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Structure of a nanobody-stabilized active state of the β2 adrenoceptor

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GPCRs activated by diffusible ligands have a spectrum of functional states2. A GPCR may activate more than one G protein isoform or a G-protein-independent pathway such as arrestin. In the absence of a ligand, many GPCRs exhibit some basal, agonist independent activity towards one or more of these signalling pathways. Orthosteric ligands (compounds that occupy the native hormone-binding pocket) are classified according to their efficacy, that is, the effect that they have on receptor signalling through a specific pathway. Inverse agonists inhibit basal activity whereas agonists maximally activate the receptor. Partial agonists submaximally activate, but sterically block the activity of other ligands. Moreover, the efficacy profile of ligands for a given GPCR can differ for different downstream signalling pathways. The presence of some activity in the unliganded receptor implies low energy barriers between functional states, such that thermal fluctuations significantly sample activating conformations, and ligands with distinct efficacy profiles act by stabilizing distinct subsets of conformations.

We know little about the structural basis for the functional versatility of GPCRs. Only rhodopsin has been crystallized in different conformational states2–4. The first structures of rhodopsin covalently bound to 11-cis-retinal represent a completely inactive state with virtually no basal activity2. Structures of opsin, the ligand-free form of rhodopsin, obtained from crystals grown at pH 5.6 are likely to represent active conformations5, as the Fourier transform infrared (FTIR) spectrum of opsin at acidic pH resembles that of metarhodopsin II, the light-activated form of rhodopsin6. For rhodopsin, the light-induced transition from the inactive to the active state is very efficient.

Crystal structures of low-pH opsin reveal that the protein conformation is the same in the presence or absence of a peptide from the alpha subunit of transducin (Gt), its cognate G protein, consistent with the notion that metarhodopsin II can adopt a fully active conformation in the absence of Gt.

The crystal structures of GPCRs activated by diffusible ligands, including the human β2AR7–10, the avian β1AR11, and the human adenosine A2A receptor12,13, represent inactive conformations bound by inverse agonists. Unlike the activation of rhodopsin by light, agonists are much less efficient at stabilizing the active state of the β2AR, making it difficult to capture this state in a crystal structure. Fluorescence lifetime studies show that even saturating concentrations of the full agonist isoproterenol do not stabilize a single active conformation13. This may be due to the relatively low affinity and rapid rates of association and dissociation for β2AR agonists. However, in a companion manuscript we show that, even when bound to a covalent agonist, the β2AR crystallizes in an inactive conformation14. Experiments using a β2AR labelled with a conformationally sensitive fluorescent probe show that stabilization of the active state requires both agonist and Gs, the stimulatory G protein for adenylyl cyclase15. Efforts to obtain an agonist-GPCR-G protein complex are of great importance; however, this is a particularly difficult endeavour due to the biochemical challenges in working with both GPCRs and G proteins, and the inherent instability of the complex in detergent solutions. As an alternate approach, we developed a binding protein that preferentially binds to and stabilizes an active conformation, acting as a surrogate for Gs.

**Nanobody-stabilized β2AR active state**

The active G protein coupled state of the β2AR (and many other family A GPCRs) has characteristic functional properties. Agonists promote Gs binding to the β2AR and G protein binding to the receptor increases agonist affinity. We identified a camelid antibody fragment...
that exhibits G protein-like behaviour towards the β2AR. Tylopo- 
dida (camels, dromedaries and llamas) have developed a unique class of 
functional antibody molecules that are devoid of light chains14. A nano- 
body (Nb) is the recombinant minimal-sized intact antigen-binding 
domain of such a camels heavy chain antibody and is approximately 
25% the size of a conventional Fab fragment. To generate receptor- 
specific nanobodies, a llama was immunized with purified agonist- 
bound β2AR reconstituted at high density into phospholipid vesicles. A 
library of single-chain nanobody clones was generated and screened 
against agonist bound receptor. We identified seven clones that recog- 
nized agonist-bound β2AR. Of these, Nb80 was chosen because it 
showed G-protein-like properties upon binding to both wild-type 
β2AR and β2AR–T4L, the β2AR–T4 lysozyme fusion protein used to 
obtain the high-resolution inactive state crystal structure2,9.

