

Cryo-EM structures of a pentameric ligand-gated ion channel in liposomes

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The reported cryo-EM imaging of a pentameric ligand-gated ion channel in liposomes as opposed to nanodiscs has both broad implications and contributes **valuable** methodological advances to the structural investigation of membrane receptors. The comparison of structures assigned to distinct functional states in liposomes versus nanodiscs is **convincing** and will aid membrane protein structural biologists in selection of functionally relevant membrane reconstitution environments.

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Abstract

Detergents and lipid nanodiscs affect the cryo-EM structures of pentameric ligand-gated ion channels (pLGICs) including ELIC. To determine the structure of a pLGIC in a membrane environment that supports ion channel function, we performed single particle cryo-EM of ELIC in liposomes. ELIC activation and desensitization were confirmed in liposomes with a stopped-flow thallium flux assay. Using WT ELIC and a non-desensitizing mutant (ELIC5), we captured resting, activated and desensitized structures at high resolution. In the desensitized structure, the ion conduction pore has a constriction at the 9' leucine of the pore-lining M2 helix, indicating that 9' is the desensitization gate in ELIC. The agonist-bound structures of ELIC in liposomes are distinct from those in nanodiscs. In general, the transmembrane domain is more loosely packed in liposomes compared to nanodiscs. It has been suggested that large nanodiscs are superior for supporting membrane protein function. However, ELIC localizes to the rim of large circularized nanodiscs, and structures of ELIC in large nanodiscs deviate from the liposome structures more than those in small nanodiscs. Using liposomes for cryo-EM structure determination of a pLGIC increases our confidence that the structures are snapshots of functional states.

Introduction

There are many cryo-EM structures of pentameric ligand-gated ion channels (pLGICs) that have provided insight into the architecture of these ion channels and the determinants of activation and desensitization. Ideally, structure determination should be performed under conditions in which ion channel function (i.e. ion flux or conduction) can also be measured. However, all

available high-resolution structures of pLGICs have used proteins solubilized in detergent or reconstituted in one of a variety of lipid nanoparticles or nanodiscs. In many cases, the structures vary depending on the detergent or nanodiscs used. In the $\alpha 1$ glycine receptor (GlyR), the proportion of particles contributing to open and desensitized conformations differed when using detergent, MSP (membrane scaffold protein) nanodiscs, or SMA (styrene maleic acid) extracted nanoparticles [1]. In other pLGICs, different structures were obtained in detergent or various nanodiscs for the GABA_A receptor (GABA_AR) [2, 3], serotonin 3A receptor (5-HT3aR) [4–6], $\alpha 7$ nicotinic acetylcholine receptor ($\alpha 7$ nAChR) [7–9], and muscle nAChR [10, 11]. In a systematic study of the prokaryotic pLGIC, ELIC, in which various lipid nanoparticles or nanodiscs were tested, it was shown that the choice of nanodisc affects the agonist-bound structure of ELIC [12]. Taken together, these studies indicate that detergent or nanodisc conditions impact the structure of pLGICs. Without knowledge of ion channel function under these conditions, the functional annotation of these structures is less certain.

It has been suggested that large nanodiscs, which have proportionally more lipid at the core than rim (the 1–2 nm shell adjacent to the scaffold), may be superior for structural studies of pLGICs. This is because molecular dynamics simulations of ELIC in small nanodiscs show frequent contact of the scaffold with the membrane-facing M4 helix, altering the conformation and dynamics of this helix [12]. The MSP also perturbs the structure of the lipid bilayer (i.e. thickness and order) at the rim [13], and this too may be undesirable. Therefore, it is possible that larger nanodiscs are better membrane mimetics, reducing interactions of the membrane protein with the scaffold or having more homogeneous lipid bilayer properties. In support of this notion, the function of the ABC transporter was found to be sensitive to nanodisc size with larger nanodiscs yielding functional properties that are more similar to the ABC transporter in liposomes [14].

Here, we report cryo-EM structures of ELIC in liposomes where the ion channel is confirmed to be in resting, activated, and desensitized states. By performing structural and functional characterization under the same reconstitution conditions, we increase our confidence in the functional annotation of these structures. Comparison of structures in liposomes and nanodiscs show differences in the packing of the transmembrane domain and M4 transmembrane helix. Contrary to what was suggested previously [12], structures of ELIC in large nanodiscs deviate the most from those in liposomes.

Results

Resting, activated, and desensitized structures of ELIC in liposomes

Optimal reconstitution of ELIC in liposomes to facilitate single particle cryo-EM was achieved by dialysis. Reconstitution of ELIC in liposomes at low protein:lipid molar ratios can be accomplished by detergent removal with Biobeads [15]; however, reconstitution at a higher protein:lipid molar ratio (1:500 in this study) with efficient incorporation of ELIC in the liposomes required dialysis. The method was adapted from protocols previously reported for the reconstitution of muscle nAChR [16], 5-HT3aR [17], and ELIC [18]. Although dialysis was performed for 5–7 days to ensure complete removal of detergent, the minimum time of dialysis necessary was not tested. A shorter dialysis protocol could likely be implemented for less stable proteins depending on the detergent and dialysis conditions [19]. Proteoliposomes were formed using a 2:1:1 molar ratio of POPC (1-palmitoyl-2-oleoyl-phosphatidylcholine): POPE (1-palmitoyl-2-oleoyl-phosphatidylethanolamine): POPG (1-palmitoyl-2-oleoyl-phosphatidylglycerol); these lipids are known to support ELIC activity [15], and phosphatidylethanolamine and phosphatidylglycerol are the two principal phospholipids found in gram-negative bacteria in which ELIC is expressed. Using a stopped-flow thallium flux assay, we confirmed that WT ELIC activates and then mostly desensitizes in response to the agonist, propylamine (**Fig. 1A**). The time constant of activation

and desensitization were 10 ± 2 ms and 5.1 ± 2.1 s ($\pm$ SD, $n=6$), respectively, which matches the kinetics of ELIC activation and desensitization from excised patch-clamp recordings in liposomes or HEK293 cells [20–22]. We previously identified a combination of five mutations in ELIC, P254G/C300S/V261Y/G319F/I320F, called ELIC5 which eliminates channel desensitization [15]. We confirmed that ELIC5 in 2:1:1 POPC:POPE:POPG liposomes activates and does not desensitize for at least 20 minutes (Fig. 1A). The open probability of ELIC5 when activated by 10 mM propylamine in 2:1:1 POPC:POPE:POPG membranes is estimated to be close to 1 [15]. Therefore, proteoliposome preparations of WT ELIC in the absence and presence of propylamine is expected to yield resting and desensitized channels, respectively, and ELIC5 in the presence of propylamine is expected to yield activated channels. The same reconstitution protocol was used for the stopped-flow thallium flux assay and single particle cryo-EM.

We determined structures of WT ELIC with and without agonist, and ELIC5 with agonist. Side views from the 2D class averages showed that ELIC is oriented in both directions in the liposomes with a preference for the extracellular domain (ECD) facing the extra-liposomal solution (i.e. outward-facing orientation) (Fig. 1B, Supplementary Figure 1, 2 and 3). Heterogeneous refinement in CryoSPARC separated the particles into two classes that generated outward-facing and inward-facing 3D reconstructions (Fig. 1C). One caveat to this analysis is that top/down views of outward- and inward-facing channels may not be distinguishable without the curvature of the liposome membrane as a reference. Therefore, it is possible that outward- and inward-facing ELIC particles could not be rigorously separated using 3D heterogeneous refinement or 3D classification in CryoSPARC or Relion. Accordingly, the proportion of particles assigned to outward- and inward-facing 3D classes may not accurately reflect the relative orientation of ELIC in the liposomes. Nevertheless, final maps were obtained for apo WT ELIC at a resolution of 3.4 Å for outward-facing and 3.6 Å for inward-facing channels, agonist-bound WT ELIC at a resolution of 3.8 Å for outward-facing and 4.2 Å for inward-facing channels, and agonist-bound ELIC5 at a resolution of 2.8 Å for outward-facing and 4.2 Å for inward-facing channels (Fig. 2A, Supplementary Figure 1, 2, 3 and 4, and Supplementary Table 1). In all samples, the inward- and outward-facing structures of ELIC were not significantly different. However, we cannot be certain that ELIC structure is insensitive to membrane curvature due to the limitations of distinguishing inward- and outward-facing particles. In addition, the inward-facing structures were of significantly lower resolution and quality compared to the outward-facing structures. The reason for this is uncertain, but could be due to fewer inward-facing particles, increased structural heterogeneity, and contamination within the liposomes. We focused our analysis on the outward-facing structures since these have better resolution. Moreover, only outward-facing channels are activated by agonist in the stopped-flow thallium flux assay.

The structures of ELIC in liposomes have the same overall architecture as structures of ELIC or other pLGICs in nanodiscs, consisting of a homopentameric assembly around a central ion conduction pore (Fig. 2B). Each subunit consists of an ECD and transmembrane domain (TMD). In the agonist-bound structures, propylamine binds in a conserved site between β -sheets from two adjacent subunits. Comparison of the apo WT ELIC and agonist-bound ELIC5 structures shows the conformational changes for activation, and comparison of agonist-bound ELIC5 and agonist-bound WT ELIC structures shows the conformation changes for desensitization. ELIC activation consists of a contraction of the agonist binding site, counter-clockwise twisting of the ECD, and outward translation of M2-M3 linker and pre-M1 linker in the TMD (Supplementary Figure 5). These changes are also associated with an outward translation and counter-clockwise twisting of the transmembrane helices (M1-M4) that leads to opening of the ion channel pore lined by the M2 helix (Supplementary Figure 5). ELIC desensitization consists of a partial return of the transmembrane helices (clockwise twisting and contraction), but without significant change in the ECD or the M2-M3 and pre-M1 linkers in the TMD (Supplementary Figure 5).

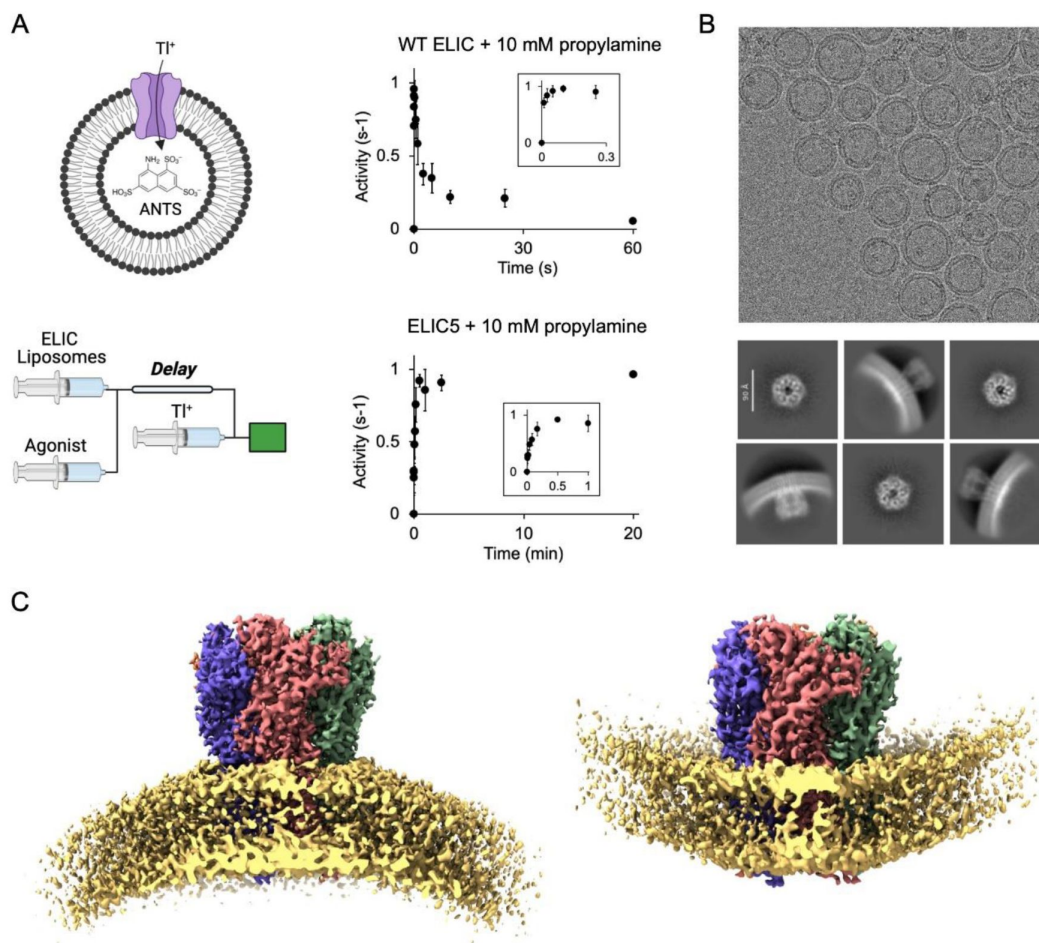


Figure 1

Single particle cryo-EM of ELIC in liposomes.

