docking were subjected to three replicas of conventional MD (cMD). Analysis of cMD trajectories revealed various degrees of the stability of bound cholesterol. The quantitative analysis of interactions between receptor and cholesterol molecules is in (Figure 3). Fractions of time-frames at which cholesterol binds to a given residue were calculated in the Maestro Simulation Interactions Diagram. Residues interacting with cholesterol in at least 20 % of time-frames in at least one replica are shown. The principal (the most frequent in the site) receptor residues interacting with cholesterol are listed in Table 1. Differences in cholesterol binding to receptors in inactive versus active conformations were detected.

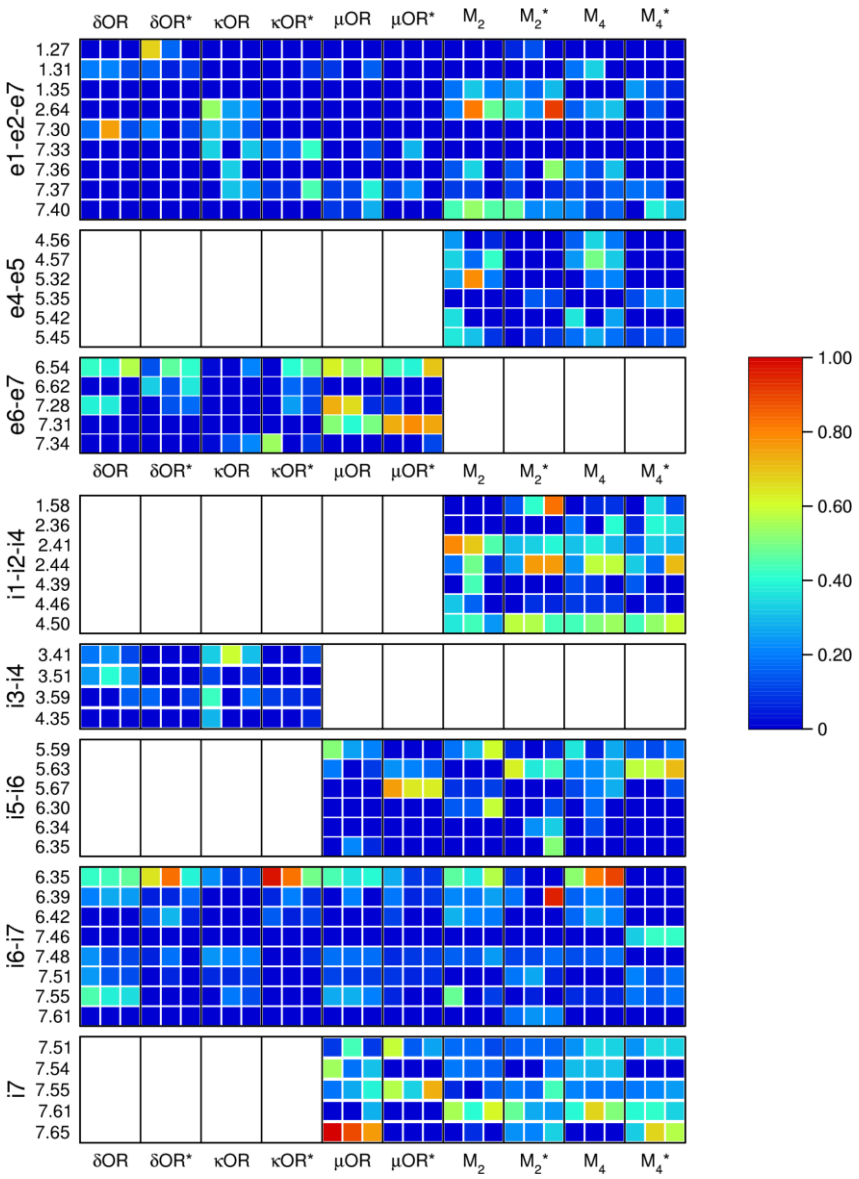

Figure 3 Interactions between cholesterol and receptor

Histograms of interactions between receptors indicated on x-axis and cholesterol molecules in the extracellular leaflet interacting with e1-e2-e7 bundle, e4-e5 groove or e6-e7 groove and in the intracellular leaflet interacting with i1-i2-i4 bundle, i3-i4 groove, i5-i6 groove, i6-i7 groove or i7 helix indicated on y-axis were calculated from MD trajectories using Ligand Interaction Diagram in Maestro. Only residues interacting with cholesterol at more than 20% of time-frames in at least one MD replica are displayed. Each square represents one of 3 independent MD replicas. Values over

1.0 are possible as some protein residues may make multiple contacts with cholesterol within one timeframe. However, no values greater than 1 were obtained.

Table 1 - Principal residues interacting with cholesterol during conventional MD
Principal residues of interaction between receptor (the first column) and cholesterol molecule in the extracellular leaflet interacting with TM1-TM2-TM7 (e1-e2-e7) bundle or TM4-TM5 (e4-e5) or TM6-TM7 (e6-e7) groove and in the intracellular leaflet interacting with TM1-TM2-TM4 (i1-i2-i4) bundle or TM3-TM4 (i3-i4), TM5-TM6 (i5-i6) or TM6-TM7 (i6-i7) groove or TM7 (i7) helix throughout MD trajectory are listed. Superscript, Ballesteros-Weinstein numbering; ECL3, the third extracellular loop; ICL3, the third intracellular loop.

Structure	e1-e2-e7	e4-e5	e6-e7	i1-i2-i4	i3-i4	i5-i6	i6-i7	i7
δ-OR 4EJ4 inactive	L295$^{7.30}$		F280$^{6.54}$ D293$^{7.28}$		F137$^{3.41}$ Y147$^{3.51}$		R261$^{6.35}$ V265$^{6.39}$ F320$^{7.55}$	
δ-OR 6PT2 active	S44$^{1.27}$		F280$^{6.54}$ D288$^{6.62}$		K155$^{3.59}$		R261$^{6.35}$ G268$^{6.42}$	
κ-OR 4DJH inactive	Y119$^{2.64}$ S310$^{7.33}$ Y313$^{7.36}$ F314$^{7.37}$		F293$^{6.54}$ S311$^{7.34}$		F147$^{3.41}$ K165$^{3.59}$		R274$^{6.35}$	
κ-OR 6B73 active	S310$^{7.33}$ F314$^{7.37}$		F239$^{6.54}$ S305$^{7.28}$ S311$^{7.34}$				R274$^{6.35}$ L325$^{7.48}$ F332$^{7.55}$	
μ-OR 4DKL inactive	F320$^{7.37}$ A323$^{7.40}$		Y299$^{6.54}$ T311$^{7.28}$ Q314^{ECL3}			Y252$^{5.59}$	R280$^{6.35}$ L331$^{7.48}$ F338$^{7.55}$	V334$^{7.51}$ A337$^{7.54}$ R348^{Helix8}
μ-OR 5C1M active	S317$^{7.33}$ F320$^{7.37}$		Y299$^{6.54}$ Q314^{ECL3}			I256$^{5.63}$ K260^{ICL3}	R280$^{6.35}$	V334$^{7.51}$ F338$^{7.55}$
M_2 3UON inactive	I26$^{1.35}$ Y84$^{2.64}$ W427$^{7.40}$	W155$^{4.57}$ F180$^{5.32}$ T190$^{5.42}$		Y60$^{2.41}$ F63$^{2.44}$ T137$^{4.39}$ W148$^{4.50}$		Y206$^{5.58}$ E382$^{6.30}$	R387$^{6.35}$ A391$^{6.39}$ L394$^{6.42}$ L442$^{7.55}$	K448^{Helix8}
M_2 4MQS active	I26$^{1.35}$ Y84$^{2.64}$ W427$^{7.40}$			K49$^{1.58}$ Y60$^{2.41}$ F63$^{2.44}$ W148$^{4.50}$		S210$^{5.63}$ T386$^{6.34}$ R387$^{6.35}$	A391$^{6.39}$ A438$^{7.51}$ K448^{Helix8}	L442$^{7.55}$ K448^{Helix8} K452^{Helix8}
M_4 5DSG inactive	E31$^{1.31}$ Y92$^{2.64}$ S290$^{7.36}$	W164$^{4.57}$ T199$^{5.42}$		F72$^{2.44}$ W157$^{4.50}$		S219$^{5.63}$	R354$^{6.35}$	A405$^{7.51}$ A408$^{7.54}$ K415^{Helix8}
M_4 8FX5 active	F34$^{1.35}$ W440$^{7.40}$			F72$^{2.44}$ W157$^{4.50}$		S219$^{5.63}$	R400$^{7.46}$	K415^{Helix8} R419^{Helix8}

Opioid receptors

Four unique cholesterol-binding sites were identified on the δ-opioid receptor (Table 1, Supplementary information Figure S5). Binding to e6-e7 and i3-i4 sites was similar for receptors at inactive and active conformations, respectively. In the e6-e7 site, the cholesterol binding was mediated by hydrophobic

interaction with F280$^{6.54}$ (superscript, Ballesteros-Weinstein numbering[10]) (Figure 3**Error! Reference source not found.**). Cholesterol binding to the i3-i4 site was weak at both conformations. In an inactive conformation (4EJ4), binding was mediated by hydrophobic interactions with F137$^{3.41}$. In an active conformation (6PT2), binding was mediated by hydrogen bonding to K155$^{3.59}$. While cholesterol binding to the e1-e2-e7 site at an inactive conformation was primarily mediated by hydrophobic interaction with L295$^{7.30}$, at an active conformation it was mediated by hydrogen bonding to S44$^{1.27}$. Cholesterol binding to the i6-i7 site of the δ-opioid receptor was via hydrogen bond to R261$^{6.35}$ that was more frequent in an active conformation than in an inactive conformation. In an active conformation, cholesterol was shifted towards TM7 interacting with F320$^{7.55}$ (Figure 2).

