**STRUCTURAL BIOLOGY**

**Structure-based mechanism of cysteinyl leukotriene receptor inhibition by antiasthmatic drugs**

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The G protein–coupled cysteinyl leukotriene receptor CysLT1R mediates inflammatory processes and plays a major role in numerous disorders, including asthma, allergic rhinitis, cardiovascular disease, and cancer. Selective CysLT1R antagonists are widely prescribed as antiasthmatic drugs; however, these drugs demonstrate low effectiveness in some patients and exhibit a variety of side effects. To gain deeper understanding into the functional mechanisms of CysLTRs, we determined the crystal structures of CysLT1R bound to two chemically distinct antagonists, zafirlukast and pranlukast. The structures reveal unique ligand-binding modes and signaling mechanisms, including lateral ligand access to the orthosteric pocket between transmembrane helices TM4 and TM5, an atypical pattern of microswitches, and a distinct four-residue–coordinated sodium site. These results provide important insights and structural templates for rational discovery of safer and more effective drugs.

**INTRODUCTION**

Cysteinyl leukotriene receptor type 1 (CysLT1R) along with CysLT2R are two G protein (heterotrimeric GTP-binding protein)–coupled receptors (GPCRs) activated by the endogenous leukotrienes LTC4, LTD4, and LTE4, produced from arachidonic acid (1). CysLT1R is a nanomolar affinity receptor for LTD4, with lower affinities for LTC4 and LTE4 (2). It is broadly expressed in most types of leukocytes, lung, spleen, intestines, pancreas, prostate, and smooth muscle, predominantly activating Gq/11, while also signaling through Gq/o and through G protein–independent pathways (1). CysLT1R is a key player in allergic and inflammatory disorders, such as asthma, allergic rhinitis, atopic dermatitis, and urticaria, and is involved in cardiovascular diseases and several types of cancer (3–8). The selective CysLT1R antagonists montelukast, zafirlukast, and pranlukast are often used for the treatment of asthma, allergic rhinitis, and rhinosinusitis (9).

Despite their bronchodilator and anti-inflammatory properties, they have shown low effectiveness in some patients and gastrointestinal symptoms and neuropsychiatric side effects have been reported (8, 10–12), although no causal relationship has yet been established. To gain deeper understanding into the functional mechanisms of CysLTRs, we determined the crystal structures of CysLT1R in complexes with zafirlukast and pranlukast at 2.5- and 2.7-Å resolution, respectively.

**RESULTS**

**CysLT1R structure determination using synchrotron and x-ray free-electron laser (XFEL) sources**

Human CysLT1R was engineered for crystallization by fusion of a thermostabilized apocytochrome b562 RIL (13) into the third intracellular loop (ICL3) and a truncation of the C terminus. This minimally modified construct was crystallized in lipidic cubic phase (LCP) (14) as a complex with zafirlukast or pranlukast. Crystals of CysLT1R bound to pranlukast (CysLT1R-pran) reached an average size of 250 μm by 15 μm by 15 μm, and the structure was obtained using four cryocooled crystals at a synchrotron source. Crystals of CysLT1R bound to zafirlukast (CysLT1R-zafir), however, could not be optimized to grow larger than 10 μm, and therefore, the structure was obtained with an x-ray free-electron laser (15) at room temperature (RT) using 5 μm by 2 μm by 2 μm microcrystals. CysLT1R-pran structure was solved in a monoclinic P21 space group with one monomer per asymmetric unit, while CysLT1R-zafir structure was obtained in a triclinic P1 space group with two monomers per asymmetric unit, forming a parallel dimer through the TM4 (transmembrane helix 4)–TM6 interface (figs. S1 to S3 and table S1).