(A) Schematic of the fluorescence stopped-flow liposomal flux assay: a sequential mixing experiment is performed. ELIC proteoliposomes are mixed with agonist followed by thallium (Tl^+) after a variable delay time. ELIC activity at each delay time is measured as the rate of fluorescence quenching by the influx of Tl^+ . Shown is WT ELIC and ELIC5 activity after mixing with 10 mM propylamine over varying delay times ($n = 3-6$, $\pm$ SEM). (B) Representative cryo-EM micrograph of WT ELIC in 2:1:1 POPC:POPE:POPG liposomes and 2D class averages. (C) Cryo-EM maps of WT ELIC without agonist in liposomes showing inward- and outward-facing orientations. The lipid bilayer density is shown at a lower contour level for illustration.

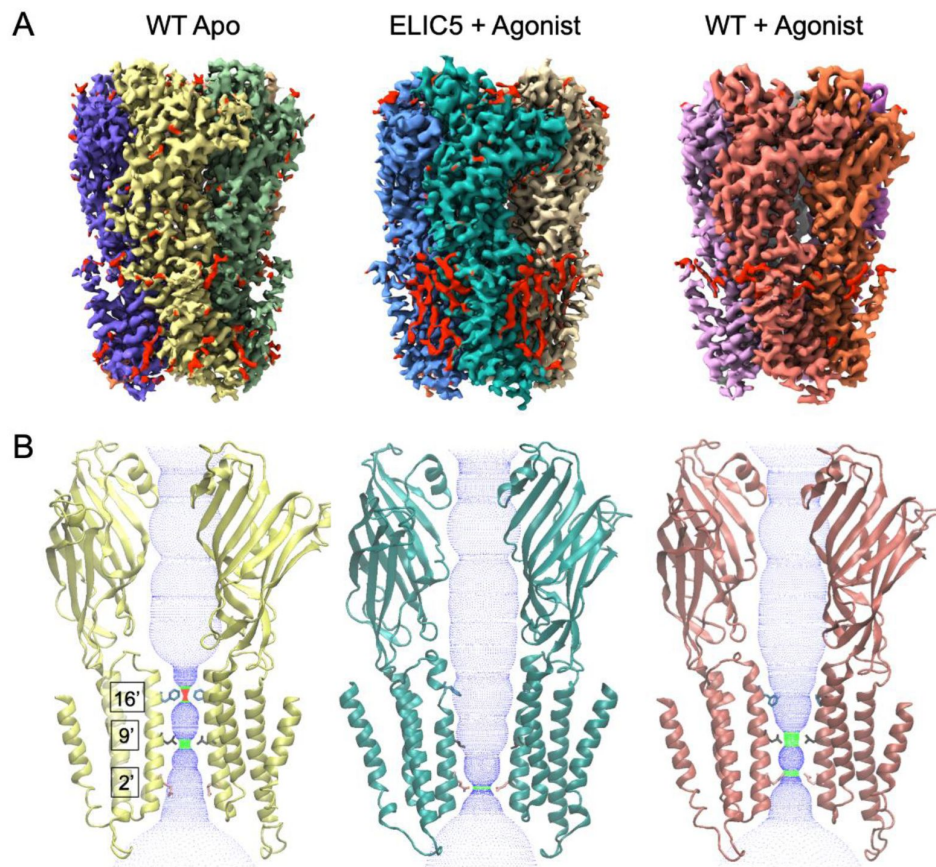


Figure 2

Structure and pore conformation of resting, activated, and desensitized states.

(A) Cryo-EM maps of WT ELIC without agonist (resting state), ELIC5 with 10 mM propylamine (activated state), and WT ELIC with 10 mM propylamine (desensitized state) in liposomes. In the ELIC5 + Agonist map, red shows non-protein densities. (B) Two opposing subunits from models of the structures shown in (A) along with a dot plot of the pore dimensions generated using HOLE [45]. Shown are the side chains for F247 (16'), L240 (9') and Q233 (2').

The structure of the pore also reveals the conformational state of ELIC: the presence or absence of a continuous and sufficiently wide water-accessible pathway indicates whether the ion channel is open or closed, respectively. Apo WT ELIC shows a pore with two hydrophobic constrictions at F247 and L240 (also known as 16' and 9' positions of M2), where the ion conduction pathway is dehydrated and therefore, closed (**Fig. 2B**, **Supplementary Fig. 6**). In contrast, the agonist-bound ELIC5 pore is hydrated and open because M2 rotates and F247 and L240 orient away from the pore axis towards the adjacent subunit (**Fig. 2B**, **Supplementary Fig. 6**). There is some narrowing of the pore at 2' (Q233, diameter of 4.4 Å), but this hydrophilic side chain, which can take on different rotameric states [15], is not anticipated to impede ion conduction. Agonist-bound WT ELIC shows conformational heterogeneity at F247, and two states were modeled with different conformations for F247 and Y248 (**Supplementary Fig. 6**). In state 1, F247 orients towards the pore axis, while in state 2, F247 orients towards M2 of the adjacent subunit. The latter has a wider pore at 16' (F247), but still 9' (L240) forms a hydrophobic constriction (diameter of 3.3 Å) like Apo WT ELIC (diameter of 2.6 Å) (**Fig. 2B**, **Supplementary Fig. 6**). There is also a narrowing of the pore at 2' (Q233) in the agonist-bound WT ELIC structure (diameter of 3.7 Å). Nevertheless, the pore diameter at 9' (L240) and the hydrophobicity of this residue suggests that 9' is the highest barrier to ion conduction in the agonist-bound WT ELIC structure. In summary, apo and agonist-bound WT ELIC are closed structures with hydrophobic constrictions at 9' consistent with resting and desensitized states, and agonist-bound ELIC5 is an open structure consistent with an activated state. It has been proposed that the activation and desensitization gates in the GABA_AR and GlyR are distinct with 9' being the activation gate and -2' the desensitization gate [1, 23–26]. However, in agonist-bound structures of the α7 nAChR and 5-HT3aR, which are expected to be desensitized conformations, 9' is the only constriction in the pore that poses an energetic barrier to ion and water permeation [4, 7, 27, 28]. It was previously suggested that the agonist-bound structures of ELIC and 5-HT3aR may be pre-active states [15, 29], and that the channel may somehow be limited from entering a desensitized state due to detergent or nanodisc conditions [12]. Based on the liposome structures, we conclude that 9' is the desensitization gate for ELIC and possibly other cation-selective pLGICs. This conclusion is consistent with studies showing that mutation of 9' (L240A) in ELIC appears to eliminate desensitization [30].

Lipid-like densities are also resolved in the agonist-bound ELIC5 structure (**Supplementary Figure 7**). The most prominent lipid densities are in the outer TMD consisting of four lipid-like tails. Two of these tails fill intersubunit (M1-M3) and intrasubunit (M3-M4) grooves, and meet to form a putative phospholipid headgroup near R117 of the β6-β7 interfacial loops. A very similar phospholipid density was observed previously in agonist-bound ELIC5 in nanodiscs (e.g. MSP1E3D1) (**Supplementary Figure 7**), and streamlined free energy perturbation calculations determined that this is likely POPG and not POPE or POPC [15]. Another lipid-like tail adjacent to M1 joins with the density in the intersubunit site making a three-pronged lipid-like density. The ELIC5 structure in MSP1E3D1 also showed a similar but weaker density. Therefore, the lipid densities observed in the liposome structure of the activated state of ELIC are very similar to those observed in a nanodisc structure, suggesting that ELIC and not the nanodisc are primarily determining the interaction of these phospholipids. Lipid-like densities are not well appreciated in the apo WT ELIC or agonist-bound WT ELIC structures, possibly due to the lower resolution of these structures or differences in the nature of the lipid interactions [15].

ELIC is associated with the MSP even in large nanodiscs

Nanodiscs affect the structure of ELIC possibly through interactions of ELIC with the membrane scaffold protein (MSP) [12, 14]. Larger nanodiscs may decrease the probability of interactions with the MSP and therefore be superior membrane mimetics [14]. To test this possibility, we reconstituted WT ELIC in spNW25, a circularized nanodisc with an average diameter of 25 nm [31], for single particle cryo-EM analysis, and determined a structure of ELIC in the presence of agonist (propylamine). spNW25 nanodiscs are significantly larger than the 11 nm (spMSP1D1) and 15 nm (spNW15) nanodiscs previously used for agonist-bound WT ELIC structures [12]. Initial

inspection of the micrographs showed multiple ELIC particles in most nanodiscs, and localization of the particles to the rim of the nanodisc (**Fig. 3A**). Consistent with this observation, side views of the 2D class averages (**Fig. 3B**) and the resulting 3D reconstruction using C1 symmetry (**Fig. 3C**, **Supplementary Figure 8**) showed significant MSP density on one side of the TMD. A recent study showed that MSP densities can be resolved in the structures of many membrane proteins [32]. We therefore re-analyzed the dataset of agonist-bound WT ELIC in spMSP1D1 with C1 symmetry; the resulting map showed strong MSP densities associated with ELIC (**Fig. 3E**). Taken together, the structures indicate that ELIC has a strong affinity for the MSP or nanodisc rim irrespective of nanodisc size.

We next examined whether the C1 reconstructions of agonist-bound WT ELIC in spMSP1D1 or spNW25 nanodiscs exhibit any asymmetric features associated with contact with the MSP. In the spMSP1D1, the cryo-EM map showed stronger densities for M4 in subunits adjacent to the MSP, and the local resolutions of those subunits are higher in both the TMD and ECD (**Fig. 3E** and **3F**). This agrees with the finding in other nanodisc-reconstituted membrane proteins that interactions with the MSP stabilize the local conformation of the protein [32]. In contrast, the C1 reconstruction of agonist-bound ELIC in spNW25 showed better local resolution in subunits facing the lipid bilayer (**Fig. 3D**). In addition, M4 was only resolved in one of the lipid bilayer-facing subunits (**Fig. 3C**). A C5 reconstruction of agonist-bound WT ELIC in spNW25 also did not show densities for M4 (**Supplementary Figure 8**). The C1 maps of agonist-bound ELIC in nanodiscs suggest that the MSP can influence the local dynamics of the protein.

The micrographs and 2D class averages of ELIC in spNW25 showed multiple ELIC particles in each nanodisc. ~10% of particles from the 2D class averages showed two adjacent pentamers (**Supplementary Figure 8**), but these dimers of pentamers did not yield high resolution reconstructions. 2D class averages of dimers of pentamers were never observed in the liposome datasets. This observation suggests that reconstitution of membrane proteins in large nanodiscs may be a strategy to promote the association of multiple membrane proteins. Whether the formation of dimers of pentamers alters the function of ELIC is not known.

Comparison of ELIC structures in liposomes and nanodiscs

The structures of ELIC in nanodiscs differ from the structures in liposomes to varying degrees. From this and previous studies [12, 15], the following structures of ELIC in nanodiscs have been determined: apo WT ELIC in MSP1E3D1 (PDB 8D65) and spMSP1D1 (PDB 8F35), agonist-bound ELIC5 in MSP1E3D1 (PDB 8VUW) and spNW15 (PDB 8TWV), and agonist-bound WT ELIC in MSP1E3D1 (PDB 8D66), spMSP1D1 (PDB 8F34), spNW15 (PDB 8TWZ), and spNW25 (PDB 9NH4). To examine the effect of nanodisc size on ELIC structure, we compared agonist-bound WT ELIC in liposomes with spMSP1D1 (11 nm), spNW15 (15 nm) and spNW25 (25 nm). Unexpectedly, the structure in the largest nanodisc, spNW25, deviates most from the liposome structure. There is a shortening of M1 and M2, and tilting of M3 towards the membrane that decreases the height of these transmembrane helices along the pore axis by ~1-1.5 Å compared to the liposome and spMSP1D1 structures (**Fig. 4A**, **Supplementary Table 2**). Along with this, M2 is tilted towards the pore axis, narrowing the pore even further at L240 (9°) and Q233 (2°) (**Fig. 4B**). In spNW15, M2 tilts towards the pore axis at the intracellular end slightly narrowing the pore, as was reported previously [12]. The spMSP1D1 structure most closely matches the liposome structure, except there is ~1 Å outward (away from the pore axis) translation of M4 in the liposome structure compared to the spMSP1D1 structure (**Fig. 4C**). There is no M4 density in the C5 maps of agonist-bound WT ELIC in spNW15 and spNW25, suggesting that larger nanodiscs increase the structural heterogeneity of this helix.

