

## Perspectives

## Cholesterol footprint in high-resolution structures of serotonin receptors: Where are we now and what does it mean?

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## ABSTRACT

An emerging feature of several high-resolution GPCR structures is the presence of closely bound cholesterol molecules. In this Perspective, we share the excitement of the recent advancements in GPCR structural biology. We further highlight our laboratory's journey in comprehensively elucidating functional sensitivity of GPCRs (using the serotonin<sub>1A</sub> receptor as a representative neurotransmitter GPCR) to membrane cholesterol and validation using a variety of assays and molecular dynamics simulations. Although high-resolution structures of many GPCRs have been reported in the last few years, the structure of the serotonin<sub>1A</sub> receptor proved to be elusive for a long time. Very recently the cryo-EM structure of the serotonin<sub>1A</sub> receptor displaying 10 bound cholesterol molecules has been reported. We conclude by providing a critical analysis of caveats involved in GPCR structure determination.

Serotonin (5-hydroxytryptamine, 5-HT) receptors are a large family of receptors involved in regulating a diverse array of physiological signaling pathways in organisms that span a wide evolutionary range. Except the members of the serotonin<sub>3</sub> receptor subfamily which act as ligand-gated ion channels, all other serotonin receptors belong to the family of seven transmembrane domain G protein-coupled receptors (GPCRs) (Nichols and Nichols, 2008; Sarkar et al., 2018, 2021; Barnes et al., 2021). Serotonin receptors constitute the largest class of non-odorant GPCRs (Nichols and Nichols, 2008) and predate the emergence of other biogenic amine receptors (Peroutka and Howell, 1994). Among the members of serotonin receptors belonging to the GPCR superfamily, the serotonin<sub>1A</sub> receptor occupies a central position due to a number of reasons (Pucadyil et al., 2005a; Lacivita et al., 2008; Fiorino et al., 2014; Sarkar et al., 2018). For example, it was the first serotonin receptor to be cloned, sequenced and antibodies were raised against it (Fargin et al., 1988). Another factor that helped is the early availability of a selective agonist, 8-hydroxy-2-(di-*N*-propylamino)tetralin (8-OH-DPAT), that allowed biochemical, physiological and pharmacological analysis of the serotonin<sub>1A</sub> receptor (Gozlan et al., 1983). Importantly, the serotonin<sub>1A</sub> receptor also represents a popular drug target (Lacivita et al., 2008; Fiorino et al., 2014).

In the late 1990's, one of us (A.C.) became interested in lipid interactions of GPCRs. Till then, there were very few reports on this topic in the literature. However, it was well known by that time that integral

membrane proteins such as Ca<sup>2+</sup>/Mg<sup>2+</sup>-ATPase (London and Feigenson, 1981; Simmonds et al., 1982) and ion channels such as the nicotinic acetylcholine receptor (Criado et al., 1984; Fong and McNamee, 1986) exhibit lipid-dependent function due to lipid-protein interactions. The GPCR of interest was a recently 'deorphanized' GPCR (Fargin et al., 1988), namely, the serotonin<sub>1A</sub> receptor. As mentioned above, this receptor attained appreciable popularity in a few years after its discovery due to its key role in serotonergic signaling, anxiety and depression, and as a drug target (Müller et al., 2007; Lacivita et al., 2008; Fiorino et al., 2014). For example, knockout mice lacking the serotonin<sub>1A</sub> receptor and displaying increased anxiety-related behavior were simultaneously generated by several groups and the resulting publications appeared in the same year, even in the same journal (Heisler et al., 1998; Parks et al., 1998; Ramboz et al., 1998). Importantly, these results showed how a single gene knockout could alter complex behavior and offered relevant animal models for conditions such as anxiety disorders and aggression (Gingrich and Hen, 2001). The choice of this receptor therefore appeared to be appropriate from a functional perspective.