We compared the effect of Nb80 with Gs on β2AR structure and 
agonist binding affinity. β2AR was labelled at the cytoplasmic end of 
transmembrane helix 6 (TM6) at Cys 265 with the fluorophore mono- 
brombobimane and reconstituted into high-density lipoprotein (HDL) 
particles. TM6 moves relative to TM3 and TM5 upon agonist activa-
tion (Fig. 1a), and we have shown previously that the environment 
around bimane covalently linked to Cys 265 changes with both ago-
nist binding and G protein coupling, resulting in a decrease in fluo-
rescence intensity and a red shift in $\lambda_{\text{max}}^{11}$. As shown in Fig. 1b, the 
catecholamine agonist isoproterenol and Gs both stabilize an active-
like conformation, but the effect of Gs is greater in the presence of 
isoproterenol, consistent with the cooperative interactions of agonist 
and Gs on β2AR structure. Nb80 alone has an effect on bimane fluo-
rescence and $\lambda_{\text{max}}$ of unliganded β2AR that is similar to that of Gs 
(Fig. 1c). This effect was not observed in β2AR bound to the inverse 
agonist ICI-118,551. The effect of Nb80 was increased in the presence 
of 10 μM isoproterenol. These results show that Nb80 does not recog-
nize the inactive conformation of the β2AR, but binds efficiently to 
agonist-occupied β2AR and produces a change in bimane fluo-
rescence that is indistinguishable from that observed in the presence 
of Gs and isoproterenol.

Figure 1d and e shows the effect of Gs and Nb80 on agonist affinity 
for β2AR. β2AR was reconstituted into HDL particles and agonist 
competition binding experiments were performed in the absence or 
presence of Nb80 and Gs. In the absence of either protein, isoproterenol 
has an inhibition constant (Ki) of 107 nM. In the presence of Gs two 
affinity states are observed, because not all of the β2AR is coupled to Gs. 
In the Gs-coupled state the affinity of isoproterenol increases by 100-
fold (Ki = 1.07 nM) (Fig. 1d and Supplementary Table 1). Similarly, in 
the presence of Nb80 the affinity of isoproterenol increases by 95-fold 
(Ki = 1.13 nM) (Fig. 1e and Supplementary Table 1). In contrast, Nb80 
had little effect on β2AR binding to the inverse agonist ICI-118,551 
(Supplementary Fig. 1 and Supplementary Table 1). These binding data 
indicate that Nb80 stabilizes a conformation in wild-type β2AR that is 
very similar to that stabilized by Gs, such that the energetic coupling 
of agonist and Gs binding is faithfully mimicked by Nb80.

The high-resolution structure of the inactive state of the β2AR was 
obtained with a β2AR–T4L fusion protein. We showed previously that 
β2AR–T4L has a higher affinity for isoproterenol than wild-type β2AR2. 
Nevertheless, in the presence of Nb80 the affinity increased by 60-fold, 
resulting in an affinity (Ki = 0.56 nM) comparable to that of wild-type 
β2AR bound to Nb80 (Fig. 1f and Supplementary Table 1). Although 
we cannot study G protein coupling in β2AR–T4L due to steric hind-
rance by T4L, the results show that T4L does not prevent binding of 
Nb80, and the nearly identical Ki values for agonist binding to wild-type 
β2AR and β2AR–T4L in the presence of Nb80 indicate that Nb80 
stabilizes a similar conformation in these two proteins. The most likely 
explanation for the ability of Nb80 to bind to β2AR–T4L whereas Gs 
does not is the difference in size of these two proteins. Nb80 is approxi-
mately 14 kDa whereas the Gs heterotrimer is approximately 90 kDa.

Figure 1 | Effect of Nb80 on β2AR structure and function. a, The cartoon 
illustrates the movement of the environmentally-sensitive bimane probe 
attached to Cys 265 in the cytoplasmic end of TM6 from a more buried, 
hydrophobic environment to a more polar, solvent-exposed position during 
agonist activation that results in a decrease in fluorescence in Fig. 1b–c and 
Supplementary Fig. 2c, d. b, c, Fluorescence emission spectra showing ligand-
induced conformational changes of monobromobimane-labelled β2AR 
reconstituted into high density lipoprotein particles (mBB-β2AR/HDL) in the 
absence (black solid line) or presence of full agonist isoproterenol (ISO, green 
wide dashed line), inverse agonist ICI-118,551 (ICI, black dashed line), Gs 
heterotrimer (red solid line), nanobody-80 (Nb80, blue solid lines), and 
combinations of Gs with ISO (red wide dashed line), Nb80 with ISO (blue wide 
dashed line), and Nb80 with ICI (blue dashed line). d–f, Ligand binding curves 
for ISO competing against [3H]-dihydroalprenolol ([3H]-DHA) for d, β2AR/ 
HDL reconstituted with Gs heterotrimer in the absence or presence GTPyS; e, 
β2AR/HDL in the absence and presence of Nb80; and f, β2AR–T4L/HDL in the 
absence and presence of Nb80. Error bars represent standard errors.