In apo WT ELIC, the structures in MSP1E3D1 or spMSP1D1 are not significantly different from the structure in liposomes. In agonist-bound ELIC5, M4 is translated (2 Å) and tilted (~5 degrees) outward (away from the pore axis) in the liposome structure compared to the MSP1E3D1 or

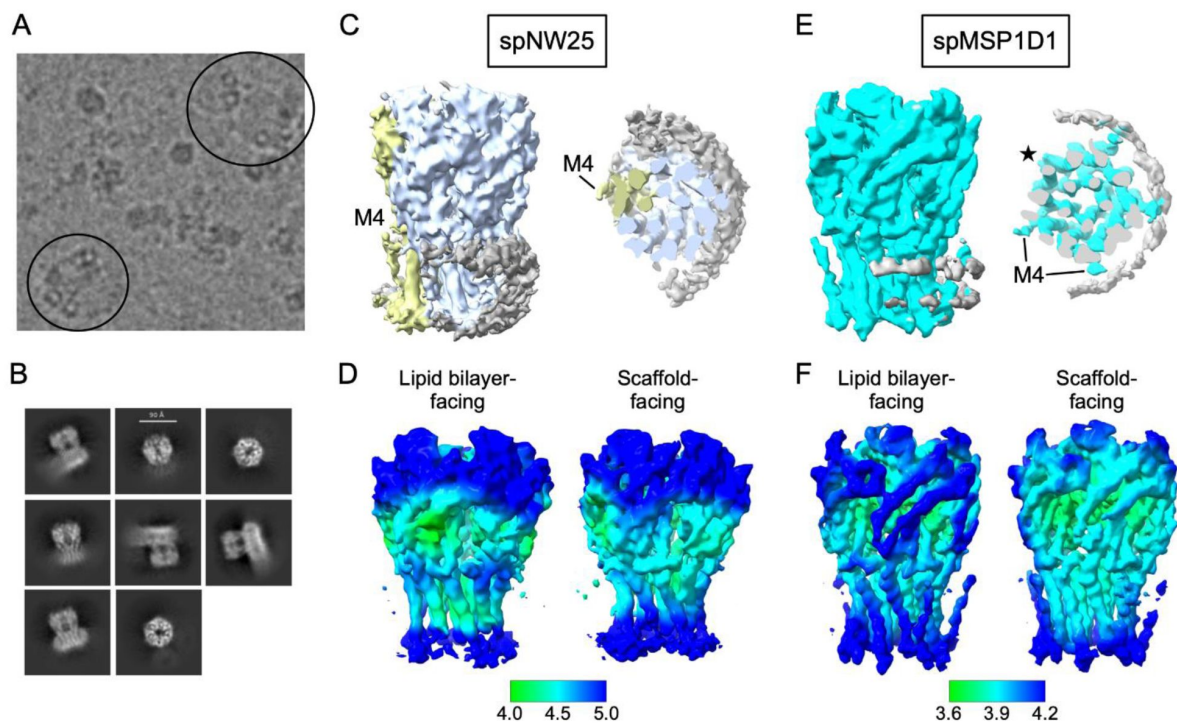


Figure 3

Single particle cryo-EM of ELIC in spNW25 nanodiscs.

(A) Cryo-EM micrograph of WT ELIC with 10 mM propylamine in spNW25 nanodiscs. The circles indicate top-down views of spNW25 nanodiscs with multiple ELIC ion channels at the rim of the nanodisc. (B) 2D class averages of WT ELIC in spNW25. (C) C1 cryo-EM map of agonist-bound WT ELIC in spNW25 at low contour showing the nanodisc scaffold density (gray). M4 is resolved in one of the ELIC subunits colored yellow. (D) Displays of the local resolution for the map in (C). Shown are the aspects of ELIC facing the lipid bilayer and the nanodisc scaffold. (E) C1 cryo-EM map of agonist-bound WT ELIC in spMSP1D1 at low contour showing the nanodisc scaffold density (gray). M4 densities can be appreciated in all subunits except one of the lipid bilayer-facing subunits (star). (F) Displays of the local resolution for the map in (E). Shown are the aspects of ELIC facing the lipid bilayer and the nanodisc scaffold.

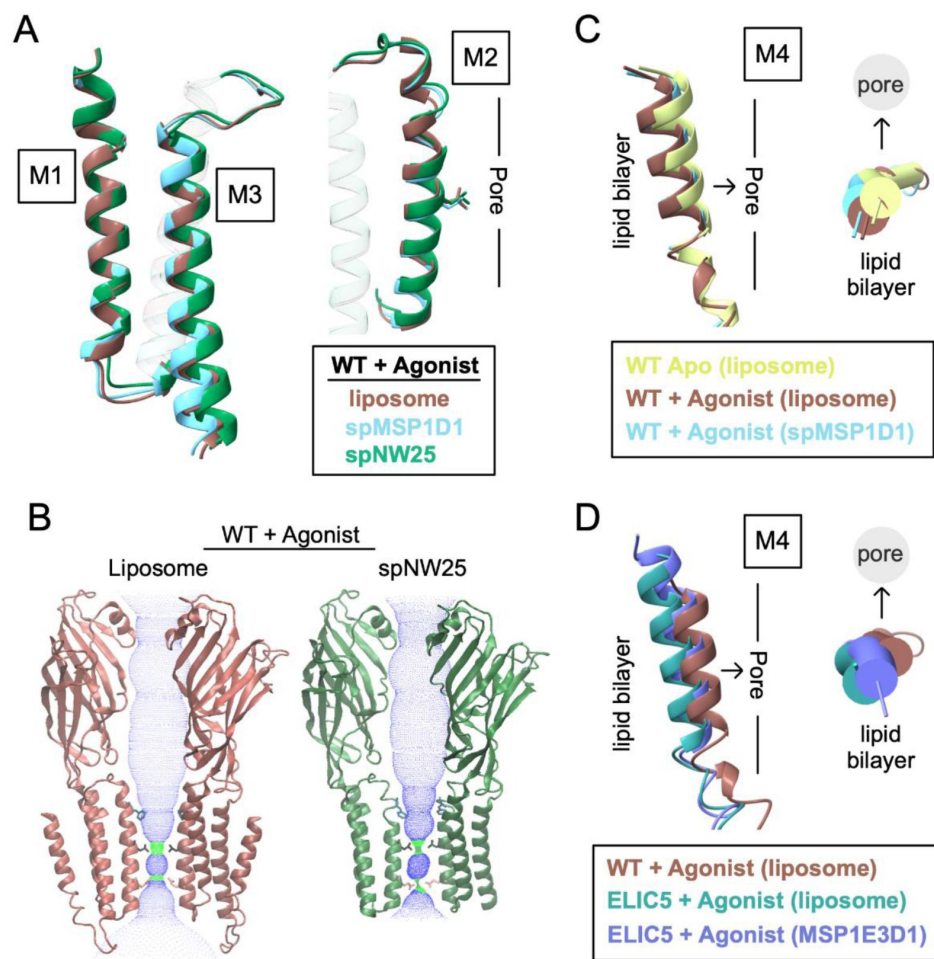


Figure 4

Comparison of ELIC structures in liposomes and nanodiscs.

(A) Comparison of the M1, M2, and M3 helices in structures of WT ELIC with agonist in liposomes, spMSP1D1 and spNW25. Shown in M2 is the side chain of L240 and the approximate location of the ion conduction pore relative to M2. Images are from a global superposition of the structures. (B) Two opposing subunits from structures of WT ELIC with agonist in liposomes and spNW25. Shown are dot plots of the pore dimensions generated using HOLE [45], and the side chains for F247 (16'), L240 (9') and Q233 (2'). (C) Comparison of M4 in WT ELIC in liposomes, WT ELIC with agonist in liposomes, and WT ELIC with agonist in spMSP1D1 showing a side view and top view (from extracellular side) of the helix. The approximate location of the lipid bilayer and ion conduction pore are indicated relative to M4. Images are from a global superposition of the structures. (D) Same representation as (C) comparing M4 in WT ELIC with agonist in liposomes, ELIC5 with agonist in liposomes, and ELIC5 with agonist in MSP1E3D1.

spNW15 structures (**Fig. 4D**). Along with this, there is a slight outward expansion of the M1, M2 and M3 transmembrane helices away from the pore axis, indicating that the liposome is producing an activated structure that is more loosely packed.

We further analyzed the agonist-bound WT ELIC and ELIC5 structures by measuring the area between subunit interfaces in the TMD and the buried surface area between M4 and the rest of the protein. There is an overall trend where the liposome structures having a smaller area between subunit interfaces in the TMD and a smaller buried surface area between M4 and the rest of the protein (**Supplementary Table 3**). This means that the TMD is more loosely packed in the agonist-bound structures in liposomes compared to nanodiscs. Accordingly, the total buried surface area is also consistently smaller in the liposome structures compared to the nanodisc structures (**Supplementary Table 3**).

In summary, the agonist-bound structures of WT ELIC or ELIC5 in liposomes deviate from the nanodisc structures, particularly in M4. The structure of the TMD in liposomes is generally more loosely packed than in nanodiscs. This is consistent with MD simulations of ELIC in nanodiscs showing that the outward tilt of M4 is reduced by interactions with the MSP [12]. Contrary to what was previously suggested [12], the agonist-bound WT ELIC structure in a large nanodisc (spNW25) deviates most from the structure in liposomes indicating that such large nanodiscs do not recapitulate the membrane environment of a liposome.

Discussion

Single particle cryo-EM of ion channels in liposomes provides the opportunity to study structure and function in the same preparation [33, 34]. There has been uncertainty as to whether agonist-bound structures of ELIC in lipid nanodiscs represent a desensitized state [12, 35]. Using liposomes that support ELIC function, we have greater confidence that the structures presented in this study capture resting, activated and desensitized conformations. The desensitized conformation shows that the 9' leucine is likely the desensitization gate in ELIC. The ability to obtain structures of ELIC in liposomes sets the stage for time-resolved cryo-EM structural analysis of a pLGIC where the rates of activation and desensitization can be monitored [36].

We previously observed variation in agonist-bound structures of ELIC in nanodiscs of different size [12]. The nanodisc scaffold could affect the structure of ELIC by perturbing the lipid bilayer or by directly interacting with ELIC itself. Therefore, we predicted that larger nanodiscs with a larger lipid bilayer area may better recapitulate the environment of a lipid bilayer that is not surrounded by a nanodisc scaffold. This prediction is not supported by the agonist-bound structure of ELIC in large ~25 nm nanodiscs, which shows the greatest deviation from the liposome structure. Strikingly, ELIC localizes only to the rim of this large nanodisc. This is anticipated to produce a non-uniform environment (i.e. MSP on one side and a lipid bilayer on the other), and the differences in the local resolution of C1 reconstructions of ELIC in nanodiscs may be a consequence of direct interactions with the MSP. It is also likely that the spNW25 nanodisc alters lipid bilayer properties particularly at the rim of the nanodisc, and that this contributes to the observed changes in the TMD structure. There is evidence that other membrane proteins in nanodiscs have an affinity for the MSP [32, 37], suggesting that the perturbing effects of large nanodiscs on ELIC structure may apply to other membrane proteins.

In pLGICs, M4 is in the periphery of the TMD, and is thought to be a lipid sensor due to its contact with the membrane [38]. In ELIC, the structure and dynamics of M4 influence agonist responses [39]. Based on the liposome structures, activation of ELIC involves an outward translation and tilting of M4 towards the membrane; this movement of M4 is greatest in the activated state and intermediate in the desensitized state. In both activated and desensitized structures, nanodiscs limit this agonist-induced conformational change in M4, and in desensitized structures, some

nanodiscs (i.e. spNW15 and spNW25) appear to increase the conformational heterogeneity of M4. Therefore, we infer from the structural data that nanodiscs affect agonist responses in ELIC, suggesting that structure determination in liposomes is necessary to capture snapshots of activated and desensitized states of this pLGIC.

Methods

Expression, purification and liposome reconstitution of ELIC

ELIC was expressed from pET-26-MBP-ELIC provided by Raimund Dutzler (Addgene plasmid #39239) in OverExpress C43 (DE3) *E. coli* (Lucigen 60446-1) as previously described [40]. The ELIC5 mutant (P254G/C300S/V251Y/G319F/I320F) was made using Quikchange and confirmed by Sanger sequencing (Genewiz). Cultures were grown with Terrific Broth (Sigma T0918) using 0.1 mM IPTG (Sigma I6758) for induction. The cells were lysed with an Avestin C5 emulsifier, and membranes solubilized with 1% DDM (Anatrace D310S). The extracted protein was purified with amylose resin (New England Biolabs E8022L), and eluted with 40 mM maltose in buffer A (10 mM Tris pH 7.5, 100 mM NaCl, 0.02% DDM). The maltose binding protein was removed by overnight digestion with HRV-3c protease (ThermoFisher Scientific 88947). Lastly, the protein was purified over a Sephadex 200 Increase 10/300 size exclusion column (Cytiva 28-9909-44) in Buffer A.

Reconstitution of WT ELIC or ELIC5 in liposomes was performed using dialysis. 2:1:1 POPC:POPE:POPG was dried overnight in a vacuum desiccator to remove chloroform, resuspended in 50 mM HEPES pH 7, 150 mM NaCl, 2% cholate at 10 mg/ml, and sonicated to clarity. The lipid solution was diluted to 5 mg/ml to 1% cholate. For each sample, 0.5 mg of lipid (100 μ l) was mixed with 250 μ g of WT ELIC or ELIC5 at $\sim$ 7 mg/ml, producing a ELIC(pentamer):lipid molar ratio of $\sim$ 1:500. For samples with agonist, propylamine was added at this step to a final concentration of 10 mM such that the proteoliposomes will have propylamine in both the extraliposomal and intraliposomal space. The sample was incubated on ice for 1h, and then dialyzed (ThermoScientific 88402-20K MWCO) against 50 mM HEPES pH 7, 150 mM NaCl with or without agonist over 5-7 days with 6x solution changes of 14 ml each. After dialysis, the sample was $\sim$ 150 μ l. The sample was centrifuged at 10,000xg for 5 min to remove large aggregates, and concentrated to $\sim$ 50-75 μ l using a Amicon Ultra-0.5 100 kDa MWCO centrifugal filter (Millipore Sigma UFC910024). The final lipid concentration was $\sim$ 5 mg/ml, and this was used directly for freezing for cryo-EM analysis.