Although the serotonin<sub>1A</sub> receptor enjoyed a functional advantage, literature on its structure and lipid interaction was missing at this point (the first GPCR structure, that of rhodopsin, appeared in 2000 (Palczewski et al., 2000)). Our initial hunch of exploring cholesterol sensitivity of the serotonin<sub>1A</sub> receptor had its origin in two (unconnected at that point) facts: (i) localization of the serotonin<sub>1A</sub> receptor in several

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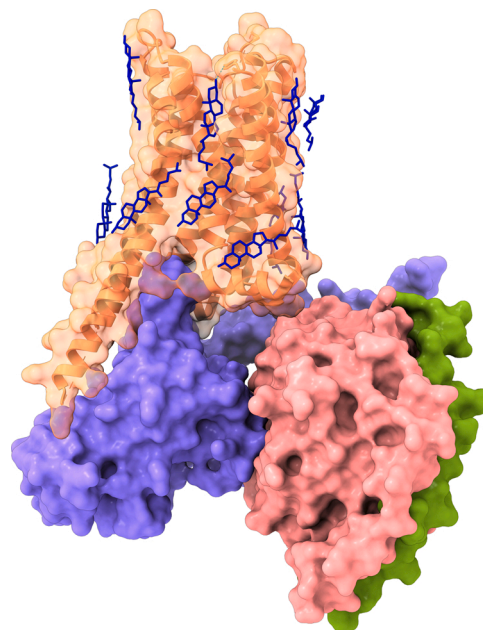
regions of the brain detected by mRNA (Kobilka et al., 1987; Albert et al., 1990; Chalmers and Watson, 1991), and (ii) the important physiological role of brain cholesterol (Dietschy and Turley, 2001; Chattopadhyay and Paila, 2007). Our early experiments showed that depletion of cholesterol from membrane preparations from hippocampal tissue, an excellent source of the serotonin<sub>1A</sub> receptor, using methyl- $\beta$ -cyclodextrin (M $\beta$ CD), a soluble sterol carrier that can be effectively used to physically deplete membrane cholesterol (Zidovetzki and Levitan, 2007; Mahammad and Parmryd, 2015; Jafurulla et al., 2019), resulted in a concentration-dependent loss in ligand binding and G-protein coupling of the serotonin<sub>1A</sub> receptor (Pucadyil and Chattopadhyay, 2004, 2005). The change in ligand binding could be reversed upon replenishment of cholesterol using M $\beta$ CD-cholesterol complex, thereby implying that the changes were indeed due to cholesterol depletion. Our initial hypothesis was that membrane cholesterol at certain sites in the receptor was instrumental in maintaining an active conformation (capable of ligand binding). To validate that this was indeed the underlying mechanism behind cholesterol-dependent activity of the serotonin<sub>1A</sub> receptor, in the next step, we carried out a series of experiments to test this hypothesis. These included experiments using (i) cholesterol oxidase which oxidizes cholesterol to cholestenone (Pucadyil et al., 2005b), (ii) sterol-complexing agents such as nystatin (Pucadyil et al., 2004) and sterol-binding detergents like digitonin (Paila et al., 2005), and (iii) eventually metabolic inhibition of cholesterol biosynthesis using proximal and distal inhibitors (Paila et al., 2008; Shrivastava et al., 2010). The common underlying theme behind all these experiments was to prevent receptor-cholesterol interaction by oxidizing, sequestering and binding of cholesterol, or inhibiting its biosynthesis (Pucadyil and Chattopadhyay, 2006; Paila and Chattopadhyay, 2010). Since all these diverse treatments resulted in loss of receptor activity, we concluded that membrane cholesterol is necessary for the function of the serotonin<sub>1A</sub> receptor, irrespective of the actual experimental strategy by which cholesterol-receptor interaction was prevented. Another group around this time reported that cholesterol depletion using M $\beta$ CD lead to attenuation of signaling of the serotonin<sub>1A</sub> receptor (Sjögren et al., 2008).