Similar to the δ-opioid receptor, four unique cholesterol-binding sites were identified on the κ-opioid receptor (Table 1, Supplementary Information Figure S5). In contrast to the δ-opioid receptor, however, cholesterol binding to the extracellular e1-e2-e7 site was more frequent at an inactive conformation (4DJH) than at an active conformation (6B73) (Figure 3). In an inactive conformation, it was mediated by frequent hydrogen bonding with Y119$^{2.64}$ and S310$^{7.33}$, and in an active conformation by less-frequent hydrogen bonding with S310$^{7.33}$ only. Cholesterol binding to the e6-e7 site was mediated by hydrogen bonding to S311$^{7.34}$ and hydrophobic integrations with F293$^{6.54}$ that were more frequent in an active than inactive conformation. Cholesterol binding to the i3-i4 site of the receptor in an inactive conformation was mediated by F147$^{3.41}$ and K165$^{3.59}$. At the receptor in an active conformation, cholesterol binding was weak and cholesterol dissociated from the binding site. In the i6 site, the cholesterol binding was primarily mediated via a hydrogen bond with R274$^{6.35}$, which was more frequent at an active conformation than an inactive one (Figure 2).

Five unique cholesterol-binding sites were identified on the μ-opioid receptor (e1-e2-e7, e6-e7, i3-i4, i6-i7, i7), three being common with δ- and κ-opioid receptors (Table 1, Supplementary Information Figure S5). The strongest cholesterol binding was identified at the i7 site (Figure 3**Error! Reference source not found.**). In an inactive conformation (4DKL), cholesterol binding to the i7 site was mediated by R348 in the Helix8. In an active conformation (5C1M), cholesterol binding to the i7 site was mediated by V334$^{7.51}$ and F338$^{7.55}$. The cholesterol binding to the i7 site was more frequent to an inactive conformation than to an active one. Also binding to the e6-e7 site was relatively strong. It was mediated by hydrophobic interaction with Y299$^{6.54}$ and hydrogen bonding to Q314 in the third extracellular loop. At inactive conformation, hydrogen bonding to Q314 was less frequent in expense for hydrogen bonding to T311$^{7.28}$. Cholesterol binding to the i5-i6 site was mediated by hydrogen bonding to K260 in the third intracellular loop of an active conformation or less frequent binding to Y252$^{5.59}$ in the TM5 helix of an inactive conformation. Like at other tested receptors, cholesterol binding to the i6-i7 site was mediated via a hydrogen bond with R280$^{6.35}$, interacting more frequently with it at an inactive conformation (Figure 2). In an inactive conformation, cholesterol binding was further stabilised by hydrophobic interactions with TM7 via L331$^{7.48}$ and F338$^{7.55}$ (Figure 3).

Muscarinic receptors

Six unique cholesterol-binding sites were identified on muscarinic receptors (Table 1, Supplementary Information Figure S6). Integration patterns of M_2 and M_4 receptors were similar. The most profound differences between inactive and active conformations were observed for cholesterol binding to the e4-e5 and i6-i7 sites (Figure 3). In an inactive conformation of the M_2-muscarinic receptor (3UON) cholesterol at the e4-e5 site primarily interacted with W155$^{4.57}$ and T190$^{5.42}$. Identically in an inactive conformation of the M_4-muscarinic receptor (5DSG) cholesterol primarily interacted with W164$^{4.57}$ and T199$^{5.42}$. In active conformations (M_2 4MQS; M_4 8FX5), these principal interactions were missing as cholesterol binding was unstable. Like opioid receptors, cholesterol binding to the i6-i7 site of the M_2 and M_4 receptors in inactive conformations was mainly mediated by hydrogen bonding to R387$^{6.35}$ and

R354$^{6.35}$, respectively. In active conformations, cholesterol moved towards Helix8 and bound to K448 of M_2 or R400 of M_4 receptor. Cholesterol binding to the e1-e2-e7 site of the M_2 receptor in an inactive conformation was mainly mediated by Y84$^{2.64}$ and W427$^{7.40}$. In an active conformation, these interactions persisted but bonding to W427$^{7.40}$ was about 5 times less frequent. Cholesterol binding to the e1-e2-e7 site of the M_4 receptor was in principle the same but much weaker and at an inactive conformation of the receptor unstable. Cholesterol binding to the i1-i2-i4 site of the M_2 and M_4 receptors was strong. At M_2-receptor cholesterol binding was mainly mediated by Y60$^{2.41}$, F63$^{2.44}$, T237$^{4.39}$ and W148$^{4.50}$ at an inactive conformation and K49$^{1.58}$, Y60$^{2.41}$, F63$^{2.44}$ and W148$^{4.50}$ at an active conformation. At M_4-receptor cholesterol binding to the i1-i2-i4 site was mainly mediated by F63$^{2.44}$ and W148$^{4.50}$ at both conformations. Cholesterol binding to the i5-i6 site of the M_2 receptor was mainly mediated by Y206$^{5.58}$ and E382$^{6.30}$ at an inactive conformation and by S210$^{5.63}$, T386$^{6.34}$ at an active conformation. In an active conformation, cholesterol moves towards R387$^{6.35}$ and forms hydrogen bonds with it (Figure 2). Cholesterol binding to the i5-i6 site of the M_4 receptor was mainly mediated by S219$^{5.63}$ at both conformations (Figure 3). Cholesterol binding to the i7 site was mediated by hydrogen bonding to lysine (M_2 K448, M_4 K415)in Helix 8 at both active and inactive conformations. At active conformations, it moves further from the TM7 helix and forms a hydrogen bond with K452 (M_2) or R419 (M_4).

Common features of cholesterol binding

Taken together, the sites e1-e2-e7 and i6-i7 were detected in all structures (Table 1, Figure 3, Supplementary Information Figure S5 and S6). Cholesterol binding to the e1-e2-e7 bundle varied among receptor families and subtypes. Cholesterol binding to the e1-e2-e7 bundle was weak at μ-opioid and M_4-muscarinic receptors. Cholesterol binding to e1-e2-e7 bundle was mediated mainly by Y$^{2.64}$ at M_2-muscarinic and κ-opioid receptors, by L$^{7.30}$ at δ-opioid receptor in an inactive conformation and S$^{1.27}$ at δ-opioid receptor in an active conformation. The principal interaction residue of cholesterol binding to the i6-i7 groove was R$^{6.35}$ (Figure 2). Cholesterol binding to R$^{6.35}$ was more frequent at inactive than active conformations of M_2, M_4 and μ receptors (Figure 3). In contrast, cholesterol binding to R$^{6.35}$ was more frequent to active conformations than to inactive conformations of κ and δ-opioid receptors.

Functional responses – membrane-cholesterol depletion

To assess the effects of membrane cholesterol on the functional response of muscarinic and opioidreceptors, membrane cholesterol was depleted in CHO cells expressing individual receptor subtypes by treatment with methyl-β-cyclodextrin (MβCD). The treatment lowered the concentration of membrane cholesterol from 225 ± 22 to 85 ± 13 nmol/mg of protein. The cholesterol removal by this procedure was shown reversible[11, 17]. Such drastic decrease in cholesterol concentration is needed to remove cholesterol from receptor binding as cholesterol may exert high affinity, up to 1 nM[18]. To avoid the effects of cholesterol removal on downstream signalling membrane proteins, functional response was measured close to the receptor as [^{35}S]GTPγS binding to membranes prepared from CHO cells. The M_2-, and M_4-muscarinic receptors were activated by the agonist carbachol, δ- and κ- opioid receptors by Leu-enkephalin and μ-opioid by endomorphin I. After subtraction of non-specific binding, [^{35}S]GTPγS binding was normalized to total GTPγS binding sites. The effects of cholesterol depletion varied among receptors. Cholesterol depletion changed basal GTPγS binding (% of total GTPγS binding sites in the absence of an agonist) to membranes, increasing it at M_2- and M_4-muscarinic receptors (Figure 4, red and turquoise) and decreasing it at δ- and μ-opioid receptors (Figure 4, yellow and blue). Basal GTPγS binding to membranes expressing κ-opioid receptors remained unchanged. Membrane-cholesterol depletion increased maximum GTPγS binding at both muscarinic receptors by about 20 % and decreased maximum GTPγS binding at all opioid receptors by 20 (μ-opioid) to 50 % (κ-opioid). Membrane-cholesterol depletion decreased the half-efficient concentration EC_{50} at both

muscarinic and μ-opioid receptors and increased it at κ-opioid receptor. EC_{50} was not affected at δ-opioid receptors (Supplementary Information Table S1). Agonists used did not affect GTPγS binding to membranes from non-transfected cells (Supplementary Information Figure S7) demonstrating that GTPγS binding is specific to activation of transfected receptors.