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**High affinity β2AR agonist**

To stabilize further the active state of the β2AR, we screened over 50 commercial and proprietary β2AR ligands. Of these, BI-167107 (Boehringer Ingelheim) had the most favourable efficacy, affinity and off-rate profile. BI-167107 is a full agonist that binds to the β2AR with a dissociation constant \(K_d\) of 84 pM (Supplementary Fig. 2a and b). As shown in Supplementary Fig. 2c and d, BI-167107 induces a larger change in the fluorescence intensity and \(\lambda_{max}\) of bimane bound to Cys265 than does the agonist isoproterenol. Moreover, the rate of dissociation of BI-167107 was extremely slow. Displacement of BI-167107 with an excess of the neutral antagonist alprenolol required 150 h to complete, compared with 5 s for isoproterenol.

**Crystallization of β2AR–T4L–Nb80 complex**

The β2AR was originally crystallized bound to the inverse agonist carazolol using two different approaches. The first crystals were obtained from β2AR bound to a Fab fragment that recognized an epitope composed of the amino and carboxyl terminal ends of the third intracellular loop connecting TMs 5 and 6 (ref. 8). In the second approach, the third intracellular loop was replaced by T4 lysozyme (β2AR–T4L)\(^7\). Efforts to crystallize β2AR–Fab complex and β2AR–T4L bound to BI-167107 and other agonists failed to produce crystals of sufficient quality for structure determination. We therefore attempted to crystallize BI-167107 bound to β2AR and β2AR–T4L in complex with Nb80. Although crystals of both complexes were obtained in lipid bicelles and lipidic cubic phase (LCP), high-resolution diffraction was only obtained from crystals of β2AR–T4L–Nb80 grown in LCP. These crystals grew at pH 8.0 in 39–44% PEG400, 100 mM Tris, 4% DMSO and 1% 1,2-heptanetriol.

A merged data set at 3.5 Å was obtained from 23 crystals (Supplementary Table 2). The structure was solved by molecular replacement using the structure of the carazolol-bound β2AR and a nanobody as search models. Supplementary Fig. 3a shows the packing of the β2AR–T4L–Nb80 complex in the crystal lattice. The receptor has interactions with lattice neighbours in several directions, and is relatively well ordered (Supplementary Fig. 3a and b), with readily interpretable electron density for most of the polypeptide. Nb80 binds to the cytoplasmic end of the β2AR, with the third complementarity-determining region (CDR) loop projecting into the core of the receptor (Fig. 2a, and Supplementary Fig. 4).

**Figure 2**

**Comparison of the agonist-Nb80 stabilized crystal structures of the β2AR with inverse agonist bound β2AR and opsins.** The structure of inverse agonist carazolol-bound β2AR–T4L (β2AR–T4L) is shown in blue with the carazolol in yellow. The structure of BI-167107 agonist-bound and Nb80-stabilized β2AR–T4L (β2AR–Nb80) is shown in green. These two structures were aligned using the PyMOL align function. a, Side view of the β2AR-Nb80 complex with β2AR in orange and CDRs of Nb80 in light blue (CDR1) and blue (CDR3). b, Side view of the superimposed structures showing significant structural changes in the extracellular and G protein facing part of the receptors. c, Comparison of the extracellular ligand binding domains showing modest structural changes. d, Cytoplasmic view showing the ionic lock interaction between Asp 3.49 and Arg 3.50 of the DRY motif in TM3 is broken in the β2AR–Nb80 structure. The intracellular ends of TM3 and TM6 is moved outward and away from the core of the receptor. The arrow indicates an 11.4 Å change in distance between the α-carbon of Glu 6.30 in the structures of β2AR–Cz and β2AR–Nb80. The intracellular ends of TM3 and TM7 move towards the core by 4 and 2.5 Å, respectively, while TM5 moves outward by 6 Å. e, The β2AR–Nb80 structure superimposed with the structure of opsin crystallized with the C-terminal peptide of Gt (transducin)\(^2\). PyMOL (http://www.pymol.org) was used for the preparation of all structure figures.
are relatively small changes in the extracellular surface (Fig. 2c). The second intracellular loop (ICL2) between TM3 and TM4 adopts a two-turn alpha helix (Fig. 2d), similar to that observed in the turkey β1AR structure. The absence of this helix in the inactive β2AR structure may reflect crystal lattice contacts involving ICL2.