In general, lipid sensitivity of membrane proteins and receptors is believed to originate either due to direct interaction of cholesterol with the membrane protein (specific effect) or due to lipid-induced modulations of membrane physical properties (general effect) (Lee, 2005; Paila and Chattopadhyay, 2009). Our interpretation of the above results made us propose that the cholesterol sensitivity of the serotonin<sub>1A</sub> receptor was due to closely interacting cholesterol molecules (Paila et al., 2009). How does one ‘see’ such closely located cholesterol molecules in the receptor structure? This became possible with the availability of increasingly high-resolution crystal structures (subsequently, cryo-EM structures) of GPCRs. Although individual lipid molecules could be observed in high-resolution crystal structures of membrane proteins since late 1990’s (Luecke et al., 1999; Gonen et al., 2005), generating high-resolution structures of GPCRs turned out to be more challenging. This is due to the inherent conformational plasticity (flexibility) exhibited by GPCRs. Whereas this structural plasticity is vital for the functional diversity exhibited by GPCRs, it poses considerable challenge for structural biology of GPCRs. A number of approaches have been utilized to tackle this problem (Ghosh et al., 2015). These include stabilizing the flexible regions of GPCRs using monoclonal antibody (Day et al., 2007), replacing the dynamic third intracellular loop with lysozyme (Cherezov et al., 2007; Rosenbaum et al., 2007) or more recently, a nanobody (Manglik et al., 2017). With these advancements, more high-resolution structures of GPCRs started emerging from 2007 onward (Cherezov et al., 2007; Rosenbaum et al., 2007; Hanson et al., 2008). A novel feature of many of these GPCR structures was the presence of closely bound cholesterol molecules (Jafurulla and Chattopadhyay, 2013; Chattopadhyay, 2014). For example, structures of the  $\beta_2$ -adrenergic receptor (Cherezov et al., 2007; Hanson et al., 2008), A<sub>2A</sub> adenosine receptor (Liu et al., 2012) and metabotropic glutamate receptor 1

(Wu et al., 2014) displayed bound cholesterol molecules. These observations gave rise to the question: how important are these bound cholesterol molecules for cholesterol-sensitive function of these GPCRs? As we write this Perspective, the list of GPCRs displaying bound cholesterol molecules has gone up significantly (~40 % of published GPCR structures display bound cholesterol molecule(s) (Sarkar and Chattopadhyay, unpublished observations)).

In spite of the fact that the serotonin<sub>1A</sub> receptor was one of the first GPCRs whose function was shown to be modulated by cholesterol (Pucadyil and Chattopadhyay, 2004, 2005), the structure of the serotonin<sub>1A</sub> receptor became available only recently (Xu et al., 2021). Interestingly, the high-resolution cryo-EM structure of the apo-form of the serotonin<sub>1A</sub> receptor shows the maximum number of bound cholesterol molecules (10 per receptor monomer) in its structure (see Fig. 1). The other structures reported in this paper include the serotonin-bound and aripiprazole-bound forms with 4 and 3 molecules of bound cholesterol, respectively. Whereas these are interesting observations, the biological relevance of this diversity in bound cholesterol molecules is not apparent at this point. Importantly, in a recent work from our laboratory (Kumar et al., 2021), we showed using all-atom molecular dynamics simulations that a cholesterol molecule is found near a cholesterol recognition/interaction amino acid consensus (CRAC) motif (see later) in a position almost identical to the one reported in the cryo-EM structure of the serotonin<sub>1A</sub> receptor (PDB ID: 7E2X). It is envisioned that with more reports of well-resolved GPCR structures with bound cholesterol molecule(s), accompanied with more information on their function, could help generate certain pattern in this large, diverse and emerging structural database.