Expression and purification of spNW25, and nanodisc reconstitution

spNW25 was expressed and purified from Addgene plasmid #173484 provided by Huan Bao exactly as previously described using Ni-NTA affinity purification, but without size exclusion chromatography [31]. Reconstitution of WT ELIC in spNW25 was performed using a liposome destabilization technique as described previously [15]. 2:1:1 POPC:POPE:POPG in 50 mM HEPES pH 7, 150 mM NaCl at 7.5 mg/ml was freeze-thawed 3x and extruded with a 400 nm filter (Avanti Polar Lipids). These lipids were destabilized by adding 0.4% DDM and incubating at RT for 3 h. ELIC and spNW25 was added to the sample with a molar ratio of 1:2:600 of ELIC:spNW25:lipid and incubated at RT for 1.5 h. DDM was removed to form nanodiscs with Biobeads SM-2 Resin (Bio-Rad 1528920) over night at 4 $^{\circ}$ C. Nanodiscs were further purified over a Sephadex 200 Increase 10/300 column in 50 mM HEPES pH 7 with 150 mM NaCl. The nanodisc fractions were concentrated to $\sim$ 0.5 mg/ml, and propylamine was added to a final concentration of 50 mM at least 30 min prior to freezing for cryo-EM analysis.

Cryo-EM sample preparation and imaging

Cryo-EM samples for agonist-bound WT ELIC in spNW25 were prepared as previously described [12]. 3 μ l of sample was applied to Quantifoil R2/2 copper grids, previously negatively glow discharged using a GloQube (Quorum Technologies) for 60 s. The grids were blotted for 2 s in a 95% humidity environment and vitrified in liquid ethane with a Vitrobot Mark IV (ThermoFisher Scientific). Images were collected on a Glacios 200 kV Cryo-EM equipped with a Falcon 4 Direct Electron Detector (ThermoFisher Scientific). The single particle cryo-EM data was acquired by counting mode on the Falcon 4 with EPU software (version 3.5.1). The movies were collected with a pixel size of 1.184, and defocus range of -0.8 to -2.4 μ m. Each movie consisted of 45 individual frames with a total dose of 46.6 electrons per $\text{\AA}^2$.

For the proteoliposome samples, 3 μ l of sample was applied to a Quantifoil R2/2 gold grid and incubated for 3 min in a 95% humidity environment. The grid was then blotted for 2 s, followed by a second sample application. After the second sample application, the grid was incubated at 95% humidity for 30 s, blotted for 2 s, and vitrified in liquid ethane. Images were collected on a Krios 300 kV Cryo-EM equipped with a Falcon 4 Direct Electron Detector. Single particle cryo-EM data was acquired using counting mode on the Falcon 4 with the EPU software 3.8.1. For apo WT ELIC and agonist-bound ELIC5, movies were collected with a pixel size of 0.868, and for agonist-bound WT ELIC, movies were collected with a pixel size of 0.865. A total dose of 55.4 electrons per $\text{\AA}^2$ was used for apo WT ELIC, 54.4 electrons per $\text{\AA}^2$ for agonist-bound WT ELIC, and 56.9 electrons per $\text{\AA}^2$ for agonist-bound ELIC5.

Single particle analysis and model building

Single particle cryo-EM analysis of WT ELIC in spNW25 with 50 mM propylamine was performed using CryoSPARC v4.6.0 [41] and Relion5.0. Initial processing was performed with CryoSPARC including Patch Motion Correction, Patch CTF and particle picking using templates from a previously determined ELIC map. Extracted particles were cleaned up with multiple rounds of 2D classification. To increase the number of picked particles, Topaz particle picking was performed by separately training with top/down, tilted and side views of ELIC from the last 2D classification job, and these particles underwent multiple rounds of 2D classification. The resulting $\sim 787,500$ particles underwent multiple heterogeneous refinement jobs using C1 symmetry. For the C1 reconstruction, the best class from the final heterogeneous refinement job was further analyzed in Relion5.0 using multiple rounds of 3D classification with blush regularization and C1 symmetry. The final post-processed map was generated in Relion5.0. For the C5 reconstruction, the $\sim 787,500$ particles underwent multiple heterogeneous refinement jobs in CryoSPARC using C5 symmetry, followed by multiple 3D classifications in Relion5.0 with blush regularization and C5 symmetry. The final post-processed map was generated in Relion5.0.

Each of the three proteoliposome samples were analyzed in a similar fashion as the approach used for the ELIC spNW25 structure, and the workflow is highlighted in **Supplementary Figures 1–3**. Movies were motion corrected and CTF estimation was performed in cryoSPARC. Particle picking was performed with blob picker, which yielded poor results, but many rounds of 2D classification eventually yielded a small number of particles (several thousand) producing class averages that resembled top/down, tilted and membrane-embedded side views. These particles were used for Topaz training and the extracted particles were further processed by 2D classification. The resulting 2D class averages were improved and, again, used for Topaz training separating top/down and tilted from side views. This was performed 2–3 times for each dataset. When there was no significant increase in the number of good particles from Topaz picking, an ab-initio reconstruction was performed to generate initial volumes for heterogeneous refinement. It was apparent from the side views of the 2D class averages that ELIC was oriented inward and outward in the liposomes. Accordingly, ab-initio reconstructions produced volumes with opposite membrane curvature indicative of inward- and outward-facing channels. Multiple rounds of

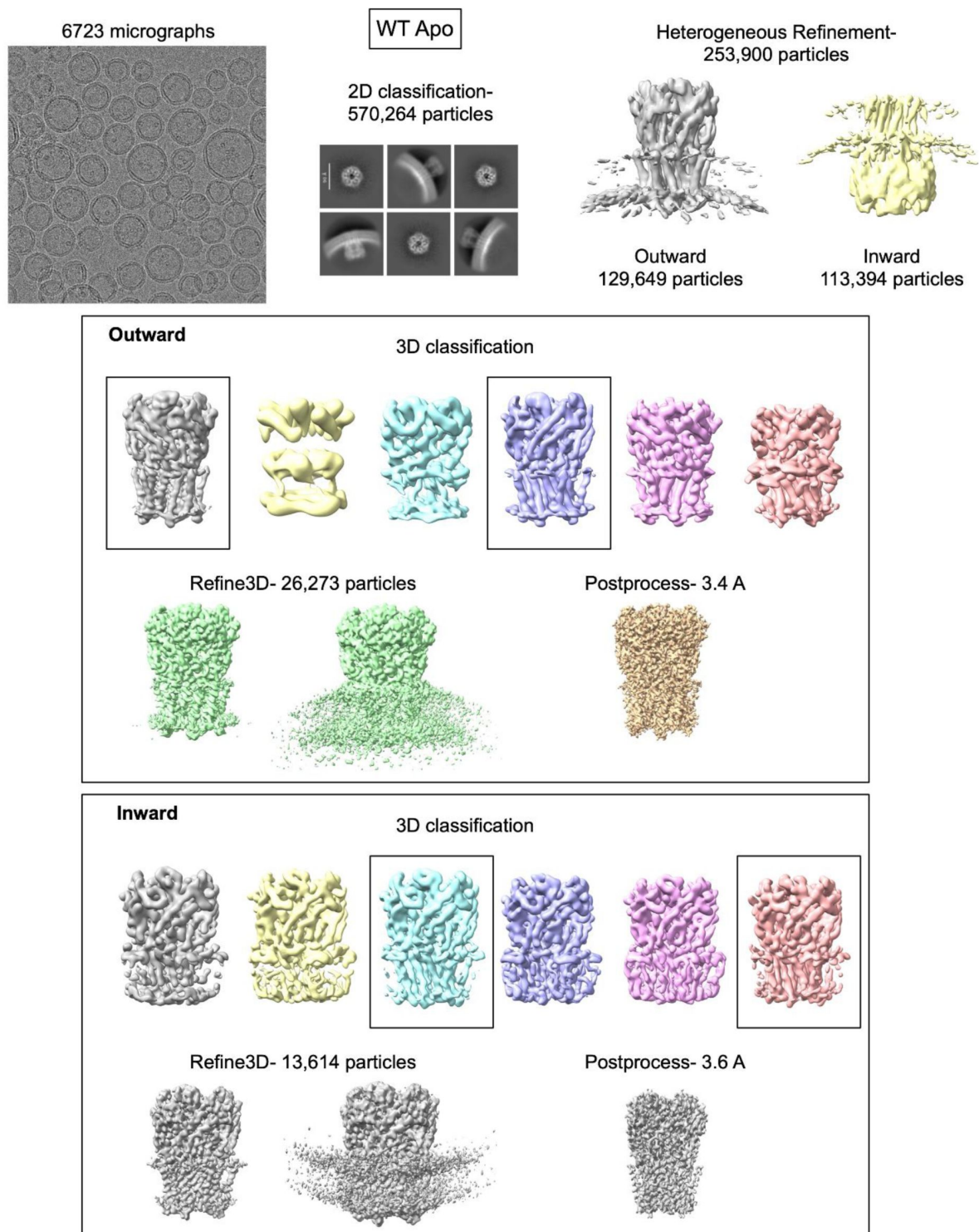
heterogeneous refinement with C1 and C5 symmetry were performed with the inward- and outward-facing volumes as well as 2-3 junk volumes. The C1 refinement jobs did not produce 3D reconstructions of sufficient quality for further refinement. Therefore, we proceeded with refinement and 3D classification using C5 symmetry. The resulting particles were used for non-uniform refinement and local refinement with a mask for the entire ELIC or ELIC5 protein. The local refinement job generally produced better maps probably because it masked out the liposome membrane from the refinement procedure. In general, better maps could be obtained with further processing in Relion5.0, except for agonist-bound ELIC5 which yielded a final outward-facing map of 2.8 Å resolution. Particles from inward- and outward-facing classes underwent multiple rounds of 3D classification in Relion5.0 without and with a mask for the entire ELIC protein. The masked 3D classification jobs yielded the best final classes for post-process refinement.

For the apo WT ELIC structures in liposomes, an initial model of ELIC was obtained from PDB 8F35. For all agonist-bound WT structures, an initial model was obtained from PDB 8F34. For the agonist-bound ELIC5 structures in liposomes, an initial model was obtained from PDB 8VUW. These were used to perform real space refinement in PHENIX 1.19.2 [42], The structure of ELIC was manually built into the cryo-EM density map using COOT 0.9.6 [43], refined in PHENIX, and this process was repeated iteratively. Propylamine was fit into the density in the agonist binding site based on the orientation predicted from MD simulations [35]. For all C5 models, a single subunit was built, refined and propagated to the other subunits. 3D volume visualization, analysis and image preparation were performed using PyMOL 2.5.2 and ChimeraX 1.6.1.

Fluorescence stopped-flow liposomal flux assay

The fluorescence stopped-flow liposomal flux measurements were performed on the SX20 stopped-flow spectrofluorometer (Applied Photophysics) as previously described [15], but with some modifications to assay ELIC activity in liposomes formed by dialysis—the same liposome reconstitution method that was used for cryo-EM. 2:1:1 POPC:POPE:POPG lipids were dried and reconstituted in 10 mM HEPES pH 7, 100 mM NaNO₃, 1% cholate at 5 mg/ml and sonicated to clarity. For each sample, 2.5 mg of lipid (0.5 ml) was used and mixed with 12.5 µg of WT ELIC or 2.5 µg of ELIC5, incubated for 1 h at 4 °C, and dialyzed for 3-5 days against 14 ml of buffer (50 mM HEPES pH 7, 100 mM NaNO₃) with 6 solution changes at 4°C. Next, the proteoliposome samples were mixed with 1.5 ml of 50 mM HEPES pH 7, 100 mM NaNO₃, and 75 mM 8-Aminonaphthalene-1,3,6-Trisulfonic Acid (ANTS, ThermoFisher Scientific). The samples underwent a single freeze-thaw to introduce ANTS into the intra-liposomal space. To remove the extra-liposomal ANTS, the samples were diluted to 2.5 ml and run through a PD-10 desalting column (Cytiva) pre-equilibrated with 50 mM HEPES pH 7, 140 mM NaNO₃ (Stopped-flow Buffer A), and eluted with 3 ml of this buffer. Lastly, the samples were diluted 3-fold with Stopped-flow Buffer A.