Figure 2a and Supplementary Fig. 4a–c show details of interaction of Nb80 with the cytoplasmic side of the β2AR. An eight-amino-acid sequence of CDR3 penetrates into a hydrophobic pocket formed by amino acids from TM segments 3, 5, 6 and 7. A four-amino-acid sequence of CDR1 provides additional stabilizing interactions with amino acids from TM segments 3, 5, 6 and 7. A four-amino-acid sequence of CDR3 penetrates into a hydrophobic pocket formed by the cytoplasmic ends of TM segments 5 and 6. CDR3 occupies a position similar to the carboxyl terminal peptide of transducin in opsin (Supplementary Fig. 4c, d). The majority of interactions between Nb80 and the β2AR are mediated by hydrophobic contacts.

When comparing the agonist- and inverse agonist-bound structures, the largest change is observed in TM6, with an 11.4-Å movement of the helix at Glu 268 (part of the ionic lock) (superscripts in structures, the largest change is observed in TM6, with an 11.4-Å movement of the helix at Glu 268 (part of the ionic lock) (Supplementary Fig. 4c, d). The majority of interactions between Nb80 and the β2AR are mediated by hydrophobic contacts.

The changes in agonist-bound β2AR–T4L–Nb80 relative to the inactive carazolol-bound β2AR–T4L are remarkably similar to those observed between rhodopsin and opsin (Fig. 2e). The salt bridge in the ionic lock between highly conserved Arg 131 and Asp/Glu 130 is broken. In opsin, Arg 131 interacts with Tyr 223, even though the tyrosine occupies a similar position in opsin and agonist-bound β2AR–T4L–Nb80. As in opsin, Tyr 326 of the highly conserved NPxxY sequence moves into the space occupied by TM6 in the inactive state. In carazolol-bound β2AR–T4L we observed a network of hydrogen bonding interactions involving highly conserved amino acids in TMs 1, 2, 6 and 7 and several water molecules. Although the resolution of the β2AR–T4L–Nb80 structure is inadequate to detect water molecules, it is clear that the structural changes we observe would substantially alter this network.

In contrast to the relatively large changes observed in the cytoplasmic domains of β2AR–T4L–Nb80, the changes in the agonist-binding pocket are fairly subtle. Figure 3 shows a comparison of the binding pockets of the inverse agonist- and agonist-bound structures. An omit map of the ligand-binding pocket is provided in Supplementary Fig. 5. Many of the interactions between the agonist BI-167107 and the β2AR are similar to those observed with the inverse agonist carazolol. The alkyamine and the β-OH of both ligands form polar interactions with Asp 113 in TM3, and with Asn 312 and Tyr 316 in TM7. The