Although the structure of the serotonin<sub>1A</sub> receptor took a relatively long time to be solved, high-resolution structures of other members of the serotonin family of GPCRs have emerged since 2013. At present, there are 25 solved structures of 7 serotonin receptor subtypes (belonging to the serotonin GPCR family) are reported. Table 1 shows a



**Fig. 1. Bound cholesterol molecules in the crystal structure of the human serotonin<sub>1A</sub> receptor.** Model of the apo-serotonin<sub>1A</sub> receptor-G<sub>i</sub> complex showing multiple (a total of 10) cholesterol molecules (represented as blue sticks) bound to the surface of the serotonin<sub>1A</sub> receptor (represented as orange semi-transparent surface). The G<sub>i</sub> complex is shown as surface (G $\alpha_{11}$  in light blue, G $\beta_1$  in pink and G $\gamma_2$  in green). The snapshot of cholesterol-bound structure of the serotonin<sub>1A</sub> receptor was generated from its cryo-EM structure (Xu et al., 2021) (PDB: 7E2X) using UCSF ChimeraX (<https://www.rbvi.ucsf.edu/chimera/>) (Pettersen et al., 2021).

**Table 1**  
Current Available Structures of Serotonin Receptors<sup>a</sup>.

Receptor	# <sup>b</sup>	Method	PDB	Resolution (Å)	Bound ligand/effector	Missing structural region(s)	Refs.
Serotonin <sub>1A</sub>	3	cryo-EM	7E2X	3.0	(apo)/G $\alpha_{i1}\beta_{1\gamma 2}$	N	Xu et al., 2021
		cryo-EM	7E2Y	3.0	Serotonin/G $\alpha_{i1}\beta_{1\gamma 2}$	N	Xu et al., 2021
		cryo-EM	7E2Z	3.1	Aripiprazole/G $\alpha_{i1}\beta_{1\gamma 2}$	N	Xu et al., 2021
		x-ray	4IAQ	2.8	Dihydroergotamine	N, ICL3	Wang et al., 2013
Serotonin <sub>1B</sub>	5	x-ray	4IAR	2.7	Ergotamine	N, ICL3	Wang et al., 2013
		x-ray	5V54	3.9	Methiothepin	N, ICL3	Yin et al., 2018
		cryo-EM	6G79	3.78	Donitriptan/G $\alpha_{o1}\beta_{1\gamma 2}$	N	Garcia-Nafria et al., 2018
		x-ray	7C61	3.0	Ergotamine	N, ICL3	Miyagi et al., 2020
Serotonin <sub>1D</sub>	1	cryo-EM	7E32	2.9	Serotonin/G $\alpha_{i1}\beta_{1\gamma 2}$	N, ICL3	Xu et al., 2021
Serotonin <sub>1E</sub>	1	cryo-EM	7E33	2.9	BRL-54443/G $\alpha_{i1}\beta_{1\gamma 2}$	N, ICL3	Xu et al., 2021
Serotonin <sub>2A</sub>	5	x-ray	6A93	3.0	Risperidone	N, C, ICL3	Kimura et al., 2019
		x-ray	6A94	2.9	Zotepine	N, C, ICL3	Kimura et al., 2019
		x-ray	6WGT	3.4	LSD	N, C, ICL3	Kim et al., 2020
		x-ray	6WH4	3.4	Methiothepin	N, C, ICL3	Kim et al., 2020
Serotonin <sub>2B</sub>	8	cryo-EM	6WHA	3.36	25-CN-NBOH/G $\alpha_{q}\beta_{1\gamma 2}$	N, C	Kim et al., 2020
		x-ray	4IB4	2.7	Ergotamine	N, C, ICL3	Wacker et al., 2013
		x-ray	4NC3	2.8	Ergotamine	N, C, ICL3	Liu et al., 2013
		x-ray	5TUD	3.0	Ergotamine	N, C, ICL3	Ishchenko et al., 2017
		x-ray	5TVN	2.9	LSD	N, C, ICL3	Wacker et al., 2017
		x-ray	6DRX	3.1	Lisuride	N, C, ICL3	McCorvy et al., 2018
		x-ray	6DRY	2.92	Methylergonovine	N, C, ICL3	McCorvy et al., 2018
		x-ray	6DRZ	3.1	Methysergide	N, C, ICL3	McCorvy et al., 2018
Serotonin <sub>2C</sub>	2	x-ray	6DS0	3.19	LY266097	N, C, ICL3	McCorvy et al., 2018
		x-ray	6BQG	3.0	Ergotamine	N, C, ICL3	Peng et al., 2018
		x-ray	6BQH	2.7	Ritanserlin	N, C, ICL3	Peng et al., 2018