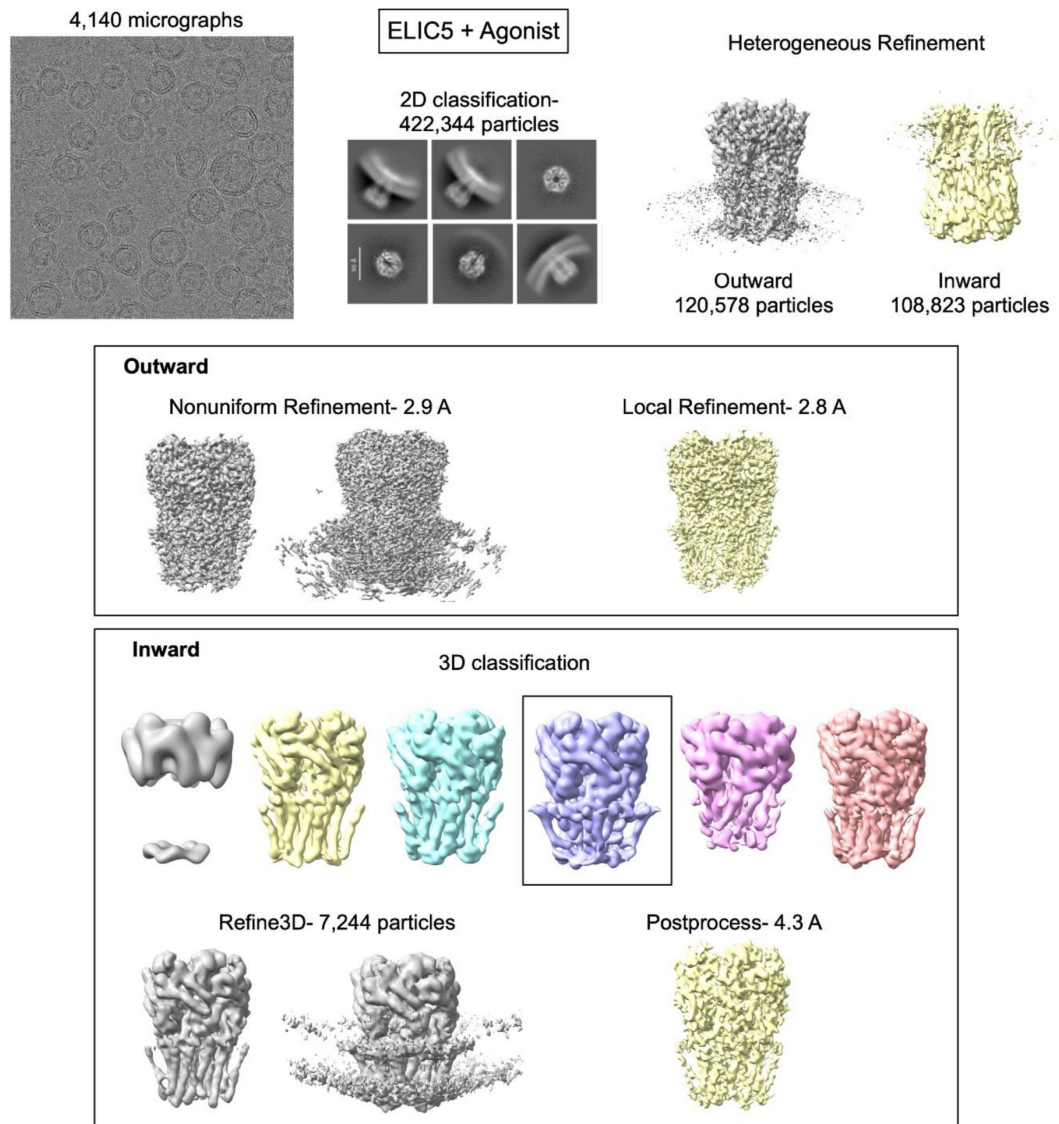
Two experiments were performed to assess activation and desensitization of WT ELIC, and activation of ELIC5. For WT ELIC, activation and desensitization proceed in the millisecond and second time scales, respectively, so a rapid sequential-mixing experiment was performed with delay times from 10 ms to 60 s. WT ELIC proteoliposomes were mixed 1:1 with Stopped-flow Buffer A containing 2x concentration of propylamine (20 mM). After a variable delay time, the sample was mixed 1:1 with quenching buffer (50 mM HEPES pH 7, 90 mM NaNO₃, 50 mM TiNO₃), and ANTS fluorescence was recorded for 1 s. Multiple repeat measurements were obtained for each delay time and averaged. For ELIC5, activation proceeds in the seconds time scale and the channel is anticipated to not desensitize. To test whether ELIC5 exhibits any desensitization over a long time scale (up to 20 minutes) we modified the assay to add propylamine manually. At predetermined times (1-20 minutes), a single mixing experiment was performed that involved 1:1 mixing with quenching buffer followed by measurement of ANTS fluorescence for 1 s. The data were analyzed using the Pro-Data SX software from Applied Photophysics. The fluorescence quenching traces were fit to a stretched exponential and the rate of Tl⁺ influx was determined at 2 ms [44].



Supplementary Figure 1

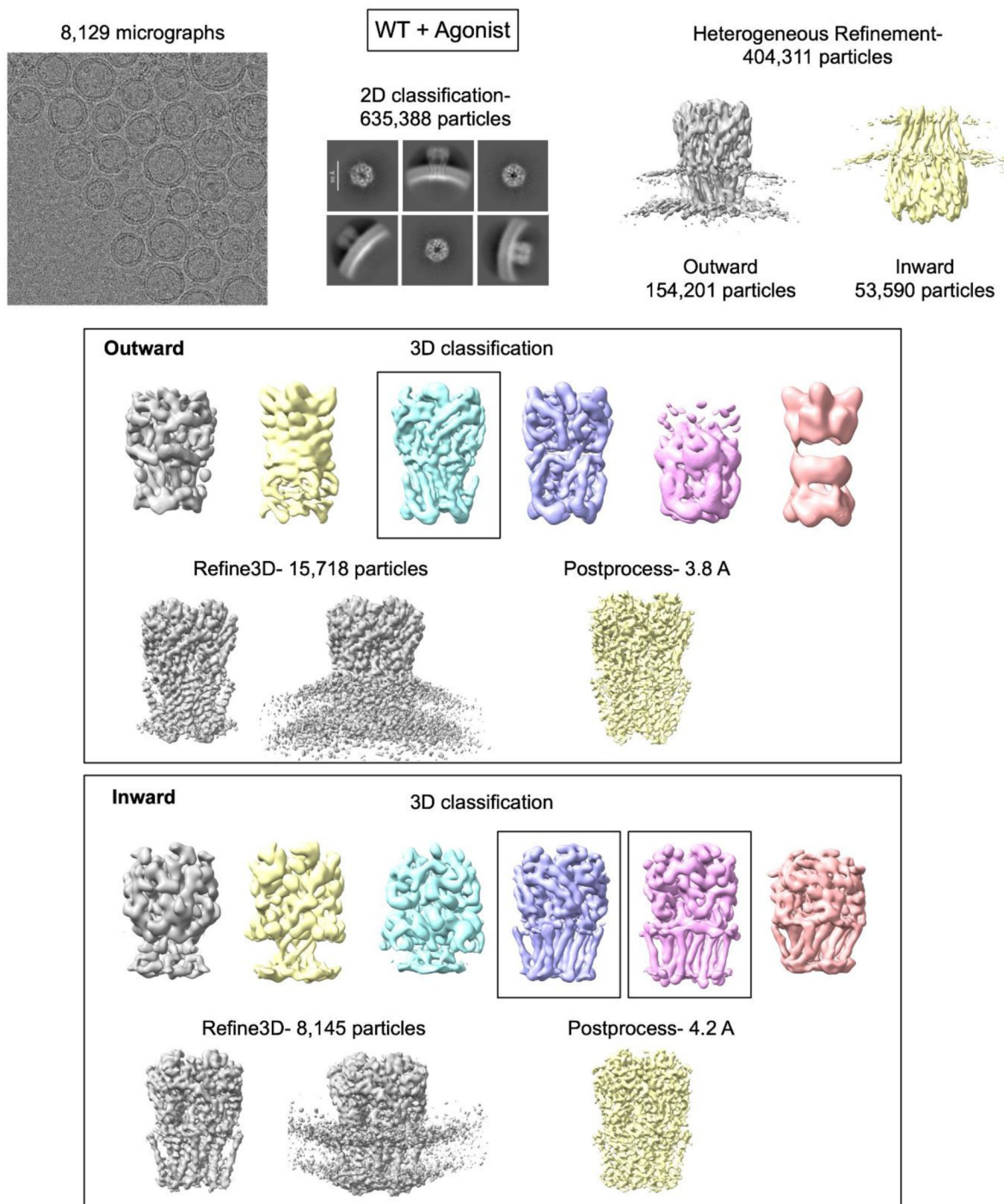
Summary of single particle cryo-EM analysis of WT ELIC in liposomes.

After multiple rounds of heterogeneous refinement in CryoSPARC to separate particles into inward- and outward-facing populations, multiple rounds of 3D classification were performed in Relion-5 to yield the final maps. The results from the final heterogeneous refinement and 3D classification jobs are shown.



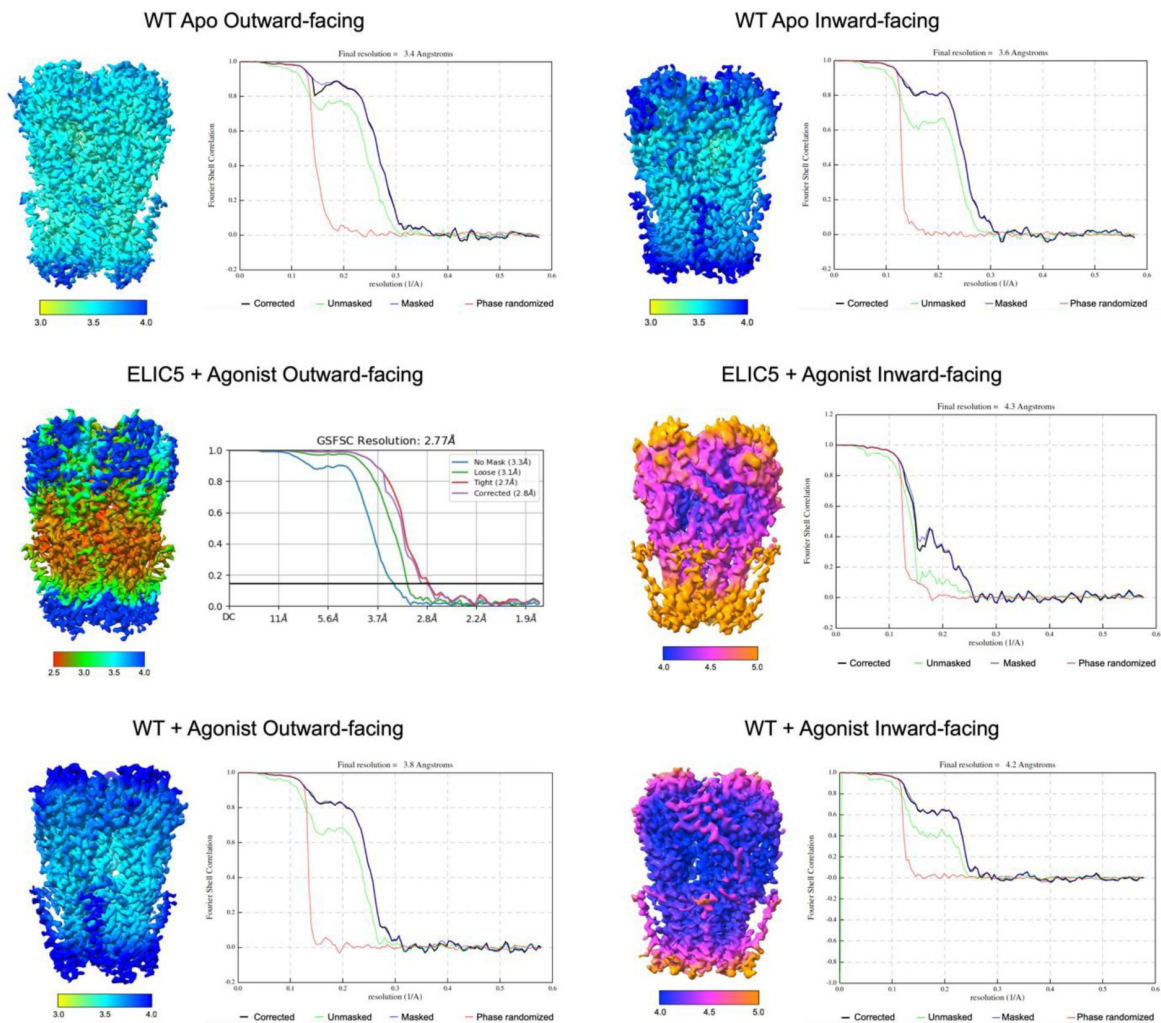
Supplementary Figure 2

Summary of single particle cryo-EM analysis of ELIC5 with agonist in liposomes, similar to Supplementary Figure 1.