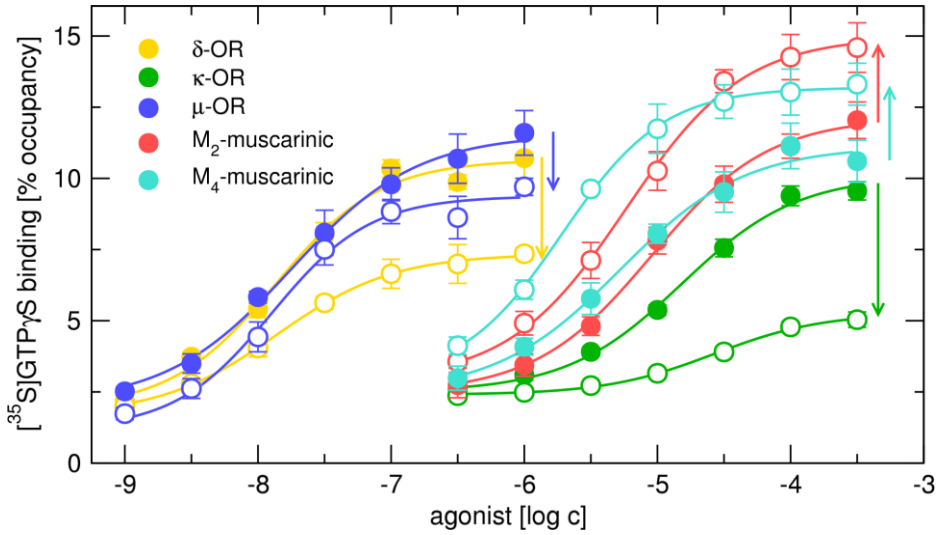

Figure 4 Effects of membrane-cholesterol depletion on functional response to agonists
Effects of membrane-cholesterol depletion (open symbols) on functional responses of δ- (yellow), κ-opioid (green) receptors to Leu-enkephalin, μ-opioid receptors (blue) to endomorphin I and M_2- (red) and M_4-muscarinic (turquoise) receptors to carbachol. Ordinate, [^{35}S]GTPγS binding is expressed as % of occupancy of G-protein binding sites. Abscissa, the concentration of agonist is expressed as a decadic logarithm of molar concentration. Data are means ± SD from 3 independent experiments performed in quadruplicates.

Functional responses – mutations

Molecular modelling (Figure 3) suggests that cholesterol binds to the i6-i7 groove at all investigated receptors and $R^{3.65}$ plays a key role in cholesterol binding at the majority of them. Therefore, $R^{6.35}$ was mutated to either alanine (neutral mutation) or glutamate (reverse charge mutation) found in some receptors (Supplementary information Figure S1) with the intention of abolishing cholesterol binding to $R^{6.35}$. The functional response of M_2- and M_4-muscarinic and δ-, κ- and μ-opioid receptors was measured as stimulation of [^{35}S]GTPγS binding to membranes prepared from CHO cells by the agonists carbachol (muscarinic), Leu-enkephalin (δ- and κ-opioid) or endomorphin I (μ-opioid receptors). The mutations of $R^{6.35}$ affected functional responses similarly to cholesterol depletion. Both mutations increased basal binding (in the absence of an agonist) of GTPγS binding to M_2- and M_4-muscarinic receptors (Figure 5, red and turquoise) and decreased basal GTPγS binding at δ- and μ-opioid receptors (Figure 5, yellow and blue). None of the mutations affected basal GTPγS binding to membranes expressing κ-opioid receptors (Figure 5, green). Both mutations increased maximum GTPγS binding at both muscarinic receptors and decreased maximum GTPγS binding at κ-opioid receptor. Mutation of $R^{6.35}$ to glutamine decreased E_{MAX} at μ-opioid receptor. Mutations of $R^{6.35}$ to alanine did not affect E_{MAX} at this receptor. Both mutations decreased EC_{50} values at both muscarinic and κ-opioid receptors. EC_{50} was not affected at δ- and μ-opioid receptors by these mutations (Supplementary Information Table S2).

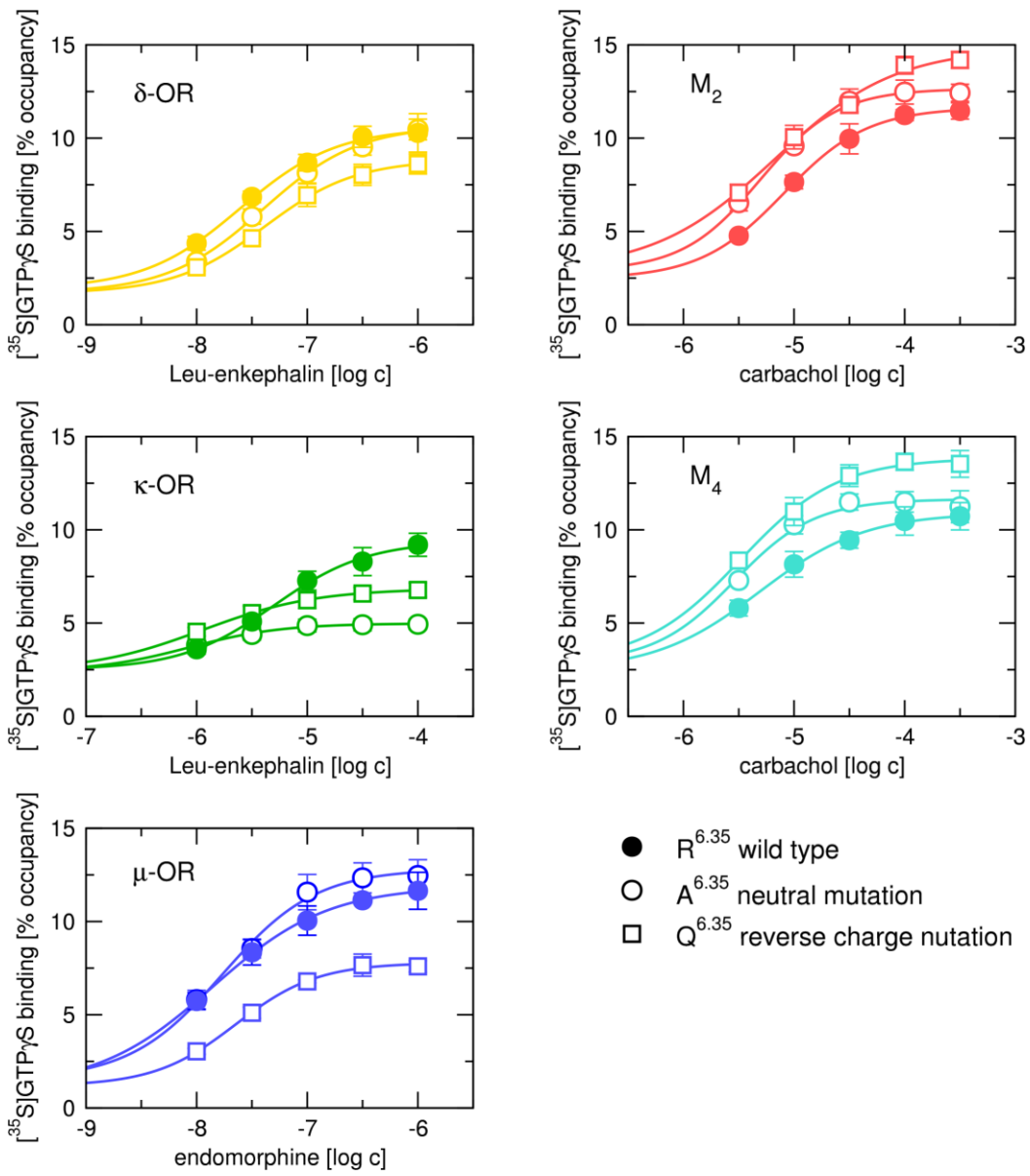

Figure 5 Effects of mutation of $R^{6.35}$ on functional response to agonists

Effects of mutations of wild type $R^{6.35}$ (full symbols) to alanine (neutral mutation, open circles) or glutamine (reverse charge mutation, open squares) on functional responses of δ- (yellow), κ-opioid (green) receptors to Leu-enkephalin, μ-opioid receptors (blue) to endomorphin I and M_2- (red) and M_4-muscarinic (turquoise) receptors to carbachol. Ordinate, [^{35}S]GTPγS binding is expressed as % of occupancy of G-protein binding sites. Abscissa, the concentration of agonist is expressed as a decadic logarithm of molar concentration. Data are means ± SD from 3 independent experiments performed in quadruplicates.

Overall, the effects of mutations on basal GTPγS binding were the same as the effects of cholesterol depletion. Also, the effects of mutations on E_{MAX} and EC_{50} at muscarinic receptors were the same as the effects of cholesterol depletion. In contrast, cholesterol depletion strongly decreased E_{MAX} of functional response of mutated M_2- and M_4-muscarinic receptors, having the opposite effect in comparison to wild-type receptors (Supplementary Information Figure S8 and Table S3), indicating additional mechanism by which cholesterol affects functional properties of muscarinic receptors.

Receptor expression level

As parameters of functional responses (EC_{50} and E_{MAX}) are dependent on the receptor expression level, the maximum binding capacity (B_{MAX}) and equilibrium dissociation constant (K_D) of radioligand were determined in saturation binding experiments (Table 2). In general, mutations of $R^{6.35}$ did not bring substantial changes in receptor B_{MAX} or radioligand K_D. Only mutations R261Q of δ-OR and R280A and R280Q of μ-OR marginally increased receptors B_{MAX} (<7 %).

Table 2 – Expression of muscarinic and opioid receptors

Maximum binding capacity B_{MAX}, expressed as fmol of binding sites per μg of membrane proteins, equilibrium dissociation constant KD, expressed in nM, of [^{3}H]NMS (muscarinic), [^{3}H]DAMGO (μ-OR), [^{3}H]delthropin (δ-OR) and [^{3}H]diprenorphine (κ-OR), respectively, of wild type (wt) and mutant receptors were obtained by fitting Eq. 2 to saturation binding data. Data are means ± SD from 3 independent experiments performed in quadruplicates.