<sup>a</sup> Abbreviations: N, N-terminus; C, C-terminus; ICL3, intracellular loop 3; cryo-EM, cryo-electron microscopy; x-ray, x-ray diffraction; BRL-54443, 5-hydroxy-3-(1-methylpiperidin-4-yl)-1H-indole; LSD, lysergic acid diethylamide; 25-CN-NBOH, 2-[(2-(4-cyano-2,5-dimethoxyphenyl)ethylamino)methyl]phenol; LY266097, 1-[(2-Chloro-3,4-dimethoxyphenyl)methyl]-2,3,4,9-tetrahydro-6-methyl-1H-pyrido[3,4-b]indole hydrochloride.

<sup>b</sup> Number of available structures.












detailed breakdown of this data. Table 2 shows available serotonin receptor structures with bound cholesterol molecule(s) as representative snapshots. The table shows that the number of bound cholesterol molecules vary between 1 (serotonin<sub>1D</sub> and serotonin<sub>2B</sub> receptors) and 10 (serotonin<sub>1A</sub> receptor, the apo-form). As individual GPCRs are characterized with multiple structures (bound to various ligands, depending on their functional state), we observe multiple available cholesterol-bound structures for serotonin<sub>1A</sub>, serotonin<sub>2A</sub> and serotonin<sub>2B</sub> receptors, with the serotonin<sub>2B</sub> receptor displaying maximum number (a total of 7) structures.

Lipid molecules which are co-crystallized with membrane proteins are often localized in protein-protein interfaces in oligomeric proteins and have been termed as 'nonannular' lipids (Lee, 2003). This prompted us to speculate that bound cholesterol molecules in GPCR structures could be occupying nonannular sites (Paila et al., 2009). Nonannular lipid sites typically display lack of accessibility to the annular lipids, i.e., these sites cannot be displaced in a competition with annular lipids. Subsequently, coarse-grain molecular dynamics simulations showed that cholesterol binding sites in GPCRs could be located deep in the hydrophobic interior of the receptor (Genheden et al., 2017). If GPCRs show bound cholesterol in their structures, what are the specific sites where cholesterol gets bound? This question has been around even before the arrival of a relatively large number of high-resolution GPCR structures. One of the first GPCR structure that addressed this issue was of the human  $\beta_2$ -adrenergic receptor (Hanson et al., 2008). In this work, two cholesterol molecules were observed in a specific cholesterol binding site, defined as the *strict* cholesterol consensus motif (CCM), formed by transmembrane helices 1-4 (TM1-4) which consists of four critical amino acids in two transmembrane helices (TM2 and 4) (Hanson et al., 2008). On the other hand, CRAC motifs were discovered much before as a linear sequence motif implicated in the interaction of cholesterol with membrane proteins such as the peripheral-type benzodiazepine receptor (Li and Papadopoulos, 1998) and caveolin-1 (Epanand et al., 2005; Epanand, 2006). The CRAC motif consists of a linear sequence of amino acids from the N-terminal to C-terminal direction. The sequence of amino acids follows the order: a branched nonpolar