Supplementary Figure 3

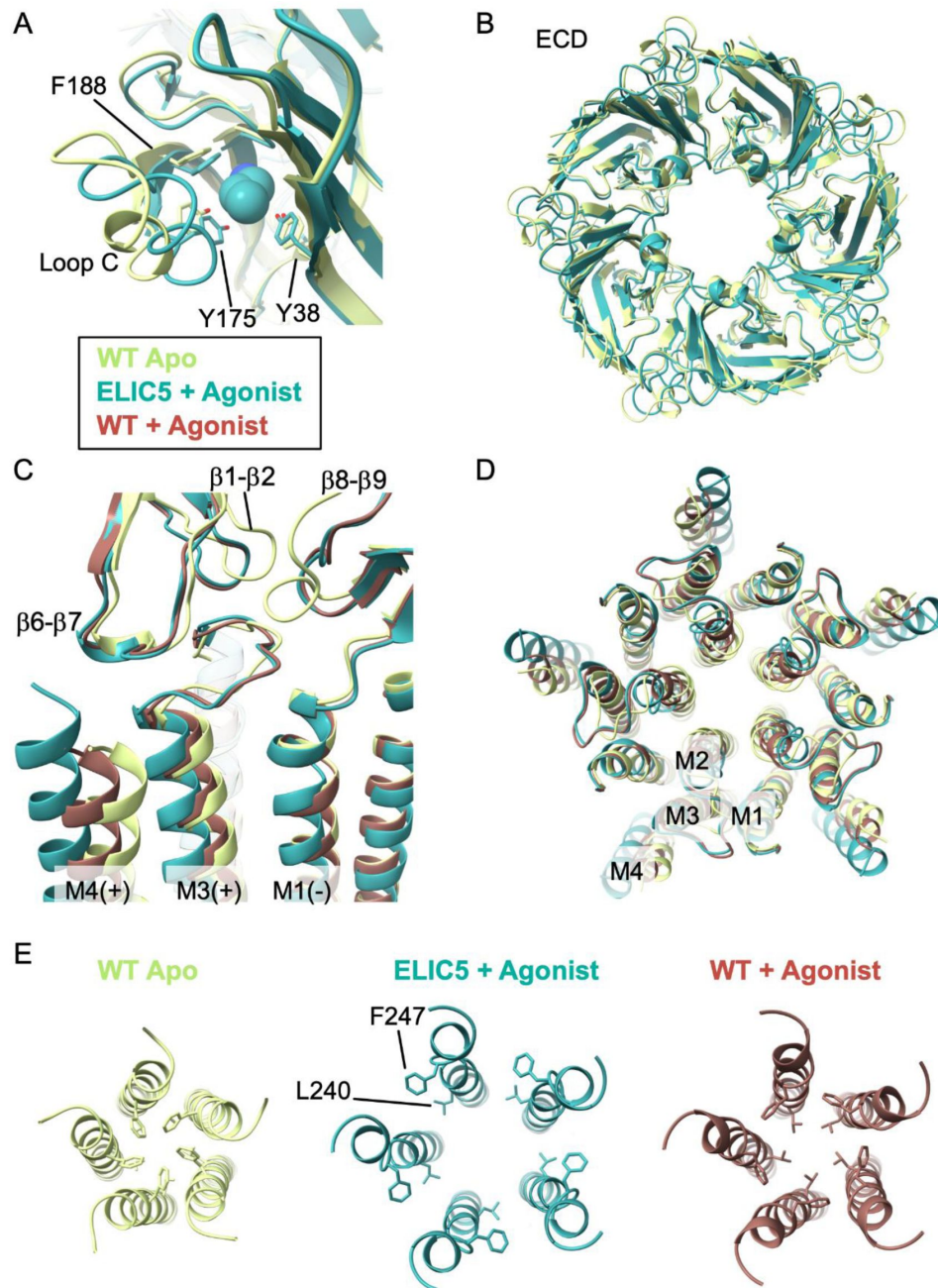
Summary of single particle cryo-EM analysis of WT ELIC with agonist in liposomes, similar to Supplementary Figure 1.



Supplementary Figure 4

Display of local resolution on sharpened maps and FSC curves from outward-facing and inward-facing ELIC structures in liposomes.

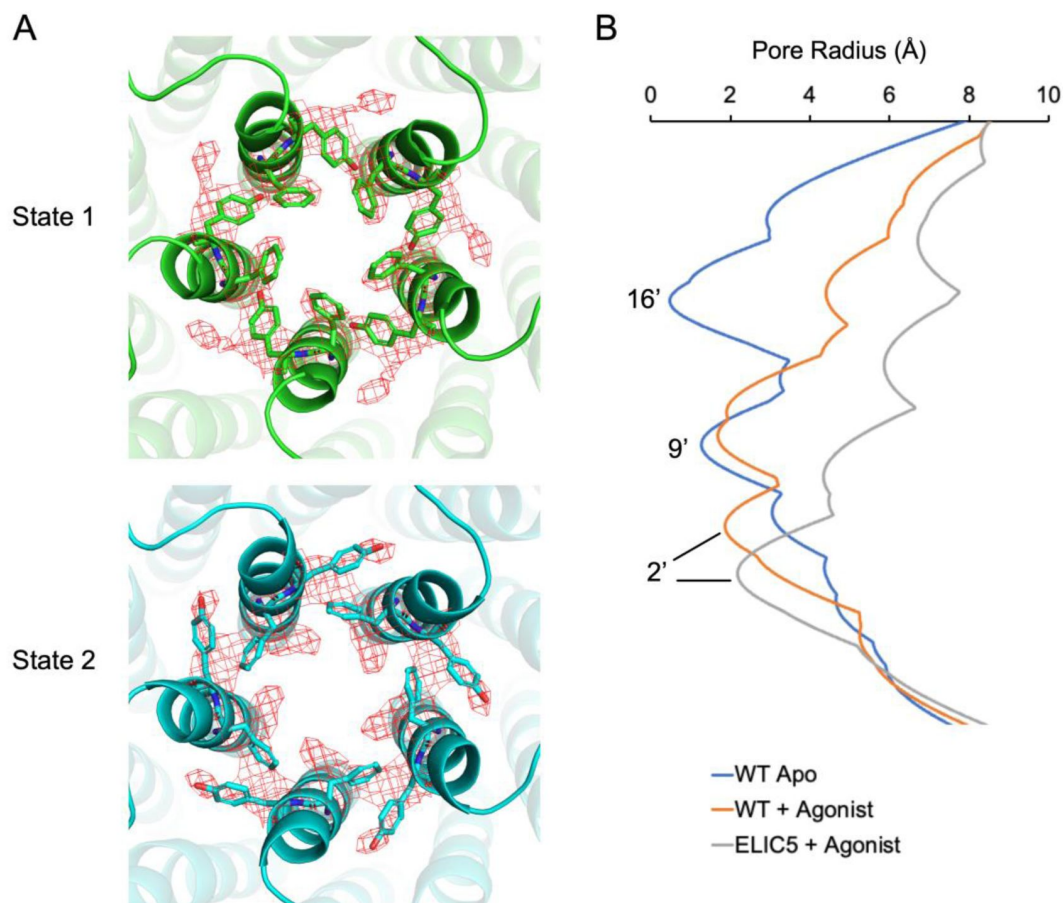
The final map of outward-facing ELIC5 with agonist in liposomes was obtained from CryoSPARC. The remaining maps were obtained from Relion-5.



Supplementary Figure 5

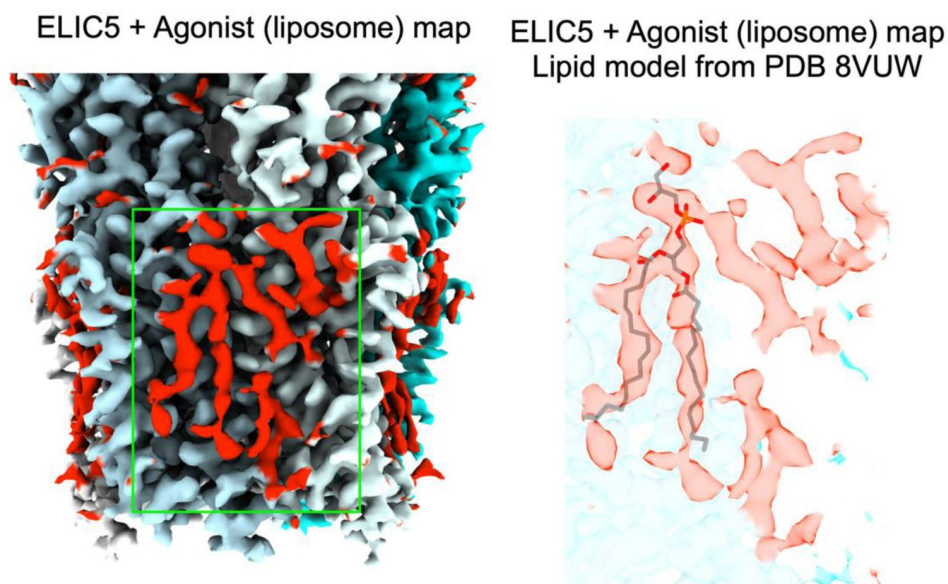
Comparison of resting (WT apo), activated (ELIC5 + agonist) and desensitized (WT + agonist) structures of ELIC in liposomes.

All images are from a global superposition of the structures. (A) View of the agonist/orthosteric binding site with bound propylamine. Loop C and three aromatic residues that interact with propylamine are labeled. The activated structure shows a contraction of the agonist binding site compared to the resting structure. (B) View of the extracellular domain (ECD) from the extracellular side along the pore axis. The activated structure shows a counter-clockwise twisting and slight contraction of the ECD. (C) View of the ECD-TMD interface. The $\beta 1-\beta 2$, $\beta 6-\beta 7$, and $\beta 8-\beta 9$ loops are labeled along with M4, and M3 and M1 from adjacent subunits. The ECD interfacial loops are similar between the activated and desensitized structures, but the transmembrane helices show a tilting and translation away from the pore axis that is greater in the activated compared to the desensitized structure. (D) View of the TMD from the extracellular side along the pore axis. (E) View of the pore-lining M2 showing the rotation of the F247 and L240 in the activated structure compared to the resting and desensitized structures.



Supplementary Figure 6

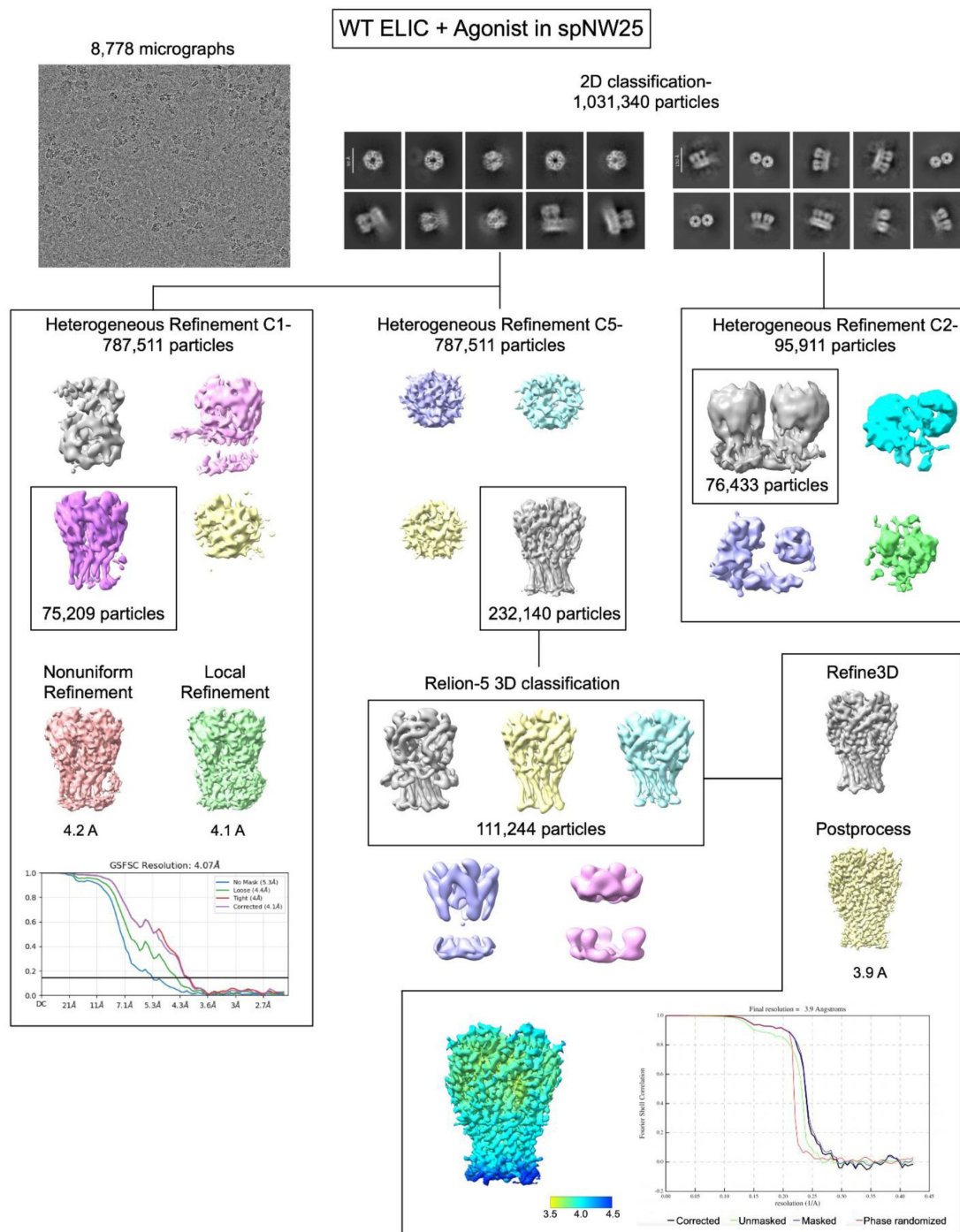
(A) View of the cryo-EM map of WT ELIC with agonist in liposomes showing the fit for State 1 and State 2 models, which differ primarily in the side chain orientation of F247 and Y248. In State 1, F247 orients towards the pore axis, while in State 2, F247 orients towards the adjacent subunit. (B) Plot of the pore radius from the liposome structures (WT apo, WT with agonist state 2 and ELIC5 with agonist) generated using HOLE [45]. The pore-lining M2 residues at 16' (F247), 9' (L240) and 2' (Q233) are labeled.