**Overall receptor architecture**

Overall, CysLT1R-zafir and CysLT1R-pran structures share the same canonical heptahelical transmembrane domain (7TM) fold and similar conformations [Cα root mean square deviation (RMSD), 1.3 Å] (Fig. 1, A and B); however, the chemically distinct ligands demonstrate

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A natural single-nucleotide variant G300<sup>8.48</sup>S was linked to a strong atopic phenotype in the Tristan da Cunha population, markedly increasing their predisposition to asthma (17). In our IP<sub>1</sub> assays, the mutation G300<sup>8.48</sup>S showed improved signal transduction in agreement with previous studies (18), while the mutation G300<sup>8.48</sup>R (as in CysLT<sub>2</sub>R) abolished cell surface expression, and the C-terminal truncation at G300<sup>8.48</sup> rendered the receptor nonresponsive to LTD<sub>4</sub> (table S2), supporting the importance of H8 and its conformational stability in signaling.

Unusual pattern of microswitches

Specific features that set CysLT<sub>1</sub>R apart from other class A receptors are evident in its unique combination of functional motifs or "microswitches" (Fig. 2) (19). Thus, the highly conserved DR<sup>3.50</sup>-Y motif is replaced by FR<sup>3.50</sup>C in CysLT<sub>1</sub>R (Fig. 2B), eliminating the common for inactive-state structures salt bridge between D<sup>3.49</sup> and R<sup>3.50</sup> and conferring more flexibility to R<sup>3.50</sup>. This residue adopts two different conformations in CysLT<sub>1</sub>R-pran and CysLT<sub>1</sub>R-zafir structures (Fig. 2B). Restoring the motif by mutating F120<sup>3.48</sup>D substantially decreases receptor expression and renders the protein nonresponsive to LTD<sub>4</sub>, while C122<sup>3.51</sup>Y mutation does not change the potency of LTD<sub>4</sub> in IP<sub>1</sub> assays (table S2).

A conserved P<sup>5.50</sup>Y<sup>3.40</sup>F<sup>6.44</sup> motif has been characterized in many class A GPCRs as a key microswitch, coupling conformational changes in the orthosteric ligand pocket with transitions in the cytoplasmic G protein– or β-arrestin–binding site (20). While the P-I-F residues are conserved in CysLT<sub>1</sub>R, they are found in a different conformation than in most other antagonist-bound GPCR structures, e.g., in β<sub>2</sub>-AR bound to carazolol [Protein Data Bank (PDB) ID 2RH1]. In both CysLT<sub>1</sub>R structures, concerted rearrangements of I<sup>3.40</sup> and F<sup>6.44</sup> rotamers result in a "switched-on" conformation of this motif, reminiscent of an active-like state (Fig. 2D). This change is apparently related to the replacement of the neighboring "toggle switch" W<sup>6.48</sup> by P<sup>6.44</sup>. Unlike W<sup>6.48</sup> in other GPCRs, the side chain of P<sup>6.44</sup> in CysLT<sub>1</sub>R adopts a "downward" conformation, where it would clash with the conformation of F<sup>6.44</sup> from the P-I-F motif found in inactive receptors. Notably, analysis of other known δ-branch GPCR structures (fig. S4) reveals that all of them also have F<sup>6.48</sup> instead of W<sup>6.48</sup> and all of them have a P-I-F motif in the same switched-on conformation as in CysLT<sub>1</sub>R, despite representing antagonist-bound inactive states. On the intracellular side (Fig. 2C), the TM6 of CysLT<sub>1</sub>R is well aligned with the inactive conformation of this helix in other receptors. However, the TM7 in the NPxxY<sup>7.53</sup> motif region is shifted (~3 Å) inward compared to the inactive-state β<sub>2</sub>-AR and most other GPCRs. This TM7 shift also appears to be common for inactive δ-branch class A GPCR structures (Fig. 2E).