leucine (or valine), followed by 1-5 amino acids (no preference), an aromatic tyrosine residue, another segment of 1-5 amino acids (no preference), and lastly, a basic lysine (or arginine) residue [(L/V)-(X)<sub>1-5</sub>-Y-(X)<sub>1-5</sub>-(R/K)]. The concept of CRAC motifs was further refined by invoking another type of CRAC motif, termed the CARC motif, that is oriented in an opposite direction of the polypeptide chain (Baier et al., 2011; Fantini and Barrantes, 2013; Fantini et al., 2016, 2019; Jafurulla et al., 2019). We reported the presence of CRAC motifs in several GPCRs (the serotonin<sub>1A</sub> receptor, the  $\beta_2$ -adrenergic receptor and rhodopsin) that exhibit cholesterol-sensitive function (Jafurulla et al., 2011). In case of the serotonin<sub>1A</sub> receptor, our analysis showed the presence of CRAC motifs in TM2, TM5 and TM7. Subsequently, presence of CRAC motif was reported for type-1 cannabinoid (CB<sub>1</sub>) receptor (Oddi et al., 2011). Interestingly, coarse-grain molecular dynamics simulations of the serotonin<sub>1A</sub> receptor showed preferential (dynamic) occupancy of membrane cholesterol in some of the CRAC sites in the serotonin<sub>1A</sub> receptor (Sengupta and Chattopadhyay, 2012). For a comprehensive account of cholesterol binding motifs in GPCRs, see Sarkar and Chattopadhyay, 2020.

To provide mechanistic insights into cholesterol sensitivity for the serotonin<sub>1A</sub> receptor, we recently examined the molecular basis of cholesterol sensitivity of the receptor function by mutating various key residues in the CRAC motifs of the receptor and monitoring corresponding functional readout (cAMP signaling) (Kumar et al., 2021). These results were complemented by all-atom molecular dynamics simulations. The take-home of our work is that the functional sensitivity of the serotonin<sub>1A</sub> receptor to membrane cholesterol is lost when the residue K101 in a CRAC motif in TM2 is mutated, indicating the role of K101 as a molecular sensor of membrane cholesterol. To the best of our knowledge, our results constitute one of the first reports that comprehensively demonstrated that cholesterol sensitivity could be knocked out by a single point mutation in a specific cholesterol binding site. We believe that future work on cholesterol-sensitive GPCR function using a combination of experimental (such as site-directed mutagenesis followed by measurement of cellular signaling) and computational approaches could be helpful in identifying structural features in receptor

**Table 2**  
Serotonin Receptor Structures with Bound Cholesterol<sup>a</sup>.

Receptor	PDB	Snapshot <sup>b</sup>	#Chol <sup>c</sup>	Refs.	Refs. for cholesterol-sensitive function
Serotonin <sub>1A</sub>	7E2X		10	Xu et al., 2021	Pucadyil and Chattopadhyay, 2004, 2005, 2007 Pucadyil et al., 2005b Paila et al., 2008 Sjögren et al., 2008 Shrivastava et al., 2010 Gutierrez et al., 2016 Jafurulla et al., 2017 Kumar and Chattopadhyay, 2020, 2021 Sarkar et al., 2020
	7E2Y		4		
	7E2Z		3		
Serotonin <sub>1D</sub>	7E32		1	Xu et al., 2021	Not available
Serotonin <sub>2A</sub>	6A93 6A94		2 2 (1/monomer)	Kimura et al., 2019	Sommer et al., 2009 Ludka et al., 2014
	6WGT		2	Kim et al., 2020	
	6WH4		2 (1/monomer)		
Serotonin <sub>2B</sub>	4IB4		1	Wacker et al., 2013	Not available
	4NC3		1	Liu et al., 2013	
	5TVN		1	Wacker et al., 2017	
	6DRX 6DRY 6DRZ 6DS0		1 1 1 1	McCorvy et al., 2018	

<sup>a</sup> Data generated by searching the PDB database for serotonin receptor structures with cholesterol as a small molecule ligand.

<sup>b</sup> Snapshots of cholesterol-bound structure of serotonin receptors (cholesterol in orange and receptor in blue) were generated using UCSF ChimeraX (Pettersen et al., 2021).