Figure 3 | Ligand binding pocket of BI-167107 and carazolol-bound β2AR structures. a, b, Extracellular views of the agonist BI-167107-bound (a) and carazolol-bound (b) structures, respectively. Residues within 4 Å of one or both ligands are shown as sticks. In all panels, red and blue represent oxygen and nitrogen, respectively. c, d, Schematic representation of the interactions between the β2AR and the ligands BI-167107 (c) and carazolol (d). The residues shown here have at least one atom within 4 Å of the ligand in the crystal structures. Mutations of amino acids in orange boxes have been shown to disrupt both antagonist and agonist binding. Mutations of amino acids in blue boxes have been shown to disrupt agonist binding. Green lines indicate potential hydrophobic interactions and orange lines indicate potential polar interactions.
agonist has a longer alkyl substituent on the amine, which ends with a phenyl ring that lies in a hydrophobic pocket formed by Trp 109β3 and Phe 193β5.32 and Ile 309β7.36. The greatest difference between inactive and active structures in the ligand-binding site is an inward bulge of TM5 centered around Ser 207β5.46, whose Cz position shifts by 2.1 Å (Fig. 4a). In addition, there are smaller inward movements of TM6 and TM7. The basal activity shown by the β2AR indicates that the protein structure surrounding the binding pocket is relatively dynamic in the absence of ligand, such that it samples active and inactive conformations. The presence of Pro 211β5.50 in the following turn, which cannot form a hydrogen bond with the backbone at Ser 207β5.46, is likely to lower the barrier to the transition between the conformations observed in the presence of carazolol and BI-167107. There are extensive interactions between the carbonyl oxygen, amine and hydroxyl groups on the heterocycle of BI-167107 and Ser 203β5.42 and 207β5.46 in TM5, as well as Asn 293β6.55 in TM6 and Tyr 308β7.35 in TM7. In contrast, there is only one polar interaction between the nitrogen in the heterocycle of carazolol and Ser 203β5.42. Interactions of Ser 203β5.42, Ser 204β5.43 and Ser 207β5.46 with catecholamine hydroxyls have been proposed, on the basis of mutagenesis studies showing that these serines are important for agonist binding and activation18,19. Whereas Ser 204β5.43 does not interact directly with the ligand, it forms a hydrogen bond with Asn 293β6.55 on TM6, which is in turn linked to Tyr 308β7.35 of extra-cellular loop 3 (ECL3) (Fig. 3a). This tyrosine packs against Phe 193β5.32 of ECL2, and both residues move to close off the ligand-binding site from the extracellular space.

Asn 293β6.55 contributes to enantiomeric selectivity for catecholamine agonists20. The β-OH of BI-167107 does not interact with Asn 293β6.55, but forms hydrogen bonds with Asp 113β3.32 and Asn 312β7.39, similar to what is observed for carazolol in the inactive structure. The chirality of the β-OH influences the spatial positioning of the aromatic ring system in β2AR ligands, so the effect of Asn 293β6.55 on β2AR enantiomeric selectivity may arise from its direct interaction with the aromatic ring system of the ligand, as well as its positioning of Ser 204β5.43 and Tyr 308β7.35, which also interact with this portion of the ligand. However, BI-167107 is not a catecholamine, and it is possible that the β-OH of catecholamine agonists, such as adrenaline and noradrenaline, has a direct interaction with Asn 293β6.55, because mutation of Asn 293β6.55 has a stronger influence on the preference for the chirality of the β-OH of catecholamine agonists, compared with non-catechol agonists and antagonists20.

Trp 6.48 is highly conserved in Family A GPCRs, and it has been proposed that its rotameric state has a role in GPCR activation (rotamer toggle switch)31. We observe no change in the side chain rotamer of Trp 286β6.48 in TM6 (Fig. 4a), which lies near the base of the ligand-binding pocket, although its position shifts slightly in concert with rearrangements of nearby residues Ile 121β3.40 and Phe 282β6.44. Although there is spectroscopic evidence for changes in the environment of Trp 6.48 upon activation of rhodopsin32, a rotamer change is not observed in the crystal structures of rhodopsin and low-pH opsin. Moreover, recent mutagenesis experiments on the serotonin 5HT4 receptor demonstrate that Trp 6.48 is not required for activation of this receptor by serotonin33. These observations indicate that, although changes in hydrophobic packing alter the conformation of the receptor in this region, changes in the Trp 6.48 rotamer do not occur as part of the activation mechanism.

It is interesting to speculate how the small changes around the agonist-binding pocket are coupled to much larger structural changes in the cytoplasmic regions of TMs 5, 6 and 7 that facilitate binding of Nb80 and Gs. A potential conformational link is shown in Fig. 4. Agonist interactions with Ser 203β5.42 and 207β5.46 stabilize a receptor conformation that includes a 2.1 Å inward movement of TM5 at position 207β5.46 and 1.4 Å inward movement of the conserved Pro 211β5.50 relative to the inactive, carazolol-bound structure. In the inactive state, the relative positions of TM5, TM3, TM6 and TM7 are stabilized by interactions between Pro 211β5.50, Ile 121β3.40, Phe 282β6.44 and Asn 312β7.45. The position of Pro 211β5.50 observed in the agonist structure is incompatible with this network of interactions, and Ile 121β3.40 and Phe 282β6.44 are repositioned, with a rotation of TM6 around Phe 282β6.44 leading to an outward movement of the cytoplasmic end of TM6.