Unique sodium-binding site

The sodium-binding site in both CysLT<sub>1</sub>R structures has a well-defined electron density for a Na<sup>+</sup> ion (fig. S3, E to G) and is distinct from previously observed sites, representing a new variant of this key functional element of class A GPCRs (21, 22). Na<sup>+</sup> ion in CysLT<sub>1</sub>R is coordinated by four side chains (D<sup>69</sup>, S<sup>110</sup>, N<sup>287</sup>, and D<sup>291</sup>), two of which are acidic, and one water molecule, with all distances within a typical for Na<sup>+</sup> coordination 2.4- to 2.6-Å range (Fig. 3). In contrast, in adenosine A<sub>2A</sub> receptor (A<sub>2A</sub>AR) and β<sub>2</sub>-AR, Na<sup>+</sup> is directly coordinated by only two side chains (D<sup>5.50</sup> and S<sup>3.39</sup>) and three waters, and in proteinate-activated receptor P<sub>1</sub> (PAR<sub>1</sub>) and delta opioid receptor (DOR) by three side chains and two waters. Moreover, the Na<sup>+</sup> position in CysLT<sub>1</sub>R is shifted by ~1.5 Å toward the...
intracellular side compared to its location in α- and γ-branch receptors, resembling another δ-branch receptor, PAR1 (PDB ID 3VW7). The difference is that in CysLT1R, the N7.45 side chain directly coordinates Na⁺ instead of making an indirect water-mediated contact with S7.45 in PAR1. Such a tight and well-defined coordination enabled reliable assignment of Na⁺ at 2.5-Å resolution, which otherwise may not be sufficient for this assessment. The tight binding of Na⁺ is also corroborated by a relatively high Na⁺ affinity of 39 ± 11 mM, estimated from its effect on receptor thermostability (fig. S5A).

In agreement with the crystal structures, we observed a pronounced specific sodium effect on CysLT1R thermostability, with melting temperature increased as much as 8°C upon addition of Na⁺ at a physiological (150 mM) concentration (fig. S5). This effect was reproducible in the Apo state and in the presence of zafirlukast. It was specific for sodium and was reduced in D692.50N and D2917.49N mutants, with an overall receptor stability decreased in these mutants. In IP1 assays at physiological sodium concentrations, three of the sodium site mutations (N1063.35A, S1103.39A, and D2917.49N) improved agonist and decreased antagonist potencies, likely by weakening sodium binding, while N1063.35A and S1103.39A also increased constitutive activity of the receptor and reduced LTD4 efficacy (fig. S6). The latter effect of reduced signaling response was also observed for sodium site mutations in A2AAR (23). For D692.50N and N2877.45A mutations, we observed decreased LTD4 potency and/or efficacy (table S2).

**CysLT1R ligand–binding pocket**

The ligand-binding pocket in both CysLT1R-zafir and CysLT1R-pran structures stretches from ECL2 all the way across the receptor toward a gap between TM4 and TM5, deep in the middle section of the 7TM bundle (Fig. 4), which is different from any previously observed pockets in GPCR structures (fig. S4). Zafirlukast and pranlukast are very similar, both the ligand binding and receptor conformation in the vicinity of the TM4-TM5 gap diverge markedly (Fig. 4, B and E). In CysLT1R-pran, the extended phenylbutyl chain of the ligand is enclosed entirely within the 7TM bundle, with only a small opening between T1544.56 and V1925.41 toward the lipid bilayer. In CysLT1R-zafir, a large-scale (~7 Å) movement of the extracellular tip of TM5 and a corresponding rearrangement in ECL2 create a wide sideways opening in the 7TM bundle, which accommodates the indole group of the ligand and is sufficient for passing the whole ligand into the pocket laterally (Fig. 4, C and F). The tilting motion of the extracellular part of TM5 is apparently facilitated by the highly conserved P2015.50 hinge, which is made even more flexible by G1975.46 as found in CysLTRs.
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...the mechanism of ligand entry in lipid receptors and provide an important example of receptor plasticity in binding of two chemically distinct antagonists. The structures suggest a new GPCR activation mechanism in which the P-I-F microswitch is pre-activated while the receptor is stabilized in the inactive state by a tightly bound sodium ion coordinated by four residues, including two acids. In addition, these structures suggest a potential binding mode for native cysteinyl leukotrienes and offer high-quality templates for the rational design of tool compounds and novel lead compounds for drug discovery and validation.