Supplementary Figure 7

Cryo-EM map of ELIC5 with agonist in liposomes with non-protein lipid-like densities colored in red.

The lipid-like densities in the green box are shown on the right along with the phospholipid from PDB 8VUW (structure of agonist-bound ELIC5 in MSP1E3D1 nanodiscs). This image was produced by fitting ELIC5 from 8VUW in the ELIC5 map from liposomes, and displaying the phospholipid from 8VUW with the non-protein densities from the map of ELIC5 in liposomes.



Supplementary Figure 8

Summary of single particle cryo-EM analysis of WT ELIC with agonist in spNW25 nanodiscs.

2D class averages were separated into single pentamers or dimers of pentamers. The particles consisting of single pentamers were processed with C1 symmetry in CryoSPARC only, or with C5 symmetry in CryoSPARC and Relion-5. Shown are the FSC curves for both C1 and C5 reconstructions, and the local resolution of the C5 map. The C1 map did not show significant asymmetry in the protein structure except for differences in the local resolution. Therefore, a model was only produced based on the C5 reconstruction, which had better resolution. The dimers of pentamers were separately processed in CryoSPARC with C2 symmetry, and this did not yield a high-resolution reconstruction.

	ELIC state 1 with propylamine facing ECD outwards in liposomes with 2:1:1 POPC:POPE:POPG EMD-49390 PDB 9NGQ	ELIC state 2 with propylamine facing ECD outwards in liposomes with 2:1:1 POPC:POPE:POPG EMD-49391 PDB 9NGR	ELIC with propylamine facing ECD inwards in liposomes with 2:1:1 POPC:POPE:POPG EMD-49392 PDB 9NGS	ELIC facing ECD outwards in liposomes with 2:1:1 POPC:POPE:POPG EMD-49383 PDB 9NGF	ELIC facing ECD inwards in liposomes with 2:1:1 POPC:POPE:POPG EMD-49384 PDB 9NGG
Data collection and processing					
Magnification	75000	75000	75000	75000	75000
Voltage (kV)	300	300	300	300	300
Electron exposure (e-/Å ²)	54.4	54.4	54.4	55.4	55.4
Defocus range (µm)	-1 to -2.4	-1 to -2.4	-1 to -2.4	-1 to -2.4	-1 to -2.4
Pixel size (Å)	0.865	0.865	0.865	0.868	0.868
Symmetry imposed	C5	C5	C5	C5	C5
Initial particle images (no)	635,388	635,388	635,388	570,264	570,264
Final particle images (no)	15,718	15,718	8,145	26,273	13,614
Map resolution (Å)	3.8	3.8	4.2	3.4	3.6
FSC threshold	0.143	0.143	0.143	0.143	0.143
Refinement					
Initial model used	PDB 8F34	PDB 8F34	PDB 8F34	PDB 8F35	PDB 8F35
Model resolution (Å)	3.8	3.8	4.2	3.5	3.7
FSC threshold	0.5	0.5	0.5	0.5	0.5

Supplementary Table 1

Summary of cryo-EM data collection and refinement parameters

Map sharpening B factor (Å ²)	-130.301	-130.301	-138.788	-117.585	-130.345
Model composition					
Non-hydrogen atoms	12551	12551	12549	12585	12617
Protein Residues	1535	1535	1535	1535	1535
Ligands	5	5	5	0	0
B factors (Å²) (0.5)					
Protein	13.55	13.55	29.12	27.02	25.93
Ligand	9.82	9.82	9.57	-----	-----
R.m.s. deviations					
Bond lengths (Å)	0.006	0.007	0.006	0.005	0.004
Bond angles (°)	1.099	1.132	1.167	1.083	1.012
Validation					
MolProbity Score	1.77	1.77	1.53	1.75	1.61
Clashscore	8.20	7.92	4	7	4.54
Poor rotamers (%)	0	0	0	0	0
Ramachandran plot					
Favored (%)	95.34	95.08	95.08	94.43	94.43
Allowed (%)	4.66	4.92	4.92	5.57	5.57
Disallowed (%)	0	0	0	0	0

Supplementary Table 1 (continued)

	ELIC5 with propylamine facing ECD outwards in liposomes with 2:1:1 POPC:POPE:POPG EMD-49382 PDB 9NGC	ELIC5 with propylamine facing ECD inwards in liposomes with 2:1:1 POPC:POPE:POPG EMD-49385 PDB 9NGI	ELIC with propylamine in spNW25 nanodiscs with 2:1:1 POPC:POPE:POPG EMD-49400 PDB 9NH4
Data collection and processing			
Magnification	75000	75000	120000
Voltage (kV)	300	300	200
Electron exposure (e-/ Å ²)	56.9	56.9	46.6
Defocus range (µm)	-1 to -2.4	-1 to -2.4	-0.8 to -2.4
Pixel size (Å)	0.868	0.868	1.184
Symmetry imposed	C5	C5	C5
Initial particle images (no)	422,344	422,344	1,031,340
Final particle images (no)	120,578	7,244	111,244
Map resolution (Å)	2.8	4.3	3.9
FSC threshold	0.143	0.143	0.143
Refinement			
Initial model used	PDB 8VUW	PDB 8VUW	PDB 8F34
Model resolution (Å)	3.1	4.1	4.2
FSC threshold	0.5	0.5	0.5
Map sharpening B factor (Å ²)	-121.1	-156.539	-258.138
Model composition			

Supplementary Table 1 (continued)

Supplementary Table 1 (continued)

Non-hydrogen atoms	12722	12729	11320
Protein Residues	1550	1550	1375
Ligands	5	5	5
B factors ($\text{\AA}^2$) (0.5)			
Protein	78.30	139.9	32.33
Ligand	59.82	93.71	16.82
R.m.s. deviations			
Bond lengths ($\text{\AA}$)	0.005	0.006	0.006
Bond angles ($^\circ$)	1.083	1.189	1.169
Validation			
MolProbity Score	1.22	1.94	2.29
Clashscore	2.33	11.19	20.80
Poor rotamers (%)	0	0	0
Ramachandran plot			
Favored (%)	96.75	94.48	92.31
Allowed (%)	3.25	5.52	7.69
Disallowed (%)	0	0	0

Supplementary Table 2

Distance along the pore axis (i.e. perpendicular to the lipid membrane) between the indicated residues (C α atoms) for each structure.

The measurements show changes in the height of each transmembrane helix along the pore axis.

	M1 (W204 to L225)	M2 (F228 to T249)	M3 (V261 to F282)
WT ELIC with agonist in liposomes	32.3 $\text{\AA}$	32.5 $\text{\AA}$	31.0 $\text{\AA}$
WT ELIC with agonist in spNW25	30.5 $\text{\AA}$	31.9 $\text{\AA}$	30.2 $\text{\AA}$
WT ELIC with agonist in spMSP1D1 (PDB 8F34)	32.0 $\text{\AA}$	32.2 $\text{\AA}$	30.6 $\text{\AA}$

	WT ELIC with agonist		
	MSP1E3D1 (PDB 8D66)	spMSP1D1 (PDB 8F34)	Liposome (PDB 9NGQ)
TMD Interface (area)	1176.7 Å	1176.8 Å	1096.3 Å
Buried surface area between M4 and the rest of ELIC	771.7 Å	757.7 Å	732.7 Å
Total buried surface area	24864.7 Å	25183.4 Å	23947.3 Å
	ELIC5 with agonist		
	MSP1E3D1 (PDB 8VUW)	spNW15 (PDB 8TWV)	Liposome (PDB 9NGC)
TMD Interface (area)	1171.1 Å	1119.0 Å	1091.7 Å
Buried surface area between M4 and the rest of ELIC	842.0 Å	986.2 Å	870.3 Å
Total buried surface area	25312.0 Å	25065.1 Å	24166.5 Å

Supplementary Table 3

Measurements of the area at the interface between subunits in the TMD and the total buried surface area were determined using the PDBePISA server [46], and the buried surface area between M4 and the rest of the ELIC protein was determined using ChimeraX1.6.1.

Data Availability

The data supporting the findings of this study are available within the paper and supplementary information files. The cryo-EM maps have been deposited in the Electron Microscopy Data Bank (EMDB) under accession codes EMD-49382, EMD-49383, EMD-49384, EMD-49385, EMD-49390, EMD-49391, EMD-49392, and EMD-49400. The structural coordinates have been deposited in the RCSB Protein Data Bank (PDB) under the accession codes 9NGC, 9NGF, 9NGG, 9NGI, 9NGQ, 9NGR, 9NGS, and 9NH4.

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Additional information

Authors Contributions Statement

W.W.C. and V.D. conceived the project and designed the experimental procedures. W.W.C. and V.D. carried out the protein expression and purification, nanodisc and liposome reconstitution and single particle analysis. B.K.T. and H.X. performed the fluorescence stopped-flow liposomal flux assay. All authors reviewed the paper.

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Reviewer #1 (Public review):

Summary:

The authors, Dalal, et. al., determined cryo-EM structures of open, closed, and desensitized states of the pentameric ligand-gated ion channel ELIC reconstituted in liposomes, and compared them to structures determined in varying nanodisc diameters. They argue that the liposomal reconstitution method is more representative of functional ELIC channels, as they were able to test and recapitulate channel kinetics through stopped-flow thallium flux liposomal assay. The authors and others have described channel interactions with membrane scaffold proteins (MSP), initially thought to be in a size-dependent manner. However, the authors reported their cryo-EM ELIC structure interacts with the large nanodisc spNW25, contrary to their original hypotheses. This suggests that the channels interactions with MSPs might alter its structure, possibly influencing the functional states of the channel. Thus, the authors describe reconstitution in liposomes are more representative of the native structure and can recapitulate all channel states.

Strengths:

Cryo-EM structural determination from proteoliposomes is promising methodology within the ion channel field due to their large surface area and lack of MSP or other membrane memetics that could alter channel structure. The authors succeeded in comparing structures determined in liposomes to those in a wide range of nanodisc diameters. This comparison gives rise to important discussions for other membrane protein structural studies when deciding the best method for individual circumstances.

Weaknesses:

As the overarching goal of the study was to determine structural differences of ELIC in detergent nanodiscs and liposomes. The authors stated they determined open, closed, and desensitized states of ELIC reconstituted in liposomes and suggest the desensitization gate is at the 9' region of the pore. However, limited functional data was provided when determining the functional states of the channel with most of the evidence deriving from structures, which only provides snapshots of channels.

<https://doi.org/10.7554/eLife.106728.2.sa2>

Reviewer #2 (Public review):

Summary

The report by Dalas and colleagues introduces a significant novelty in the field of pentameric ligand-gated ion channels (pLGICs). Within this family of receptors, numerous structures are available, but a widely recognised problem remains in assigning structures to functional states observed in biological membranes. Here, the authors obtain both structural and functional information of a pLGIC in a liposome environment. The model receptor ELIC is captured in the resting, desensitised and open states. Structures in large nanodiscs, possibly biased by receptor-scaffold protein interactions, are also reported. Altogether these results set the stage for the adoption of liposomes as a proxy for the biological membranes, for cryoEM studies of pLGICs and membrane proteins in general.

Strengths

The structural data is comprehensive, with structures in liposomes in the 3 main states (and for each, both inward-facing and outward-facing), and an agonist-bound structure in the large spNW25 nanodisc (and a retreatment of previous data obtained in a smaller disc). It adds up to a series of work from the same team that constitutes a much-needed exploration of various types of environment for the transmembrane domain of pLGICs. The structural analysis is thorough.

The tone of the report is particularly pleasant, in the sense that the authors' claims are not inflated. For instance, a sentence such as "By performing structural and functional characterization under the same reconstitution conditions, we increase our confidence in the functional annotation of these structures." is exemplary.

Weakness

All the details necessary to reproduce the work are present in the Methods. Nevertheless, the biochemistry might have been shown and discussed in greater details. While I do believe that liposomes will be in most cases better than, say, nanodiscs, the process that leads from the protein in its membrane down to the liposome will play a big role in preserving the native structure.