Although some of the structural changes observed in the cytoplasmic ends of transmembrane domains of the β2AR–T4L–Nb80 complex arise from specific interactions with Nb80, the fact that Nb80 and Gs induce or stabilize similar structural changes in the β2AR, as determined by fluorescence spectroscopy and by agonist binding affinity, suggests that Nb80 and Gs recognize similar agonist-stabilized conformations. The observation that the transmembrane domains of rhodopsin and the β2AR undergo similar structural changes upon activation provides further support that the agonist-bound β2AR–T4L–Nb80 represents an active conformation and is consistent with a conserved mechanism of G protein activation.

However, the mechanism by which agonists induce or stabilize these conformational changes likely differs for different ligands and for different GPCRs. The conformational equilibria of rhodopsin and β2AR differ, as shown by the fact that rhodopsin appears to adopt a fully active conformation in the absence of a G protein24 whereas β2AR cannot25. Thus, the energetics of activation and conformational
sampling can differ among different GPCRs, which likely gives rise to the variety of ligand efficacies displayed by these receptors. An agonist need only disrupt one key intramolecular interaction needed to stabilize the inactive state, as constitutive receptor activity can result from single mutations of amino acids from different regions of GPCRs. Thus, disruption of these stabilizing interactions either by agonists or mutations lowers the energy barrier separating inactive and active states and increases the probability that a receptor can interact with a G protein.

METHODS SUMMARY

Crystallization. Preparation of β2AR–T4L and Nb80 are described in Methods. BI-167107-bound β2AR–T4L and Nb80 precipitated in 1:1.2 molar ratio were mixed in monolein containing 10% cholesterol in 1:1.5 protein to lipid ratio (w/w). Initial crystallization leads were identified and optimized in 24-well glass sandwich plates using 50 μl protein and lipid drops overlaid with 0.8 μl precipitant solution in each well and sealed with a glass cover slip. Crystals for data collection were grown at 20 °C in hanging-drop format using 0.8 μl reservoir solution (36 to 44% PEG 400, 100 mM Tris pH 8.0, 4% DMSO, 1% 1,2,3-heptanetriol) diluted two- to fourfold in water. Crystals grew to full size, typically 40 × 5 × 5 μm3, within 7 to 10 days. Crystals were flash-frozen and stored in liquid nitrogen with reservoir solution as cryoprotectant. Diffraction data collection and processing, and structure solution and refinement are described in Methods.

Full Methods and any associated references are available in the online version of the paper at www.nature.com/nature.

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Author Contributions S.G.F.R. screened and characterized high affinity agonists, identified and determined dissociation rate of Bi-167107, screened, identified and characterized MNG-3, performed selection and characterization of nanobodies, purified and crystallized the receptor with Nb80 in LCP, optimized crystallization conditions, grew crystals for data collection, reconstituted receptor in HDL particles and determined the effect of Nb80 and Gs on receptor conformation and ligand binding affinities, assisted with data collection and preparing the manuscript. H.-J.C. processed and characterized MNG-3, performed selection and characterization of nanobodies, purified and crystallized receptor with nanobodies in bichelles, assisted with growing crystals in LCP, and assisted with data collection. E.P. performed immunization, cloned and expressed nanobodies, and performed the initial selections. J.S. supervised nanobody production. P.S.K. and S.H.G. provided MNG-3 detergent for stabilization of purified β2AR, B.T.D. and R.K.S. provided ApoA1 and Gs protein, and reconstituted β2AR in HDL particles with Gs. D.M.R. characterized the utility of MNG-3 for crystallization in LCP and assisted with manuscript preparation, F.S.T. expressed β2AR in insect cells and with T. L. K. performed the initial stage of β2AR purification. A.P., A.S. assisted in selection of the high-affinity agonist Bi-167107. L.K. synthesized Bi-167107. P.C. characterized the functional properties of Bi-167107 in CHO cells. W.J.W. oversaw data processing, structure determination and refinement, and assisted with writing the manuscript. B.K.K. was responsible for the overall project strategy and management, prepared β2AR in lipid vesicles for immunization, harvested and collected data on crystals, and wrote the manuscript.