Despite the fact that dihydroxy and cysteinyl leukotrienes are related through arachidonic acid synthetic pathways, CysLT1R shares little sequence identity with leukotriene B4 receptors (BLT1/BLT2, 26/20% identity in 7TM domain, respectively) located on the γ-branch of class A GPCRs (19, 24). Instead, CysLT1R evolutionary belongs to the δ-branch together with purinergic (29% identity with P2Y1R), proteinase-activated (29% identity with PAR1), and platelet-activating factor (29% identity with PA F) receptors. This observation is corroborated by a close structural similarity to P2Y1R (25) (Ca RMSD, 1.1 Å on 90% of residues in 7TM) compared with BLT1 (26) (Ca RMSD, 2.3 Å) (fig. S4). Such a high level of structural similarity as that between CysLT1R and P2Y1R is typically observed within members of GPCR subfamilies, which is especially noteworthy because CysLT1R and P2Y1R bind completely different types of ligands (lipids versus nucleotides) and share only 3 identical out of 30 residues in their respective orthosteric binding pockets.

Since the first observation of sodium effect distinguishing between antagonist and agonist binding in opioid receptors over 45 years ago (27) and the more recent discovery of an allosteric sodium-binding site in the A2A AR (28), sodium ion is emerging as an essential modulator of signaling in many class A GPCRs (21, 22). CysLT1R structure reveals a new type of the sodium-binding site coordinated by four residues and one water. The exact combination of the four sodium–coordinating residues, D2.50, D7.49, N7.45, and S3.39, occurs in sequences of 39 (about 6%) of nonoligofructose class A GPCRs, suggesting that tight coordination of Na+ may be important for the function of these receptors. Notably, PAR1 (29) and PAR2 (30) have so far been the only two other structures solved with D2.50 and D7.49 intact and with a Na+ ion observed in the sodium-binding pocket, while the other two GPCRs with these naturally occurring residues [P2Y1R (25) and P2Y12R (31)] had D7.49N mutations introduced to improve receptor yield and/or stability.

Cysteinyl leukotrienes are lipid signaling molecules, and in general, ligand-access routes into the orthosteric pocket directly from the membrane have been hypothesized for several lipid receptors. Thus, a small opening was observed between TM3 and TM4 in FFAR1 (free fatty acid receptor 1) (PDB ID 4PHU) (32), and between TM1 and TM7 in S1P1 (sphingosine-1-phosphate receptor 1) (PDB ID 3V2Y) (33), while access to the orthosteric pocket between TM4 and TM5 was proposed for two other δ-branch lipid receptors, PAFR (PDB ID 5ZKP) (34) and LPA4 (lysophosphatidic acid receptor 6) (PDB ID 5XSZ) (35), based on docking in PA F and the positioning of an isolated alkyl chain found in the LPAR6 crystal structure. The CysLT1R-zafir structure, however, directly captures the TM5 entry gate, jammed in its open state by the ligand, revealing details of the ligand entry and suggesting possibility for this dynamic lateral gating mechanism in other lipid receptors.

Fig. 3. Sodium-binding pocket in CysLT1R. (A) Details of Na+ (purple sphere) coordination. Water molecule is shown as a red sphere. (B) Comparison of all high-resolution GPCR structures with resolved Na+. Sodium ions are shown as purple spheres for the δ-branch receptors: CysLT1R-zafir (green), PAR1 (light purple; PDB ID 3V7W), PAR2 (PDB ID 3NDD), and as yellow spheres for receptors from the α-branch: A2AR (yellow; PDB ID 4EIY) and β2AR (turkey; PDB ID 4BVN), and the γ-branch: DOR (PDB ID 4NH8). (C and D) Frequency analysis of amino acid occurrence in the sodium pocket of the δ-branch class A GPCRs (C) and other class A receptors excluding the δ-branch (D). Yellow color marks amino acids with hydrophobic side chains; green, aromatic; red, negatively charged; blue, positively charged; purple, polar uncharged; pink, Gly and Pro. Frames indicate positions with the largest differences. The frequency analysis was performed using the weblogo.berkeley.edu server.

LPA4,5,6, and BLT1. This TM5 plasticity suggests that the opening between TM4 and TM5 can serve as an important gate for lateral ligand entry into the orthosteric pocket.