<https://doi.org/10.7554/eLife.106728.2.sa1>

Author response:

The following is the authors' response to the original reviews

Public Reviews:**Reviewer #1 (Public review):**

Summary:

The authors, Dalal, et. al., determined cryo-EM structures of open, closed, and desensitized states of the pentameric ligand-gated ion channel ELIC reconstituted in liposomes, and compared them to structures determined in varying nanodisc diameters. They argue that the liposomal reconstitution method is more representative of functional ELIC channels, as they were able to test and recapitulate channel kinetics through stopped-flow thallium flux liposomal assay. The authors and others have described channel interactions with membrane scaffold proteins (MSP), initially thought to be in a size-dependent manner. However, the authors reported that their cryo-EM ELIC structure interacts with the large nanodisc spNW25, contrary to their original hypotheses. This

suggests that the channel's interactions with MSPs might alter its structure, possibly not accurately representing/reflecting functional states of the channel.

Strengths:

Cryo-EM structural determination from proteoliposomes is a promising methodology within the ion channel field due to their large surface area and lack of MSP or other membrane mimetics that could alter channel structure. Comparing liposomal ELIC to structures in various-sized nanodiscs gives rise to important discussions for other membrane protein structural studies when deciding the best method for individual circumstances.

Weaknesses:

The overarching goal of the study was to determine structural differences of ELIC in detergent nanodiscs and liposomes. Including comparisons of the results to the native bacterial lipid environment would provide a more encompassing discussion of how the determined liposome structures might or might not relate to the native receptor in its native environment. The authors stated they determined open, closed, and desensitized states of ELIC reconstituted in liposomes and suggest the desensitization gate is at the 9' region of the pore. However, no functional studies were performed to validate this statement.

The goal of this study was to determine structures of ELIC in the same lipid environment in which its function is characterized. However, it is also worth noting that phosphatidylethanolamine and phosphatidylglycerol, two lipids used for the liposome formation, are necessary for ELIC function (PMID 36385237) and principal lipid components of gram-negative bacterial membranes in which ELIC is expressed.

The desensitized structure of ELIC in liposomes shows a pore diameter at the hydrophobic L240 (9') residue of 3.3 Å, which is anticipated to pose a large energetic barrier to the passage of ions due to the hydrophobic effect. We have included a graphical representation of pore diameters from the HOLE analysis for all liposome structures in Supplementary Figure 6B. While we have not tested the role of L240 in desensitization with functional experiments, it was shown by Gonzalez-Gutierrez and colleagues (PMID 22474383) that the L240A mutation apparently eliminates desensitization in ELIC. This finding is consistent with L240 (9') being the desensitization gate of ELIC. We have referenced this study when discussing the desensitization gate in the Results.

Reviewer #2 (Public review):

Summary

The report by Dalas and colleagues introduces a significant novelty in the field of pentameric ligand-gated ion channels (pLGICs). Within this family of receptors, numerous structures are available, but a widely recognised problem remains in assigning structures to functional states observed in biological membranes. Here, the authors obtain both structural and functional information of a pLGIC in a liposome environment. The model receptor ELIC is captured in the resting, desensitized, and open states. Structures in large nanodiscs, possibly biased by receptor-scaffold protein interactions, are also reported. Altogether, these results set the stage for the adoption of liposomes as a proxy for the biological membranes, for cryoEM studies of pLGICs and membrane proteins in general.

Strengths

The structural data is comprehensive, with structures in liposomes in the 3 main states (and for each, both inward-facing and outward-facing), and an agonist-bound structure in the large spNW25 nanodisc (and a retreatment of previous data obtained in a smaller disc). It adds up to a series of work from the same team that constitutes a much-needed exploration of various types of environment for the transmembrane domain of pLGICs. The structural analysis is thorough.

The tone of the report is particularly pleasant, in the sense that the authors' claims are not inflated. For instance, a sentence such as "By performing structural and functional characterization under the same reconstitution conditions, we increase our confidence in the functional annotation of these structures." is exemplary.

Weaknesses

Core parts of the method are not described and/or discussed in enough detail. While I do believe that liposomes will be, in most cases, better than, say, nanodiscs, the process that leads from the protein in its membrane down to the liposome will play a big role in preserving the native structure, and should be an integral part of the report. Therefore, I strongly felt that biochemistry should be better described and discussed. The results section starts with "Optimal reconstitution of ELIC in liposomes [...] was achieved by dialysis". There is no information on why dialysis is optimal, what it was compared to, the distribution of liposome sizes using different preparation techniques, etc... Reading the title, I would have expected a couple of paragraphs and figure panels on liposome reconstitution. Similarly, potential biochemical challenges are not discussed. The methods section mentions that the sample was "dialyzed [...] over 5-7 days". In such a time window, most of the members of this protein family would aggregate, and it is therefore a protocol that can not be directly generalised. This has to be mentioned explicitly, and a discussion on why this can't be done in two days, what else the authors tested (biobeads? ... ?) would strengthen the manuscript.

To a lesser extent, the relative lack of both technical details and of a broad discussion also pertains to the cryoEM and thallium flux results. Regarding the cryoEM part, the authors focus their analysis on reconstructions from outward-facing particles on the basis of their better resolutions, yet there was little discussion about it. Is it common for liposome-based structures? Are inward-facing reconstructions worse because of the increased background due to electrons going through two membranes? Are there often impurities inside the liposomes (we see some in the figures)? The influence of the membrane mimetics on conformation could be discussed by referring to other families of proteins where it has been explored (for instance, ABC transporters, but I'm sure there are many other examples). If there are studies in other families of channels in liposomes that were inspirational, those could be mentioned. Regarding thallium flux assays, one argument is that they give access to kinetics and set the stage for time-resolved cryoEM, but if I did not miss it, no comparison of kinetics with other techniques, such as electrophysiology, nor references to eventual pioneer time-resolved studies are provided.

Altogether, in my view, an updated version would benefit from insisting on every aspect of the methodological development. I may well be wrong, but I see this paper more like a milestone on sample prep for cryoEM imaging than being about the details of the ELIC conformations.

Additions have been made to the Results and Discussion sections elaborating on the following points: 1) reconstitution of ELIC in liposomes using dialysis, the advantage of this over other methods such as biobeads, and whether the dialysis protocol can be shortened for other less stable proteins; 2) the issue of separating outward- and inward-facing channels; 3) referencing the effect of nanodiscs on ABC transporters, structures of membrane proteins in

liposomes, and pioneering time-resolved cryo-EM studies; and 4) comparison of the kinetics of ELIC gating kinetics with electrophysiology measurements. With regards to the first point, it should be noted that all necessary details are provided in the Methods to reproduce the experiments including the reconstitution and stopped-flow thallium flux assay. It is also important to note that the same preparation for making proteoliposomes was used for assessing function using the stopped-flow thallium flux assay and for determining the structure by cryo-EM. This is now stated in the Results.

Recommendations for the authors:

Reviewer #1 (Recommendations for the authors):

Major revisions:

(1) The authors suggest that the desensitization gate is located at the 9' region within the pore. However, as stated by the authors, the 2' residues function as the desensitization gate in related channels. In a few of their HOLE analyzed structures (e.g. Figure 2B and 4B), there seems to be a constriction also at 2', but this finding is not discussed in the context of desensitization. Further functional testing of mutated 9' and/or 2' gates would bolster the argument for the location of the desensitization gate.

As stated above, we have included HOLE plots of pore radius in Supplementary Fig. 6B and referenced the study showing that the L240A mutation (9') in ELIC (PMID 22474383) appears to eliminate desensitization. This result along with the narrow pore diameter at 9' in the desensitized structure suggests that 9' is likely a desensitization gate in ELIC. In contrast, mutation of Q233 (2') to a cysteine in a previous study produced a channel that still desensitizes (PMID 25960405). Since Q233 is a hydrophilic residue in contrast to L240, Q233 probably does not pose the same energetic barrier to ion translocation as L240 based on the structure.

(2) In discussing functional states of ELIC and ELIC5 in different reconstitution methods, the authors reference constriction sites determined by HOLE analysis software. These constriction sites were key evidence for the authors to determine functional state, however, it is difficult to discern pore sizes based on the figures. Pore diameters and clear color designation (ie, green vs orange) with the figures would greatly aid their discussions.

HOLE plots are displayed in Supplementary Fig. 6B and pore diameters are not provided in the text.

(3) The authors had an intriguing finding that ELIC dimers are found in spNW25 scaffolds. Is there any functional evidence to suggest they could be functioning as dimers?

There is no evidence that the function of ELIC or other pLGICs is altered by the formation of dimers of pentamers. Therefore, while this result is intriguing and likely facilitated by concentrating multiple ELIC pentamers within the nanodisc, it is not clear if these interactions have any functional importance. We have stated this in the Results.

(4) Thallium flux assay to validate channel function within proteoliposomes. Proteoliposomes are known to be generally very leaky membranes, would be good to have controls without ELIC added to determine baseline changes in fluorescence.

We have established from multiple previous studies that liposomes composed of 2:1:1 POPC:POPE:POPG (PMID 36385237 and 31724949) do not show significant thallium flux as

measured by the stopped-flow assay (PMID 29058195) in the absence of ELIC activity. Furthermore, in the present study, the data in Fig. 1A of WT ELIC shows a low thallium flux rate 60 seconds after exposure to agonist when the ion channel has mostly desensitized. Therefore, this data serves also as a control indicating that the high thallium flux rates in response to agonist (at earlier delay times) are not due to leak, but rather due to ELIC channel activity.

Minor revisions:

(1) Abstract and introduction. 'Liganded' should be ligand

We removed this word and changed it to “agonist-bound” for consistency throughout the manuscript.

(2) Inconsistent formatting of FSC graphs in Supplemental Figure 4

The difference is a consequence of the different formatting between cryoSPARC and Relion FSC graphs.

Reviewer #2 (Recommendations for the authors):

Minor writing remarks:

The present report builds on previous work from the same team, and to my eye it would be a plus if this were conveyed more explicitly. I see it as a strength to explore various developments in several papers that complement each other. E.g in the introduction when citing reference 12 (Dalal 2024), later in introducing ref 15 (Petroff 2022), I wish I was reminded of the main findings and how they fit with the new results.

We have expanded on the Results and Discussion detailing key findings from these studies that are relevant to the current study.

Suggestions for analysis:

Data treatment. Maybe I missed it, but I wondered if C1 vs C5 treatment of the liposome data showed any interesting differences? When I think about the biological membrane, I picture it as a very crowded place with lots of neighbouring proteins. I would not be surprised if, similarly to what they do in discs, the receptor would tend to stick to, or bump into, anything present also in liposomes (a neighboring liposome, some undefined density inside the liposome).

We attempted to perform C1 heterogeneous refinement jobs in cryoSPARC and C1 3D classification in Relion5. For the WT datasets, these did not produce 3D reconstructions that were of sufficient quality for further refinement. For ELIC5 with agonist, the C1 reconstructions were not different than the C5 reconstructions. Furthermore, there was no evidence of dimers of pentamers from the 2D or 3D treatments, unlike what was observed in the spNW25 nanodiscs. This is likely because the density of ELIC pentamers in the liposomes was too low to capture these transient interactions. We have included this information in the Methods.

In data treatment, we sometimes find only what we're looking for. I wondered if the authors tried to find, for instance, the open and D conformations in the resting dataset during classifications.

This is an interesting question since some population of ELIC channels could visit a desensitized conformation in the absence of agonist and this would not be detected in our flux assay. After extensive heterogeneous refinement jobs in cryoSPARC and 3D classification jobs in Relion5, we did not detect any unexpected structures such as open/desensitized conformations in the apo dataset.

In the analysis of the M4 motions, is there info to be gained by looking at how it interacts with the rest of the TMD? For instance, I wondered if the buried surface area between M4 and the rest was changed. Also one could imagine to look at that M4 separately in outward-facing and inward-facing conformations (because the tension due to the bilayer will not be the same in the outer layer in both orientations - intuitively, I'd expect different levels of M4 motions)

We have expanded our analysis of the structures as recommended. We determined the buried surface area between M4 and the rest of the channel in the liganded WT and ELIC5 structures in liposomes and nanodiscs, as well as the area between the TMD interfaces for these structures. There appears to be a pattern where liposome structures show less buried surface area between M4 and the rest of the channel, and less area at the TMD interfaces. Overall, this suggests that the liposome structures of ELIC in the open-channel or desensitized conformations are more loosely packed in the TMD compared to the nanodisc structures.

We have also further discussed the issue of separating outward- and inward-facing conformations in the Results. The problem with classifying outward- and inward-facing orientations is that top/down or tilted views of the particles cannot be easily distinguished as coming from channels in one orientation or the other, unless there are conformational differences between outward- and inward-facing channels that would allow for their separation during 3D heterogeneous refinement or 3D classification. Furthermore, since the inward-facing reconstructions are of much lower resolution than the outward-facing reconstructions, we suspect that these particles are more heterogeneous possibly containing junk, multiple conformations, or particles that are both inward- and outward-facing. On the other hand, the outward-facing structures are of good quality, and therefore we are more confident that these come from a more homogeneous set of particles that are likely outward-facing (Note that most particles are outward facing based on side views of the 2D class averages). That said, when examining the conformation of M4 in outward- and inward-facing structures, we do not see any significant differences with the caveat that the inward-facing structures are of poor quality and that inward- and outward-facing particles may not have been well-separated.

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