	B_{MAX} [fmol/μg]			K_D [nM]		
δ-OR wt	1.42	±	0.02	157	±	5
δ-OR R261A	1.49	±	0.05	163	±	2
δ-OR R261Q	1.51	±	0.01*	173	±	29
κ-OR wt	1.76	±	0.09	1630	±	230
κ-OR R274A	1.74	±	0.02	1440	±	130
κ-OR R274Q	1.77	±	0.09	1240	±	100
μ-OR wt	1.49	±	0.01	175	±	18
μ-OR R280A	1.59	±	0.01*	192	±	4
μ-OR R280Q	1.57	±	0.06*	194	±	8
M_2 wt	7.50	±	0.02	403	±	6
M_2 R387A	7.59	±	0.12	397	±	6
M_2 R387Q	7.58	±	0.19	402	±	3
M_4 wt	8.21	±	0.15	233	±	3
M_4 R354A	8.26	±	0.05	235	±	5
M_4 R354Q	8.35	±	0.11	237	±	6

**, different form wild-type (P<0.01, Bonferroni multiple comparison)*

Discussion

Membrane cholesterol allosterically modulates ligand binding to and activation of GPCRs and affects the pharmacology of GPCRs[2]. Three cholesterol-binding motifs were postulated[4–6]. However, the majority of cholesterol binding in cryo-EM and X-ray structures of GPCRs occurs in the sites not conforming to these binding motifs[9]. While traditional motif-based predictions may not fully capture the complexity of cholesterol-GPCR interactions, site-specific interactions play a crucial role in modulating GPCR conformations and function. This underscores the need for detailed, residue-level analyses to better understand these interactions. In the present study, we show cholesterol binding to such a non-canonical site at TM6 of muscarinic and opioid receptors. The binding to this site is primarily mediated by hydrogen bonding to $R^{6.35}$ (Figure 1 and Figure 3).

We docked cholesterol to GPCRs by simulation of molecular dynamics of its association with receptors[12]. The procedure successfully identified all cholesterol-binding sites observed in the X-ray structures of the β_2-adrenergic receptor (3D4S)[6] and A_{2A}-adenosine receptor (5IU4)[19] (Supplementary information Figure S2), verifying a successful implementation of the procedure. Eight unique cholesterol-binding "cavities" on muscarinic and opioid receptors were identified (Figure 1, Table 1). Two of them were common for muscarinic and opioid receptors. At opioid receptors, observed cholesterol binding in the extracellular leaflet to TM6-TM7 groove (e6-e7 site) corresponds to cholesterol co-crystallized in structures 4DKL, 5C1M, 6PT2 and 6B73 further validating the procedure[20–23]. Cholesterol did not appear in the X-ray or cryo-EM structures of muscarinic

receptors. However, the observed binding of cholesterol in the intracellular leaflet to the TM1-TM2-TM4 bundle (i1-i2-i4 site) corresponds to cholesterol hemisuccinate appearing in X-ray (5CXV) and cryo-EM (6OIJ) structures of the M_1-muscarinic receptor[24, 25].

We further analysed the cholesterol binding to the putative sites by simulation of cMD of top-scoring poses (Figure 4). The binding of cholesterol to receptors in active conformations diverged from its binding to receptors in inactive conformations, indicating a modulatory role on receptor activation. We assume that preferential binding of cholesterol to one of the receptor conformations leads to stabilization of the receptor in this conformation and thus influences its activation and, consequently, the functional response. Specifically, preferential binding to the inactive conformation leads to attenuation of the functional response, and possibly a decrease in the basal response. On the other hand, preferential binding to the active conformation leads to enhancement of the functional response, and possibly an increase in the basal response. We observed major differences in binding to active versus inactive conformation for the i6-i7 site (Figure 2).

Depletion of membrane cholesterol differentially modulated activation of muscarinic and opioid receptors (Figure 4). Depletion of membrane cholesterol augmented activation of both muscarinic receptors to a similar extent and diminished to various extent (20 to 50%) activation of all opioid receptors. These findings agree with previous observations[26]. We assume that the removal of membrane cholesterol leads to the abolition of its binding to the receptor and the loss of modulatory effects. Thus, the increase in the functional response of muscarinic receptors after the removal of membrane cholesterol means that cholesterol has a negative modulatory effect. That is, it binds preferentially to the inactive conformation of the receptor. On the other hand, the decrease in the functional response of opioid receptors means that cholesterol has a positive modulatory effect. That is, it binds preferentially to the active conformation of the receptor.

Molecular modelling suggested that cholesterol hydrogen bonding to $R^{6.35}$ substantially contributes to its binding to the receptor (Figure 3). Therefore, we designed mutations of $R^{6.35}$ intended to abolish cholesterol hydrogen bonding. Effects of mutations of $R^{6.35}$ to glutamine on functional response to agonists (Figure 5) were similar to the effects of cholesterol depletion (Figure 4), suggesting these mutations indeed impair cholesterol binding to $R^{6.35}$. Thus i6-i7 groove appears to be a non-canonical cholesterol binding site through which cholesterol differentially modulates the functional response of studied receptors.

Cholesterol-mediated receptor oligomerisation via the TM6-TM7 interface was modelled for dimers of muscarinic receptors[27]. The position of cholesterol molecules in the model was given by template structures of β_2-adrenergic and 5-HT_{2B}-serotonin receptors. Binding to the e6-e7 site was not confirmed by the presented study for muscarinic receptors but was found at opioid receptors (Table 1). This may be given by the orientation of polar and acidic residues in the extracellular edge of TM6 and TM7 of muscarinic receptors out of the membrane, preventing their interaction with the hydroxy group of cholesterol.

Our findings reveal novel therapeutic opportunities by targeting non-canonical cholesterol-binding sites in GPCRs, enabling tissue-specific drug design. At muscarinic receptors, a cholesterol-binding site was shown to bind neuroactive steroids[28]. Thus, neurosteroids and steroid hormones modulating muscarinic receptors[29–31] very likely act via cholesterol-binding sites. The neurosteroid pregnanolone sulphate has been shown to increase acetylcholine release in the frontal cortex, amygdala and hippocampus and improve spatial recognition[32, 33]. The steroid whitanone blocked the negative effects of scopolamine on cholinergic signalling, exerted neuroprotective effects and promoted neuroregeneration and memory recovery[34, 35]. Like muscarinic receptors, membrane

cholesterol affected the binding and function of opioid receptors[26]. Membrane cholesterol modulated the partitioning of δ-opioid receptors to membrane rafts[36]. Also, the binding of steroids to opioid receptors affecting their functional response was observed[37, 38]. Steroid activating μ-opioid receptors was synthesised[39], indicating that similar to muscarinic receptors, opioid receptors can be modulated by steroids. However, the non-genomic effects of steroids on the function of opioid receptors have not been studied in detail yet.

Various tissues differ in the content of membrane cholesterol. For example, cholesterol content is high in neurons and low in smooth muscle cells. Steroid-based pharmaceuticals thus may be more efficient at cholesterol lean tissues due to lesser competition with cholesterol for binding to GPCRs. Membrane cholesterol affects GPCR downstream signalling and may change the pharmacological profile of GPCR agonists[40]. Reduction of the content of membrane cholesterol attenuated signalling via δ-opioid receptors in neuronal cells but enhanced it in non-neuronal cells[41]. Thus, theoretically, natural variations in the interaction of receptors with membrane allow for achieving pharmacological selectivity based on variation in membrane composition among tissues resulting in tissue-specific selectivity.

In summary, this study identifies a shared non-canonical cholesterol-binding site at TM6 in muscarinic and opioid receptors, with significant implications for drug development targeting tissue-specific GPCR modulation.

Materials and Methods

Materials

Common chemicals were purchased from Sigma (Prague, CZ) in the highest available purity. Radiolabelled [^{35}S]GTPγS, [^{3}H]DAMGO, and [^{3}H]diprenophin were Perkin Elmer NEG030H, NET902, and NET11212, respectively, and [^{3}H]N-methyl scopolamine was American Radiochemical Company ART1214 purchased from Lacomed (Kralupy nad Vltavou, CZ).

Cell culture and membrane preparation

We transfected Chinese hamster ovary (CHO) cells with the genes of individual human variants of muscarinic and opioid receptors (Missouri S&T cDNA Resource Center, Rolla, MO, USA). CHO cell cultures were prepared as described previously. Stable cell lines were grown to confluence in 75 cm^2 flasks in Dulbecco's modified Eagle's medium supplemented with 10% fetal bovine serum and 2 million cells were subcultured in 100 mm Petri dishes. The medium was supplemented with 5 mM butyrate for the last 24 hours of cultivation to increase receptor expression. Cells were detached by mild trypsinization on day 5 after subculture. For cultivation of transiently transfected cells see "Construction of mutant receptors" below. Detached cells were washed twice in 50 ml of phosphate-buffered saline and 3 min centrifugation at 250 x g. Harvested cells were stored at -20°C overnight. Thawed cells were suspended in 20 ml of ice-cold incubation medium (100 mM NaCl, 20 mM Na-HEPES, 10 mM -$MgCl_2$, pH 7.4) supplemented with 10 mM EDTA and homogenized on ice by two 30-s strokes using a Polytron homogenizer (Ultra-Turrax; Janke & Kunkel GmbH & Co. KG, IKA-Labortechnik, Staufen, Germany) with a 30 s pause between strokes. Cell homogenates were centrifuged for 5 min at 1000×g to remove whole cells and cell nuclei. The resulting supernatants were centrifuged for 30 min at 30,000×g. Pellets were suspended in a fresh incubation medium, incubated on ice for 30 min, and centrifuged again. The resulting membrane pellets were kept at -80 °C until assayed within 10 weeks.