Molecular dynamics reveals flexibility of the ligand access gate

Molecular dynamics simulations demonstrate that the open-gate conformation of the pocket as found in the CysLT1R-zafir complex is metastable: After zafirlukast is removed, the open pocket collapses typically within 200 ns into a closed conformation, resembling the one observed in the CysLT1R-pran structure (fig. S8 and movie S1). In some cases, however, the open-gate conformation lingers much longer due to a 1-palmitoyl-2-oleoyl-sn-glycero-3-phosphocholine (POPC) lipid molecule entering the pocket from the membrane (movie S2). Moreover, we observed that the gate can close and open spontaneously within a 1-μs simulation (movie S3), indicating a relatively low barrier for transitions between the open and close states, supporting the lateral ligand access route into the orthosteric pocket in CysLT1R.

DISCUSSION

As described in this study, two CysLT1R structures in complex with antiasthmatic drugs pranlukast and zafirlukast shed light on
CysLTRs control bronchodilation and inflammation in the lungs, and therefore, they have been considered as prominent targets for the treatment of asthma. According to the Centers for Disease Control and Prevention, asthma is a highly debilitating chronic condition, widespread among children, affecting quality of life and productivity of almost 10% of the population of our modern society and may result in death (36). This work should contribute toward a better understanding of the disease and development of more efficient and safe treatments against asthma and associated disorders, directly improving lives of millions of people.

**MATERIALS AND METHODS**

**Protein engineering for structural studies**

The human wild-type CysLT1R DNA was codon optimized for insect cell expression and cloned into a modified pFastBac1 vector (Invitrogen) containing an expression cassette with a hemagglutinin (HA) signal sequence, followed by a Flag tag and a 10× His tag at the N terminus. Tags were separated from the receptor sequence by the tobacco etch virus (TEV) protease cleavage site. To facilitate crystallization, a thermostabilized apocytochrome b562 RIL (BRIL; PDB ID 1M6T) was fused into ICL3 of CysLT1R (K222–K223 with S and SGlinkers, respectively) with the intact N terminus and the C terminus.
Insect cell expression and purification of the CysLT₁R construct for crystallization

High-titer recombinant baculovirus (10⁹ viral particles per milliliter) was obtained using the Bac-to-Bac Baculovirus Expression System (Invitrogen). Sf9 cells at a cell density of (2–3) × 10⁶ cells ml⁻¹ were infected with the virus at a multiplicity of infection of 10 with the addition of 8 μM zafirlukast (Cayman Chemical). Cells were harvested by centrifugation at 48 hours after infection and stored at −80°C until use.

Insect cell membranes were disrupted by thawing frozen cell pellets in a hypotonic buffer containing 10 mM Heps (pH 7.5), 10 mM MgCl₂, 20 mM KCl, and protease inhibitor cocktail (PIC; 500 μM 4-(2-aminoethyl)benzenesulfonyl fluoride hydrochloride (Gold Bio), was replaced with 50 mM Hepes (pH 7.5), 250 mM NaCl, 10% (v/v) glycerol, 0.015% (w/v) DDM, 0.02% (w/v) CHS, and 300 mM imidazole. A PD-10 desalting column (GE Healthcare) was used to remove imidazole. The TEV protease and the cleaved 10× His tag were removed by incubating the sample for 1.5 hours with TALON IMAC resin. The resin was then washed at 4°C with six column volumes of 50 mM Hepes (pH 7.5), 250 mM NaCl, 10% (v/v) glycerol, 0.05% (w/v) DDM, 0.01% (w/v) CHS, and 10 mM imidazole, and CysLT₁R was treated with PNGase F (Sigma-Aldrich) for 4.5 hours to deglycosylate the receptor. The protein was then eluted with 5 CVs of 50 mM Heps (pH 7.5), 250 mM NaCl, 10% (v/v) glycerol, 0.015% (w/v) DDM, 0.003% (w/v) CHS, and 300 mM imidazole. A PD-10 desalting column (GE Healthcare) was used to remove imidazole. The protein was then treated overnight at 4°C with His-tagged TEV protease (home-made) to remove the N-terminal Flag and His tags. The TEV protease and the cleaved 10× His tag were removed by incubating the sample for 1.5 hours with TALON IMAC resin. The receptor was then concentrated to 50 to 60 mg ml⁻¹ with a 100-kDa molecular weight cutoff concentrator (Millipore). In the case of crystallization with zafirlukast, 50 μM zafirlukast (Sigma-Aldrich) was added to the elution buffer, 200 μM after the desalt procedure, and 10 μM into the washing buffers. In the case of crystallization with pranlukast, 50 μM pranlukast (Sigma-Aldrich) was added to the elution buffer and after the desalt procedure and 10 μM into the washing buffers. Protein purity and monodispersity were tested by SDS–polyacrylamide gel electrophoresis and analytical size exclusion chromatography (aSEC). Typically, protein purity exceeded 95%, and aSEC profiles showed a single peak with less than 10% aggregation level (fig. S1A). Protein stability was assessed by a microscale thermostart assay using a 10 μM CPM [7-diethy lamino-3-[4'-maleimidylphenyl]-4-methylcoumarin, Invitrogen; λem = 384 nm; λex = 470 nm] dye on a Rotorgene-Q (QIAGEN) instrument (37). Typical melting temperatures were higher than 70°C (fig. S1B).