Author Information Coordinates and structure factors for β2AR–Nb80 are deposited in the Protein Data Bank (accession code 3POQ). Reprints and permissions information is available at www.nature.com/reprints. The authors declare no competing financial interests. Readers are welcome to comment on the online version of this article at www.nature.com/nature. Correspondence and requests for materials should be addressed to B.K.K. (kobilka@stanford.edu) or W.I.W. (bill.weis@stanford.edu).
METHODS

Preparation of β2AR–T4L and nanobody-80 for crystallography. β2AR–T4L was expressed in Sf-9 insect cell cultures infected with β2AR–T4L baculovirus, and solubilized according to methods described previously26. Functional protein was obtained by M1 Flag affinity chromatography (Sigma) before and following alprenolol-Sepharose chromatography26. In the second M1 chromatography step, receptor-bound alprenolol was exchanged for high-affinity agonist BI-167107 and dodecylmaltoside was exchanged for the MNG-3 amphiphile (11,11-bis-β-D-maltopyranosidylmethyl-heneicosane, Supplementary Fig. 6, obtained from P. S. Chae and S. H. Gellman) for increased receptor stability. The agonist-bound and detergent-exchanged β2AR–T4L was eluted in 10 mM HEPES pH 7.5, 100 mM NaCl, 0.02% MNG-3 and 10 μM BI-167107 followed by removal of N-linked glycosylation by treatment with PNGaseF (NEB). The protein was concentrated to ~50 mg ml⁻¹ with a 100kDa molecular weight cut off Vivaspin concentrator (Vivasience).

Nanobody-80 (Nb80) bearing a carboxy-terminal His₆ tag was expressed in the periplasm of Escherichia coli strain WK6 following induction with IPTG. Cultures of 0.6 l were grown to A₆₀₀ = 0.7 at 37 °C in TB media containing 0.1% glucose, 2 mM MgCl₂, and 50 μg ml⁻¹ ampicillin. Induced cultures were grown overnight at 28 °C. Cells were harvested by centrifugation and lysed in ice-cold buffer (10 mM HEPES pH 7.5, 100 mM NaCl, 0.02% MNG-3 and 10 μM BI-167107) followed by removal of residual cell debris. Nb80 was purified by nickel affinity chromatography, dialysed against buffer (10 mM HEPES pH 7.5, 100 mM NaCl, and 2 mM MgCl₂, and 50 μg ml⁻¹) and concentrated to ~120 mg ml⁻¹.

Crystalization. BI-167107 bound β2AR–T4L and Nb80 were mixed in 1:1:2 molar ratio, incubated 2 h at room temperature before mixing with liquefied monoloon (M7765, Sigma) containing 10% cholesterol (C8667, Sigma) in 1:1.5 molar ratio, incubated against buffer (10 mM HEPES pH 7.5, 100 mM NaCl, and 0.02% MNG-3) and dialysed overnight against buffer (10 mM HEPES pH 7.5, 100 mM NaCl) and spin concentrated to ~120 mg ml⁻¹.

Diffraction data were measured at beamline 23-ID of the Advanced Photon Source, using a 10-μm diameter beam. Low dose 1.0° rotation images were used to locate and centre crystals for data collection. Data were collected in 1.0° frames with exposure time typically 5–10 s with a 5× attenuated beam. Only 5–10° of data could be measured before significant radiation damage occurred. Data were integrated and scaled with the HKL2000 package26.

Structure solution and refinement. Molecular replacement phases were obtained with the program Phaser27. The search models were (1) the high-resolution carazolol-bound β2AR structure, PDB ID 2RH1, but with T4L and all water, ligand and lipid molecules removed and a nanobody (PDB ID 3DWT, water molecules and lipid molecules removed) as search models. The rotation and translation function Z scores were 8.7 and 9.0 after placing the β2AR model, and the nanobody model placed subsequently had rotation and translation function Z scores of 3.5 and 11.5. The model was refined in Phenix26 and BUSTER30, using a group B factor model with one B for each atom. Crystals grew to full size within 7 to 10 days. Crystals were flash-frozen and stored in liquid nitrogen with reservoir solution as cryoprotectant.

Microcrystallography data collection and processing. Diffraction data were measured at beamline 23-ID of the Advanced Photon Source, using a 10-μm diameter beam. Low dose 1° rotation images were used to locate and centre crystals for data collection. Data were measured in 1.0° frames with exposure time typically 5–10 s with a 5× attenuated beam. Only 5–10° of data could be measured before significant radiation damage occurred. Data were integrated and scaled with the HKL2000 package26.