Depletion of membrane cholesterol

We reduced membrane cholesterol levels by incubating whole detached cells in Krebs-HEPES buffer (KHB; final concentrations in mM: NaCl 138; KCl 4; $CaCl_2$ 1.3; $MgCl_2$ 1; NaH_2PO_4 1.2; Hepes 20; glucose

10; pH adjusted to 7.4) supplemented with 10 mM methyl-β-cyclodextrin (MβCD) at 37ºC for 30 min. The concentration of the cells in suspension was 20 million cells per ml. After incubation, the medium was removed and cells were washed twice with a triple incubation volume of fresh KHB.

Construction of mutant receptors

Plasmids coding muscarinic and opioid receptors were obtained from Missouri S&T cDNA Resource Center (Rolla, MO, USA) and used to generate sequences with the desired amino acid substitution using Q5 Site-Directed Mutagenesis Kit (NEB, via BioTek, Praha, Czech Republic). Primers were designed using NEBaseChanger (https://nebasechanger.neb.com/). CHO-K1 cells were transfected with desired plasmids using linear polyethylenimine (PEI) (Polysciences, Germany). Approximately 2 million cells were seeded in 10 ml of 1:1 mixture of Dulbeco's modified Eagle's and Ham's F-12 with L-glutamine in a 100 mm Petri dish and incubated for 24 hours at 37°C in a humidified 5% CO_2 atmosphere. DNA and PEI were mixed in a 1:3 ratio (12 ug DNA per 1 ml PBS : 36 ug PEI per 1 ml PBS) and incubated at room temperature for 30 min. Then 1 ml of transfection mix was added to a dish and incubated for 16 hours at 37°C in humidified 5% CO_2 atmosphere, Then DMEM was removed and 8 ml of fresh DMEM was added and cells incubated for additional 24 hours.

[^{35}S]GTPγS binding

Measurement of [^{35}S]GTPγS binding was carried out on membranes in 96-well plates at 30°C in the incubation medium described above supplemented with freshly prepared dithiothreitol at a final concentration of 1 mM, essentially as described by [40]. Membranes at concentrations of 10 µg of protein per well were used. The final volume was 200 µl, the final concentration of [^{35}S]GTPγS was 500 pM and the final concentration of GDP was 50 µM. Non-specific binding was determined in the presence of 1 µM unlabelled GTPγS. Total GTP binding capacity was determined in the absence of GDP. Agonist was added 15 min before [^{35}S]GTPγS. Incubation with [^{35}S]GTPγS was carried out for 20 min and the free ligand was removed by filtration through GF/C glass-fibre filtration plates (Millipore or Unifilter) using a Brandel cell harvester (Brandel, Gaithersburg, MD, USA). Filtration and washing with ice-cold water lasted for 9 seconds. Filters were dried and then 40 µl of liquid scintillator Rotiszint was added to each well. The filtration plates were counted in a Wallac-Microbeta scintillation counter.

Saturation binding

Membranes (20 -50 µg of membrane proteins per sample) were incubated in 96-well plates for 3 h at 30°C in 800 µl (200 µl for κ-OR) of incubation medium with [^{3}H]deltrophin (δ-OR), [3H]diprenorphine (κ-OR), [^{3}H]DAMGO (µ-OR) or [^{3}H]N-methylscopolamine ([^{3}H]NMS, M_2 and M_4) at six concentrations of radioligand in two-fold dilutions. Nonspecific binding was determined in the presence of 10 µM Leu-enkephalin (opioid receptors) or 1 µM atropine (muscarinic receptors). Incubations were terminated by filtration through GF/C glass-fibre filtration plates (Millipore or Unifilter) using a Brandel cell harvester (Brandel, Gaithersburg, MD, USA). Filtration and washing with ice-cold water lasted for 6 seconds. Filters were dried and then 40 µl of liquid scintillator Rotiszint was added to each well. The filtration plates were counted in a Wallac-Microbeta scintillation counter.

Experimental data analysis

Experiments were independent. Functional assays were carried out in quadruplicates. After subtraction of non-specific binding, data were normalized to the total GTP binding capacity determined in each experiment. EC_{50} values were calculated as logarithms.

Parameters of a functional response were determined by fitting Eq. 1 to experimental data.

$$y = 1 + \frac{(E_{MAX}-1)x^{n_H}}{EC_{50}^{n_H}+x^{n_H}} \qquad \text{Eq. 1}$$

Where y is the functional response at a concentration of tested compound x, E_{MAX} is the maximal response to the tested compound, EC_{50} is the concentration causing half-efficient concentration and n_H is the slope factor (Hill coefficient).

Saturation binding experiments were carried out in triplicates. After subtraction of non-specific binding, data were converted to substance amounts and concentrations. Eq. 2 was fitted to data from saturation experiments.

$$y = \frac{x * B_{MAX}}{x + K_D} \qquad \text{Eq. 2}$$

Where y is the specific radioligand binding at a concentration of the radioligand x, B_{MAX} is the maximal binding capacity and K_D is the equilibrium dissociation constant of the radioligand.

Molecular modelling

Preparation of receptor structure

Structures of the M_2 and M_4 muscarinic acetylcholine 3UON, 4MQS, 5DSG and 8FX5 and μ, κ and δ opioid 4DKL, 5C1M, 6B73, 4DJH, 6PT2 and 4EJ4, A_{2A} adenosine 5IU4 and β_2 adrenergic 3D4S receptors were downloaded from RCSB Protein Data Bank (https://www.rcsb.org/). Non-protein molecules (except ligands) and nanobody or hydrolase parts of protein were deleted, and the resulting receptor protein was processed in Maestro using Protein Preparation Wizard according to Sastry et al. guidelines[42].

Coarse-grained MD

The coarse-grained MD was used to simulate the association of cholesterol with GPCRs[13]. The Martini force field[43] coarse-grain system consisting of the receptor immersed in a 20 nm x 20 nm patch of POPC (1-palmitoyl-2-oleoyl-sn-glycero-3-phosphocholine) membrane containing 30 % of cholesterol was created using CHARMM-GUI (charmm-gui.org)[44] Membrane-Builder[45] and Martini maker[46]. After minimization and equilibration of the system, 3 independent runs of 2 μs molecular dynamics using Gromacs 2018 were run[47].

Cholesterol re-docking

Molecules of cholesterol that associated with a receptor during coarse-grained MD (cgMD) were back-mapped onto receptor structure[14]. The resulting complexes were minimized in YASARA[48] and the cholesterol molecule was re-docked using the YASARA implementation of AutoDock[49]. The binding site was defined as a 5 Å extension in all directions to the cholesterol molecule and the AutoDock local search method was employed. All resulting poses were re-scored in YASARA by energy-minimisation of ligand pose and AutoDock VINA's local search, confined closely to the original ligand pose. The top-scoring pose was taken for further evaluation.

Simulation of molecular dynamics

The conventional molecular dynamics (cMD) of the top-scoring pose (one cholesterol molecule per simulation) of individual cholesterol-receptor complexes was simulated to evaluate cholesterol binding to the receptor and assess its interactions with the receptor and potential effects on ligand binding. Simulation of cMD was performed using Desmond/GPU ver. 6.5[50]. The simulated system consisted of the receptor-ligand-cholesterol complex in the POPC membrane in water and 0.15 M NaCl. The system was first relaxed by the standard Desmond protocol for membrane proteins and then 600 ns NPγT (Noose-Hover chain thermostat at 300 K, Martyna-Tobias-Klein barostat at 1.01325 bar, isotropic coupling, and Coulombic cutoff at 0.9 nm). The quality of molecular dynamics simulation was assessed by the Simulation Quality Analysis tools of Maestro and analysed by the Simulation Event Analysis tool. Ligand-receptor interactions were identified using the Simulation Interaction Diagram tool.

Acknowledgements

We thank Prof. Esam El-Fakahany, University of Minnesota and Dr. Vladimir Dolezal, Institute of Physiology CAS for the critical reading of the manuscript.

Author contributions

N.C. constructed mutants and performed measurements of functional responses. A.R. contributed to measurements of functional responses and data analysis. D.N. contributed to molecular modelling and measurements of functional response. J.J. conceived the experimental design, secured financing, performed molecular modelling and data analysis and finalized the manuscript. All authors contributed to the manuscript preparation and approved the final version.

Competing interests

The authors declare no competing interests.

Data availability

All relevant data are contained within the manuscript and supporting information.

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Supplementary Information: Cholesterol differentially modulates the activity of opioid and muscarinic receptors via common non-canonical binding site