LCP crystallization of CysLT₁R

The CysLT₁R-BRIL in complex with pranlukast was crystallized using the LCP method by mixing 40% of protein (50 mg ml⁻¹) with 60% of lipid (monolein and cholesterol, 9:1, w/w) using a syringe lipid mixer (14). After a clear LCP formed, the mixture was dispensed onto 96-well glass sandwich plates (Marienfeld) as 40-ml drops and overlaid with 800 nl of precipitant solutions using an NT8-LCP robot (FORMULATRIX). Crystals appeared after 2 to 10 days and reached their full size within 2 weeks using 100 mM sodium citrate (pH 6), 200 to 600 mM lithium nitrate, and 30 to 38% (v/v) polyethylene glycol 400 (PEG400) as a precipitant solution. Typical crystal size was 250 μm by 15 μm by 15 μm, and crystals had a twiggly shape (fig. S1D). Crystals were harvested directly from LCP using 100- to 200-μm MicroMount loops (MiTeGen) and flash frozen in liquid nitrogen. For the XFEL data collection, CysLT₁R-BRIL purified with zafirlukast was crystallized in syringes as described (38), using 75 to 175 mM sodium phosphate, 24 to 34% (v/v) PEG400, 100 mM Heps (pH 7), and 1 μM zafirlukast as a precipitant. Typical crystal size was 5 μm by 2 μm by 2 μm (fig. S1C).

Data collection using synchrotron radiation

Crystallographic data collection of CysLT₁R-pran crystals was performed at the ID30b beamline of the European Synchrotron Radiation Facility (ESRF), Grenoble, France. Overall, nine CysLT₁R-pran datasets (two 90° and seven 10° wedges) were collected from four needle-shaped crystals using a PILATUS 6M detector and an unattenuated 20-μm beam (wavelength, 0.9771 Å). Data were collected using 0.1° to 0.2° oscillations per frame with an exposure calculated by BEST (39), so that the overall dose per dataset was 20 Mgy. Data were processed using XDS (x-ray detector software) and scaled with XSCALE (40). Rejection of outliers was performed using correlation coefficients produced by XSCALE, as described (41). Drop of R_{merge} in the lowest-resolution shell after an individual dataset exclusion was used as a supporting criterion of its nonisomorphism.

Data collection using x-ray free-electron laser

XFEL data of CysLT₁R-zafir crystals were collected at the CXI (coherent x-ray imaging) instrument of the Linac Coherent Light Source (LCLS) at SLAC National Accelerator Laboratory, Menlo Park, California. The LCLS was operated at a wavelength of 1.302 Å (9.52 keV) delivering individual x-ray pulses of 43-fs duration focused into a spot size of ~1.5 μm in diameter using a pair of Kirkpatrick-Baez mirrors. LCP laden with protein microcrystals was injected at RT inside a vacuum chamber into the beam focus region using an LCP injector (42) with a 50-μm-diameter capillary at a flow rate of 0.3 μl min⁻¹. Microcrystals ranged in size from 2 to 10 μm. Diffraction data were collected at a pulse repetition rate of 120 Hz with the 2.3-megapixel Cornell-SLAC Pixel Array Detector. The beam was attenuated to 6.3% of full intensity (1.9 × 10¹⁰ photons}