<sup>c</sup> Number of cholesterol molecules per PDB structure.

that are responsible for cholesterol sensitivity.

These recent developments on the presence of closely bound cholesterol molecules in high-resolution GPCR structures are exciting, yet its biological relevance is still emerging (Chattopadhyay, 2014). A major reason for this is that data on cholesterol-sensitivity of many GPCRs are simply not available yet (e.g., see Table 2 for cholesterol-sensitive members of the serotonin receptor family). In addition, there are certain factors involving heavy protein engineering to aid GPCR crystallization needs to be sorted out in this context (Ghosh et al., 2015). In spite of the fact that the extramembranous regions (loops) of GPCRs are critical in GPCR function and signaling (Turner et al., 2004; Wheatley et al., 2012; Pal and Chattopadhyay, 2019; Kharche et al., 2021), the flexible loops corresponding to these regions are usually stabilized using monoclonal antibody (Day et al., 2007), or

replaced with lysozyme (Cherezov et al., 2007; Rosenbaum et al., 2007), or a nanobody (Manglik et al., 2017) in the available structures. Additionally, structure determination of GPCRs is commonly carried out using a heavily engineered (mutated for thermal stability) receptor. Further, structure determinations are often carried out in detergent dispersions (micelles) or lipidic cubic phases (not in membrane bilayers). Although micelles could mimic many properties of lipid bilayers, the conformations of GPCRs in the micellar environment could differ from that in the membrane bilayer due to intrinsic difference in the radius of curvature (the micellar surface has a much larger curvature than the bilayer) (Mukherjee and Chattopadhyay, 1994). In addition, the membrane interface (a crucial part of the bilayer in terms of membrane organization, dynamics and function (Haldar et al., 2011; Pal and Chattopadhyay, 2017)) differs from the micellar interface which is much

thinner. On the other hand, although lipidic cubic phase membranes are popular for GPCR crystallization (Caffrey, 2015), the physiological significance of bound cholesterol molecules in GPCR crystal structures in lipidic cubic phases is still emerging (Khelashvili et al., 2012). It is possible that the bound cholesterol molecules observed in GPCRs in lipidic cubic phases could represent aspects of membrane lipid environment specifically in lipidic cubic phases (different from lamellar bilayer phases). Another caveat is that GPCR structures are often determined by crystallization (or cryo-EM) in lipidic cubic phases (or micelles) containing cholesterol hemisuccinate (CHS), which is used to replace cholesterol in the receptor. A number of studies addressing the ability of CHS to mimic cholesterol (Kulig et al., 2014, 2015; Augustyn et al., 2019) suggests that it could depend on actual experimental conditions and it appears that the jury is still out on this topic.

Taken together, it appears that whereas bound cholesterol molecules in emerging high-resolution GPCR structures are indeed exciting, it would perhaps be prudent to exercise sufficient caution in extrapolating bound cholesterol in GPCR structures to their cholesterol-sensitive function. The road ahead could lie in mutating specific residues of GPCRs and actually monitoring their function in a cholesterol-dependent fashion. However, this does not rule out early pointers from bound cholesterol molecules in GPCRs as an indication of functionally relevant cholesterol molecules. In any event, a comprehensive understanding of cholesterol-sensitive function of GPCRs, using a judicious combination of experimental and computational approaches, could lead to a better understanding of GPCR function in health and disease, and better therapeutics since GPCRs represent major drug targets (Sriram and Insel, 2018; Chan et al., 2019). So far as the serotonin<sub>1A</sub> receptor is concerned, the recent availability of high-resolution structures (Table 2) displaying bound cholesterol molecules provides a novel platform to set up experiments addressing the role of cholesterol in its diverse cholesterol-sensitive function, including recently reported receptor endocytosis and trafficking (Kumar and Chattopadhyay, 2020, 2021). Viewed from this perspective, the next few years could be exciting in this research area.

## Declaration of Competing Interest

The authors report no declarations of interest.

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