Nikolai Chetverikov, Alena Janoušková-Randáková, Dominik Nelic, and Jan Jakubík*

Institute of Physiology CAS, Prague, Czech Republic

*, corresponding author, jan.jakubik@fgu.cas.cz

Supplementary Figures

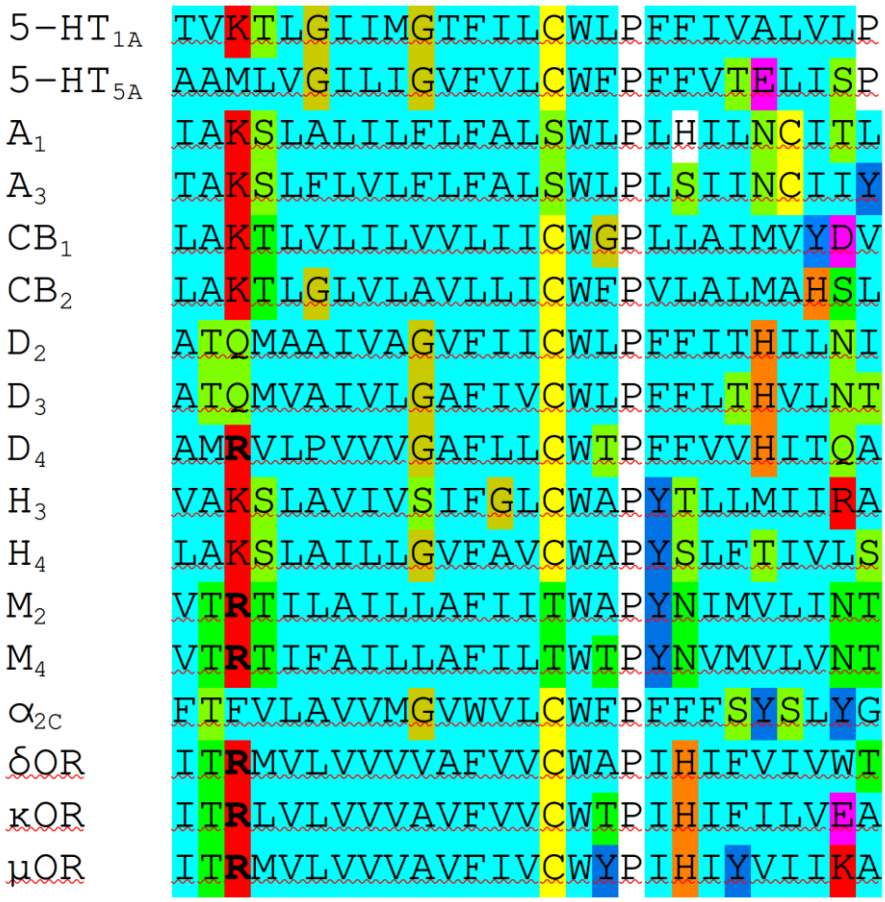

Figure S1 - Protein sequences of TM6

Aligned protein sequences of the sixth transmembrane α-helix (TM6) of selected $G_{i/o}$ coupled GPCRs of class A. Cyan, non-polar; green, polar; turquoise, aromatic polar; yellow, cysteine; gold, glycine; white, proline; magenta, acidic; red, basic amino acids. Bold, arginine.

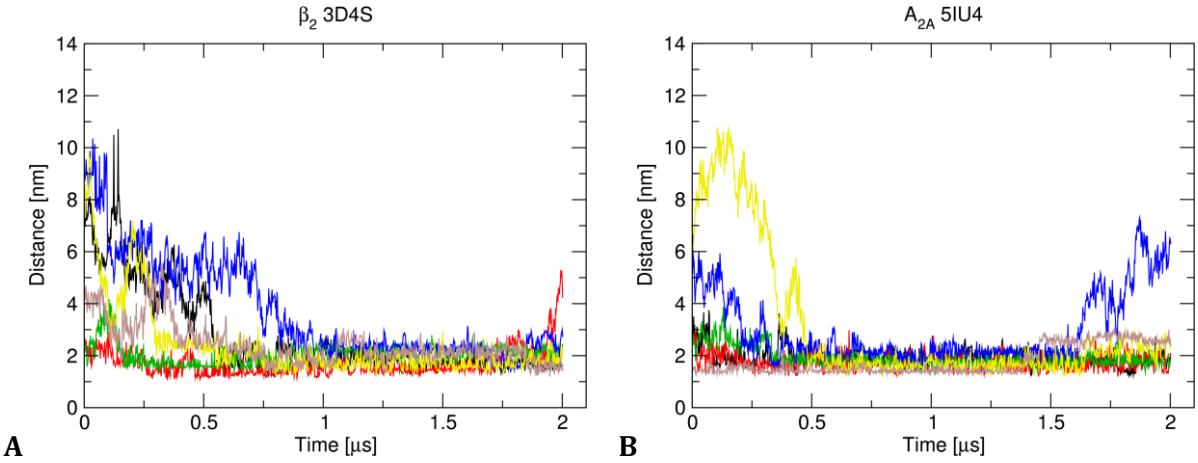

Figure S2 - Association of cholesterol with the β₂-adrenergic and A_{2A}-adenosine receptor
A*, association trajectories of six cholesterol molecules with the β₂-adrenergic receptor in an inactive conformation (PDB code: 3D4S).* ***B****, association trajectories of six cholesterol molecules with A_{2A}-adenosine receptor in an inactive conformation (PDB code: 5IU4). X-axis, duration of coarse-grained MD in µs. Y-axis, the distance of the centre of cholesterol molecule from the centre of the receptor. Data are representative of one out of three independent MD simulations.*

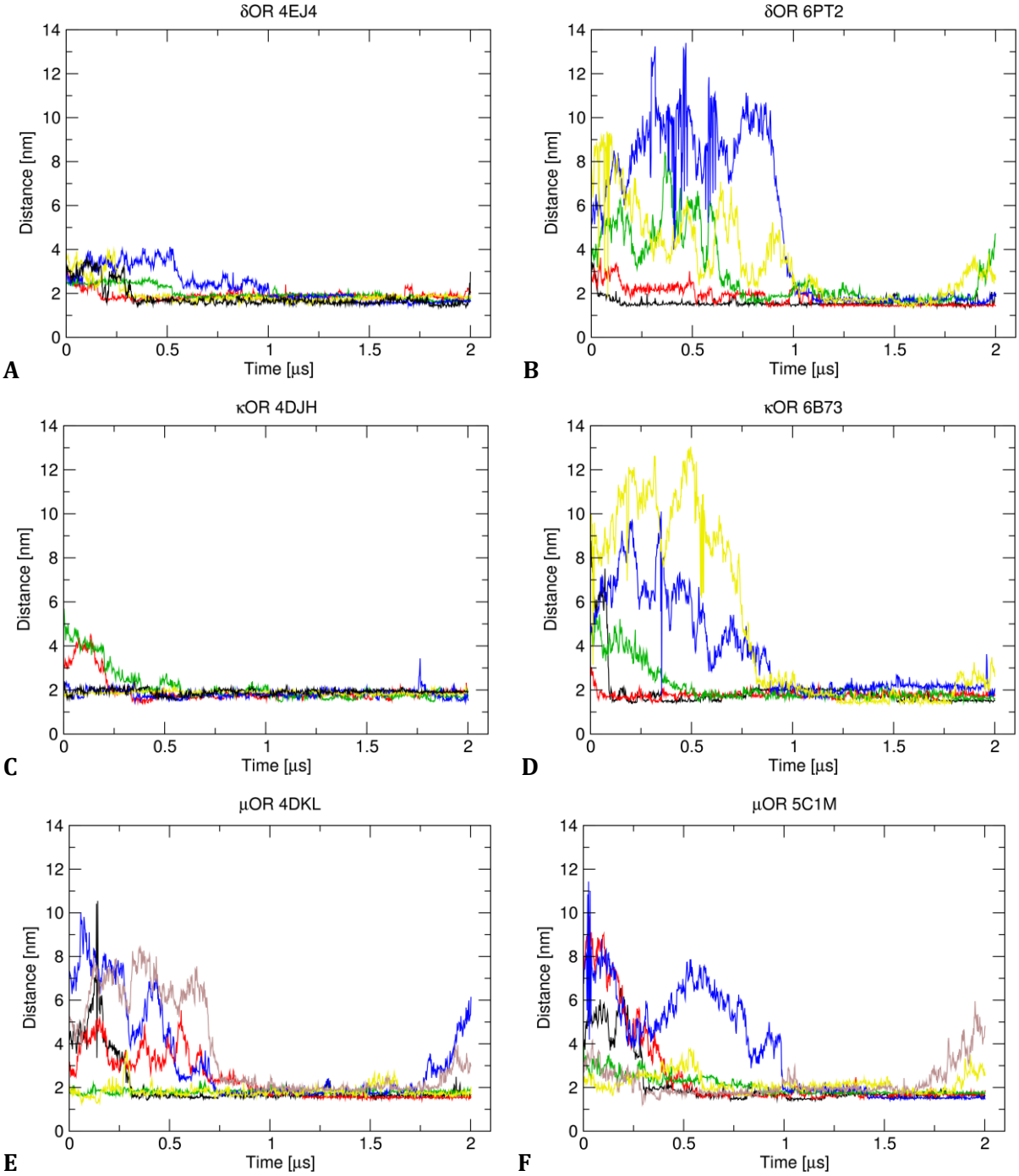

Figure S3 - Association of cholesterol with opioid receptors

*Association trajectories of five cholesterol molecules with the δ-opioid receptor in an inactive conformation (PDB code: 4EJH) (**A**) and an active conformation (PDB code: 6PT2) (**B**), the κ-opioid receptor in an inactive conformation (PDB code: 4EJH) (**C**) and in an active conformation (PDB code: 6PT2) (**D**), and the μ-opioid receptor in an inactive conformation (PDB code: 4EJH) (**E**) and an active conformation (PDB code: 6PT2) (**F**). X-axis, duration of coarse-grained MD in μs. Y-axis, the distance of the centre of cholesterol molecule from the centre of the receptor. Data are representative of one out of three independent MD simulations.*