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per pulse) to avoid detector saturation. A total number of 315,374 detector images were collected, of which 40,720 were identified as potential crystal hits with more than 20 Bragg peaks using Cheetah (43), corresponding to an average hit rate of 13%. Autoindexing and structure factor integration of the crystal hits were performed using the Monte Carlo integration routine with the “pushes 2.4” option implemented in CrystFEL (version 0.6.3 + 23ea03c7) (44). Peak detection parameters were extensively optimized for Cheetah, and experimental geometry was refined for CrystFEL with geoptimizer (45). The overall time of data collection from a sample with a total volume of about 15 μl was approximately 45 min and yielded 30,129 indexed patterns (indexing rate 90%).

Structure determination
The structure of CysLT1R-pran was initially solved by molecular replacement using the program Phaser (46) with two independent search models of the P2Y1 R 7TM domain (PDB ID 4XNW) and BRIL (10−11 to 10 −5 M), and LTD4 concentrations corresponding to the EC50 (80% of effective concentration) for each mutant. After equilibration for 30 min at 37°C, the cells were lysed with IP1-D2 and Ab-Crypt reagents in lysis buffer and then incubated at RT for 1 hour. The plate was read on a Tecxan Genios Pro plate reader using a HTRF (homogeneous time-resolved fluorescence) filter set (λex = 320 nm, λem = 620 and 655 nm). Data were plotted using the three-parameter EC50/IIC50 fit of GraphPad Prism 7 (San Diego) and represent the means ± SD of at least two independent experiments performed in quadruplicate.

Cell surface expression determined by enzyme-linked immunosorbent assay
HEK293 cells were seeded in 24-well plates coated with poly-L-lysine (Sigma-Aldrich) at 100,000 cells per well and transfected with 375 ng of plasmid coding for CysLT1R using X-tremeGENE HP (Roche). Forty-eight hours after transfection, cells were washed with fresh Hanks’ balanced salt solution. Cells were either stimulated directly with a range of LTD4 concentrations (10−12 to 10−6 M) prepared in IP1 stimulation buffer, or sequentially stimulated with a range of zafirlukast and pranlukast concentrations (10−11 to 10−5 M), and LTD4 concentrations corresponding to the EC50 (80% of effective concentration) for each mutant. After equilibration for 30 min at 37°C, the cells were lysed with IP1-D2 and Ab-Crypt reagents in lysis buffer and then incubated at RT for 1 hour. The plate was read on a Tecxan Genios Pro plate reader using a HTRF (homogeneous time-resolved fluorescence) filter set (λex = 320 nm, λem = 620 and 655 nm). Data were plotted using the three-parameter EC50/IIC50 fit of GraphPad Prism 7 (San Diego) and represent the means ± SD of at least two independent experiments performed in quadruplicate.

Effects of monovalent ions on receptor stability
Effects of monovalent ions were assayed using the CysLT1R crystalization construct and two mutants D256N and D48N based on it. Each receptor construct was purified, as described above for the crystallization setup, using KCl instead of NaCl in hypotonic and solubilization buffers. KCl was replaced with choline chloride during

Molecular docking
To prepare LTD4 for molecular docking, we extracted its chemical structure from the PubChem web database (https://pubchem.ncbi.nlm.nih.gov/compound/5280878), assigned charges at pH 7.0, and generated three-dimensional (3D) ligand structure from its 2D representation, using the Monte Carlo optimization and the MMFF-94 force field. As for the receptor, we preprocessed the CysLT1R-pran structure by adding missing residues, optimizing side-chain rotamers, and removing water molecules. Rectangular box enclosing the ligand-binding site of pranlukast in CysLT1R was used as the sampling space for docking. We kept the receptor rigid during the docking simulations and sampled ligand conformations in the internal coordinate space using biased probability Monte Carlo optimization with the sampling parameter (docking effort) set to 50. We performed three independent docking runs and selected the binding pose with the lowest docking score. All simulations were performed using the ICM-Pro software package (Molsoft, San Diego).

IP1 production assay
For the CysLT1R functional assays, the initial pcDNA3.1(+)-CYSLTR1 plasmid coding for CysLT1 wild-type receptor, cMyc tag for labeling, and β-globin intron for stability (18) was received as a gift from J. Stankova (Université de Sherbrooke, Canada). The 3× HA tag was then inserted by overlapping polymerase chain reaction (PCR) instead of cMyc for better antibody detection, and desired gene modifications (point mutations, truncations, or partner protein fusion) were introduced by overlapping PCR.

The Cisbio IP-One kit was used according to the manufacturer’s instructions. Human embryonic kidney (HEK) 293 cells were seeded onto poly-L-lysine–coated 384-well plates at 20,000 cells per well and transfected with 40 ng of DNA coding for the wild-type CysLT1R or for the CysLT1R mutants using the T-x-tremeGENE HP (Roche) agent. At 48 hours after transfection, the medium was removed, and the cells were washed with fresh Hanks’ balanced salt solution. Cells were either stimulated directly with a range of LTD4 concentrations (10−12 to 10−6 M) prepared in IP1 stimulation buffer, or sequentially stimulated with a range of pranlukast and pranlukast concentrations (10−11 to 10−5 M), and LTD4 concentrations corresponding to the EC50 (80% of effective concentration) for each mutant. After equilibration for 30 min at 37°C, the cells were lysed with IP1-D2 and Ab-Crypt reagents in lysis buffer and then incubated at RT for 1 hour. The plate was read on a Tecxan Genios Pro plate reader using a HTRF (homogeneous time-resolved fluorescence) filter set (λex = 320 nm, λem = 620 and 655 nm). Data were plotted using the three-parameter EC50/IIC50 fit of GraphPad Prism 7 (San Diego) and represent the means ± SD of at least two independent experiments performed in quadruplicate.
the washing step on the Talon resin. After elution, the protein solution was desalted from imidazole, concentrated to 1 mg ml⁻¹, and diluted 50 times with the assay buffer: 10 μM CPM dye, 25 mM Hepes (pH 7.5), 10% (v/v) glycerol, 0.05% (w/v) DDM, 0.01% (w/v) CHS, containing one of the ions (Na⁺, K⁺, or Rb⁺) at concentrations between 0 and 150 mM. The ionic strength in all samples was compensated by choline chloride to an overall ion concentration of 150 mM. The samples were then incubated at 4°C in the dark for 15 min, and their thermal stability was analyzed using a microscale fluorescence assay as previously described (37). Briefly, fluorescence from the CPM dye (see the purification methods part) was recorded during a temperature ramp from 25° to 80°C with a 1.5°C min⁻¹ rate using a Rotor–Gene Q real-time PCR machine (QIAGEN). Melting curves were collected for n = 3 independent experiments in triplicates.

Molecular dynamics simulations

The CysLT₁R-pran and CysLT₁R-rafiar structures were preprocessed to assign their protonation states and to model missing side chains using the energy-based optimization protocols available in ICM-Pro (v3.8.6-50). Missing loops were modeled using Loop modeling and regularization protocols in ICM-Pro (52). The initial membrane coordinates were assigned by aligning the receptor models to CB₁ receptor coordinates retrieved from the OPM (Orientations of Proteins in Membranes) database (53). The structure was simulated in a periodic box containing 178 POPC lipids, 11,898 water molecules, 31 sodium, and 44 chloride ions. After the initial energy minimization, the system was equilibrated for 10 ns, followed by production runs of up to 1 μs for CysLT₁R-rafiar and 650 ns for CysLT₁R-pran apo-state structures. The simulations were performed using the Gromacs (v.2018) simulation package (54), and the plots were generated using the Matplotlib plotting package available in Python. The simulations were performed either on NVIDIA P100 GPU enabled nodes made available by the Google Cloud Platform or with NVIDIA K-80 or P100 GPU enabled clusters at the High-Performance Computing Center at the University of Southern California.

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