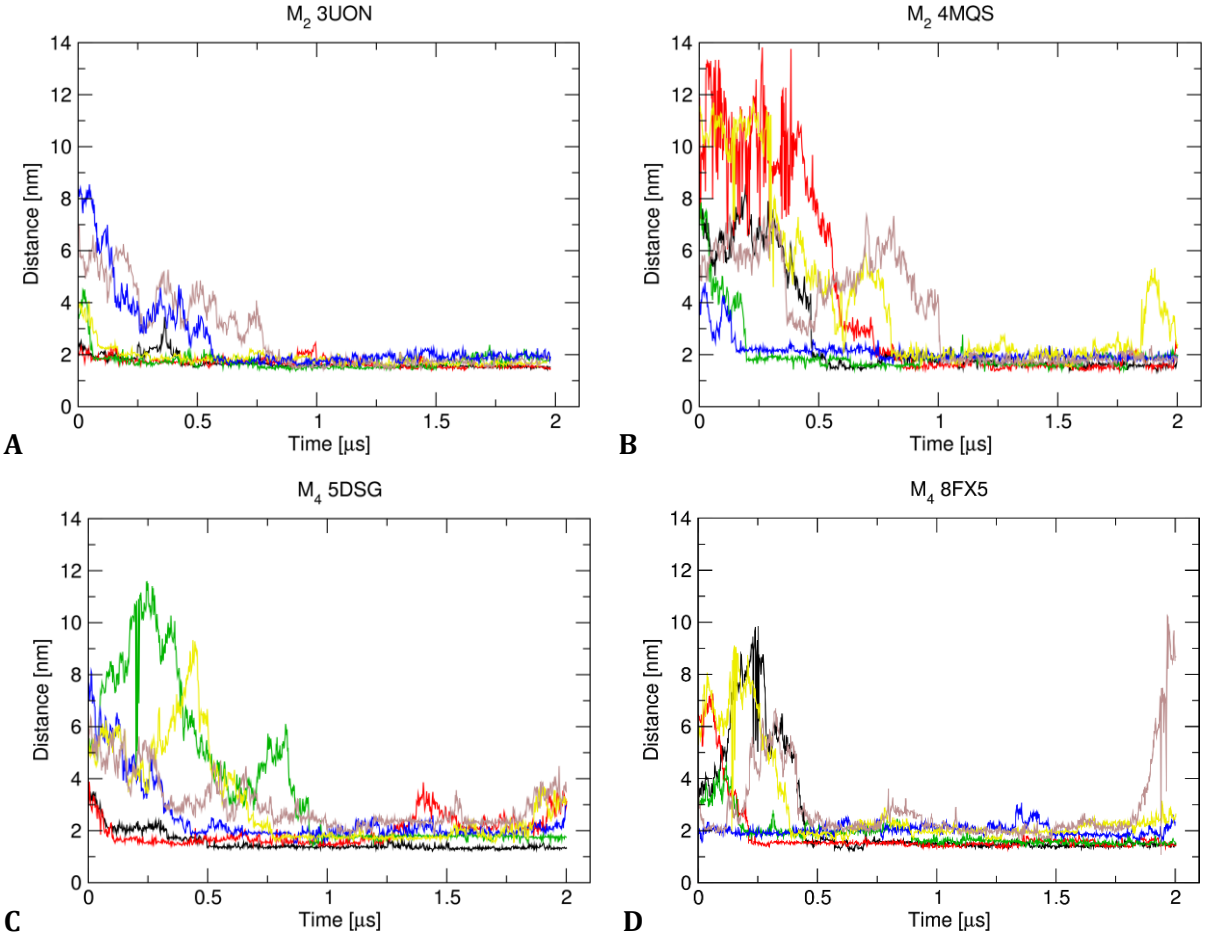

Figure S4 - Association of cholesterol with muscarinic receptors

*Association trajectories of six cholesterol molecules with M_2-muscarinic receptor in an inactive conformation (PDB code: 3UON) (**A**) and an active conformation (PDB code: 4MQS) (**B**) and M_4-muscarinic receptor in an inactive conformation (PDB code: 5DSG) (**C**) and an active conformation (PDB code> 8FX5) (**D**). X-axis, duration of coarse-grained MD in µs. Y-axis, the distance of the centre of cholesterol molecule from the centre of the receptor. Data are representative of one out of three independent MD simulations.*

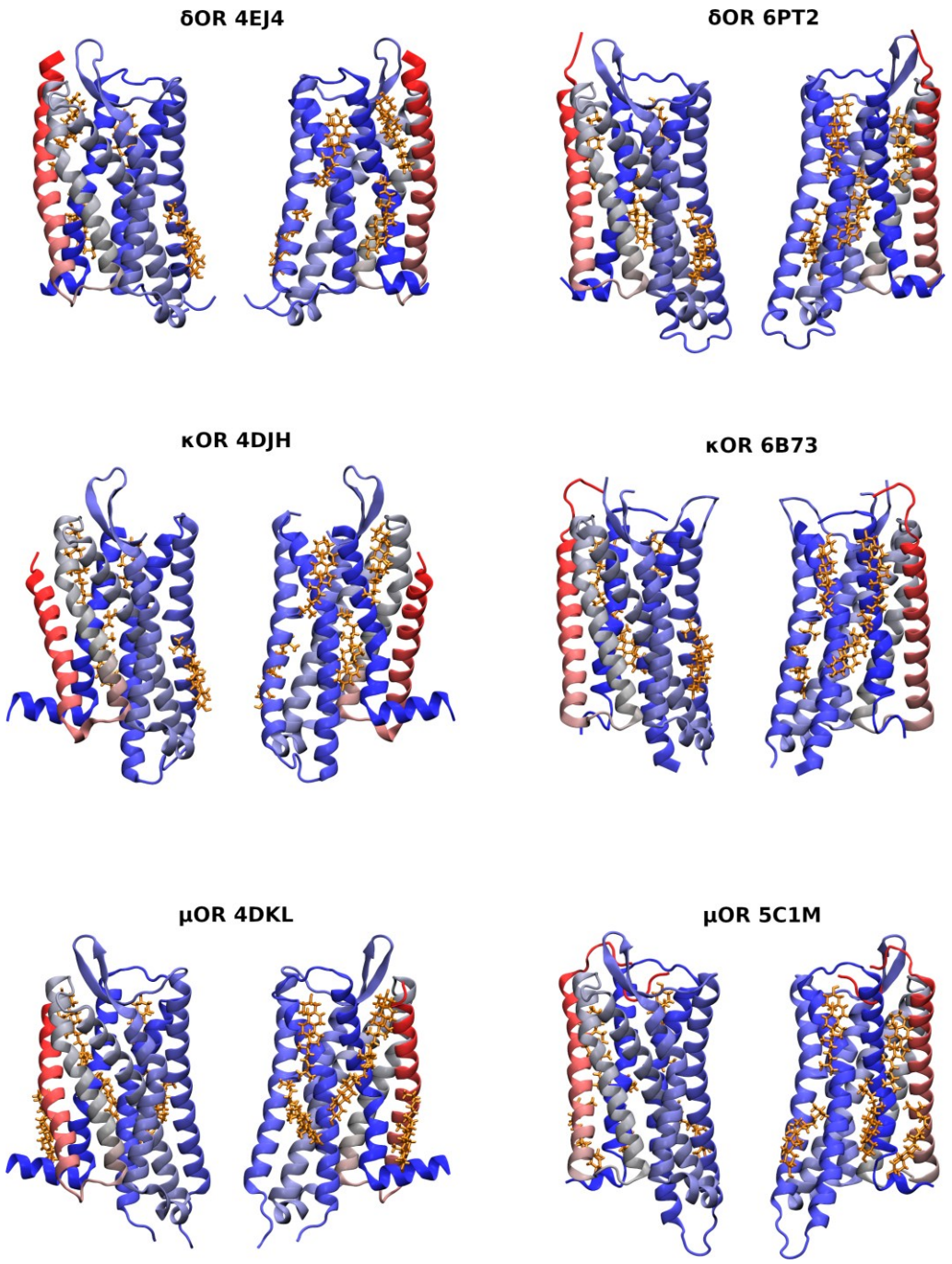

Figure S5 - Cholesterol binding to opioid receptors

Molecules of cholesterol that are associated with opioid and muscarinic receptors in an inactive or active conformation during cgMD were back-mapped and re-docked to the receptors. Cholesterol is gold. The receptor is in a red-grey-blue gradient. Orientation: extracellular up, TM3 (left) or TM6 (right) in front.

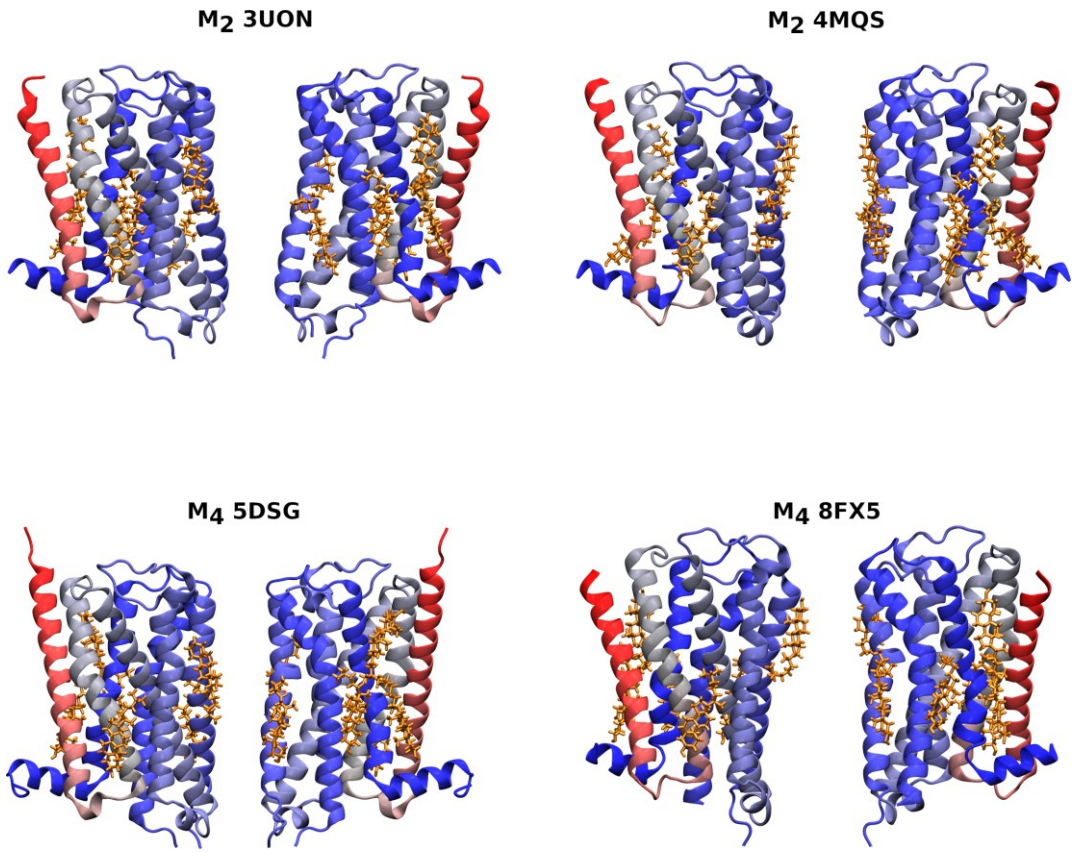

Figure S6 - Cholesterol binding to muscarinic receptors
Molecules of cholesterol that are associated with opioid and muscarinic receptors in an inactive or active conformation during cgMD were back-mapped and re-docked to the receptors. Cholesterol is gold. The receptor is in a red-grey-blue gradient. Orientation: extracellular up, TM3 (left) or TM6 (right) in front.

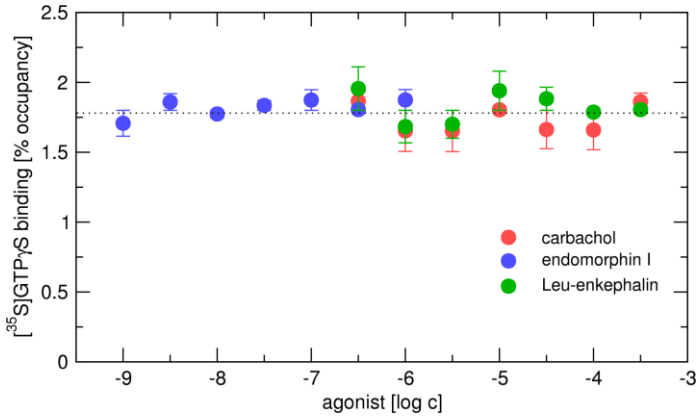

Figure S7 – Effects of agonists on GTPγS binding to non-transfected membranes
Effects of carbachol (red), endomorphin I (blue) and Leu-enkephalin (green) on [^{35}S]GTPγS binding to the membranes from CHO-K1 cells which were not transfected. Abscissa, the concentration of agonist is expressed as a decadic logarithm of molar concentration. Data are means ± SD from 3 independent experiments performed in quadruplicates.

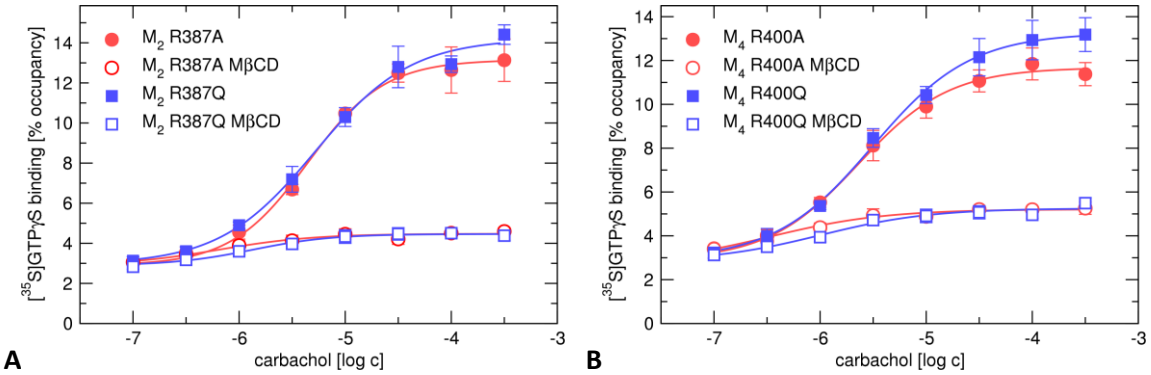

Figure S8 -Effects of cholesterol depletion on the functional response of mutated muscarinic receptors

Effects of membrane-cholesterol depletion (open symbols) on functional responses of mutated (red circles - $R^{6.35}$ to alanine; blue squares – $R^{6.35}$ to glutamine) M_2- (left) and M_4-muscarinic (right) receptors to carbachol. Ordinate, [^{35}S]GTPγS binding is expressed as % of occupancy of G-protein binding sites. Abscissa, the concentration of agonist is expressed as a decadic logarithm of molar concentration. Data are means ± SD from 3 independent experiments performed in quadruplicates.

Supplementary Tables

Table S1 Parameters of functional response to agonists at native and methyl-β-cyclodextrin-treated (MβCD) membranes.

EC_{50} values are expressed as negative decadic logarithms. E_{MAX} and basal values are expressed as % of occupancy of G-protein binding sites. Data are means ± SD from 3 independent experiments performed in quadruplicates.

	pEC_{50}			E_{MAX} [% occupancy]			Basal [% occupancy]		
δ-OR	7.87	±	0.08	10.65	±	0.38	1.92	±	0.07
δ-OR MβCD	7.86	±	0.02	7.35	±	0.07*	1.68	±	0.06*
κ-OR	4.82	±	0.06	10.1	±	0.29	2.5	±	0.08
κ-OR MβCD	4.57	±	0.05*	5.27	±	0.11*	2.4	±	0.08
μ-OR	7.75	±	0.05	11.55	±	0.28	2.09	±	0.07
μ-OR MβCD	7.89	±	0.07*	9.38	±	0.31*	1.18	±	0.05*
M_2	5.04	±	0.04	12.14	±	0.26	2.46	±	0.08
M_2 MβCD	5.23	±	0.04*	14.97	±	0.25*	2.9	±	0.09*
M_4	5.28	±	0.07	11.13	±	0.35	2.46	±	0.08
M_4 MβCD	5.72	±	0.02*	13.19	±	0.10*	2.9	±	0.09*

**, different from untreated (P<0.05, paired t-test)*

Table S2 Parameters of functional response to agonists at wild type ($R^{6.35}$) and mutated receptors.
EC_{50} values are expressed as negative decadic logarithms. E_{MAX} and basal values are expressed as % of occupancy of G-protein binding sites. Data are means ± SD from 3 independent experiments performed in quadruplicates.

	pEC_{50}			E_{MAX} [% occupancy]			basal [% occupancy]		
δ-OR $R^{6.35}$	7.55	±	0.09	10.75	±	0.58	1.92	±	0.05
δ-OR $A^{6.35}$	7.45	±	0.08	10.28	±	0.77	1.70	±	0.04*
δ-OR $Q^{6.35}$	7.37	±	0.07	9.07	±	0.99	1.68	±	0.04*
κ-OR $R^{6.35}$	5.28	±	0.02	9.56	±	0.79	2.50	±	0.07
κ-OR $A^{6.35}$	6.01	±	0.02*	5.03	±	0.27*	2.40	±	0.05
κ-OR $Q^{6.35}$	6.05	±	0.03*	6.75	±	0.49*	2.41	±	0.09
μ-OR $R^{6.35}$	7.75	±	0.09	11.61	±	1.35	2.09	±	0.08
μ-OR $A^{6.35}$	7.82	±	0.05	12.75	±	1.77	1.54	±	0.07*
μ-OR $Q^{6.35}$	7.64	±	0.06	7.92	±	1.01*	1.18	±	0.04*
M_2 $R^{6.35}$	5.05	±	0.03	12.16	±	0.10	2.46	±	0.07
M_2 $A^{6.35}$	5.26	±	0.05*	13.47	±	0.36*	2.89	±	0.10*
M_2 $Q^{6.35}$	5.23	±	0.03*	14.29	±	0.78*	2.90	±	0.09*
M_4 $R^{6.35}$	5.32	±	0.01	10.59	±	0.13	2.46	±	0.08
M_4 $A^{6.35}$	5.60	±	0.04*	11.79	±	0.08*	2.89	±	0.10*
M_4 $Q^{6.35}$	5.53	±	0.01*	13.28	±	0.69*	2.90	±	0.09*

**, different from wild type (P<0.05 after Bonferroni correction, paired t-test)*

Table S3 Parameters of functional response to agonists at mutated receptors.
EC_{50} values are expressed as negative decadic logarithms. E_{MAX} and basal values are expressed as % of occupancy of G-protein binding sites. Data are means ± SD from 3 independent experiments performed in quadruplicates.

	pEC_{50}			E_{MAX} [% occupancy]			basal [% occupancy]		
M_2 $A^{6.35}$	5.26	±	0.02	13.55	±	0.29	2.90	±	0.04
M_2 $A^{6.35}$ MβCD	6.17	±	0.03*	4.46	±	0.20*	2.88	±	0.04
M2 $Q^{6.35}$	5.26	±	0.02	14.07	±	1.01	2.94	±	0.01
M2 $Q^{6.35}$ MβCD	5.73	±	0.01*	4.50	±	0.22*	2.89	±	0.03
M4 $A^{6.35}$	5.64	±	0.02	11.71	±	0.93	2.89	±	0.04
M4 $A^{6.35}$ MβCD	6.50	±	0.02*	5.11	±	0.01*	2.71	±	0.02*
M4 $Q^{6.35}$	5.50	±	0.02	13.40	±	0.60	2.92	±	0.02
M4 $Q^{6.35}$ MβCD	5.89	±	0.02*	5.22	±	0.10*	2.82	±	0.02*

**, different from untreated (P<0.05, paired t-test)*