Ligand binding on receptor reconstituted in HDL particles. The effect of Nb80 and Gs on the receptors affinity for agonists was compared in competition binding experiments. The β2AR and β2AR–T4L (both truncated at position 365) purified as previously described26 were reconstituted in high-density lipoprotein (HDL) particles followed by reconstitution of Gs into HDL particles containing β2AR according to previously published methods26. [125I]-dihydroalprenolol ([125I]-DHA; 0.6 nM) was used as radioligand and agonist (~1-isoproterenol (ISO) or inverse agonist ICI-118,551 (ICI) as competitor. Nb80 was used at 1 μM. GTPγS was used at 10 μM. TBS (50 mM Tris pH 7.4, 150 mM NaCl) containing 0.1% BSA was used as binding buffer. Bound [125I]-DHA was separated from unbound on a Brandel harvester by passing over a Whatman GF/B filter (presoaked in TBS with 0.3% polyethyleneimine) and washed in cold TBS. Radioligand binding was measured in a Beckman LS6000 scintillation counter. Ligand binding affinity (Kᵢ) of DHA was determined from saturation binding curves using GraphPad Prism software. Normalized ISO competition binding data were fit to a two-site competition binding model by using GraphPad Prism. Binding affinities of ISO (Kᵢ values, tabulated in Supplementary Table 1) were determined from 50% inhibitory concentration (IC₅₀) values using the equation Kᵢ = IC₅₀/(1 + [L]/Kᵢ).

cAMP assay. To determine the functional potency of BI-167107, changes in intracellular cAMP levels were determined with CHO-hβ2AR cells in suspension (15 000 cells per well) by using Alphascreen technology (PerkinElmer Life and Analytical Sciences) and a 348-well plate format (Optiplate; PerkinElmer Life and Analytical Sciences), according to the manufacturer’s protocol. In brief, cells were stimulated with the respective agonists at different concentrations in Hanks’ buffered saline solution supplemented with 5 mM HEPES, 0.1% bovine serum albumin and 3-isobutyl-1-methylxanthine for 30 min at room temperature. Cells were lysed by using Alphascreen reagents. After 2 h, plates were read on an Envision plate reader (PerkinElmer Life and Analytical Sciences). The concentration of cAMP in the samples was calculated from a standard curve.

Bimane fluorescence spectroscopy on β2AR reconstituted in HDL particles. To compare the effects on receptor conformation of Gs and Nb80 binding the purified β2AR was labelled with the environmentally sensitive fluorescent probe monobromobimane (Invitrogen) at cysteine 265 located in the cytoplasmic end of TM6, and reconstituted into HDL particles (mBB-β2AR/HDL). Prior to obtaining fluorescence emission spectra, 10 nM mBB-β2AR/HDL was incubated 30 min at room temperature in buffer (20 mM HEPES pH 7.5, 100 mM NaCl) in the absence or presence of 10 μM ISO, 1 μM ICI, 300 nM Gs heterotrimer, or 300 nM Nb80, or in combinations of ISO with Gs, ISO with Nb80, and ICI with Nb80. Fluorescence spectroscopy was performed on a Spex Fluoromax-3 spectrofluorometer (Jobin Yvon) with photon-counting mode, using an excitation and emission bandwidth of 5 nm. Excitation was set at 370 nm and emission was collected from 415 to 535 nm in 1-nm increments with 0.3 nm⁻¹ integration time. Fluorescence intensity was corrected for background fluorescence from buffer and ligands. The curves shown in Fig. 1b and c are each the average of triplicate experiments.

High affinity β2AR agonist screening by bimane fluorescence spectroscopy. To obtain high affinity agonist candidates with slow dissociation rates for crystallography, a screening process of commercially available drugs and compound libraries from medicinal and biotech industry was initiated. Screening was conducted in several rounds on more than 50 compounds. Each compound (10 μM) was incubated with 100 nM purified mBB-β2AR in DDM buffer (20 mM HEPES pH 7.5, 100 mM NaCl, 0.1% dodecylmaltoside (DDMI)) for 30 min at room temperature before emission scanning, using same equipment and settings as described in the section above. Compounds inducing the largest red shift in λ_max and decrease in bimane fluorescence emission were identified. Closely related structural analogues were subsequently screened using same criteria for selection. Several lead candidate compounds were then subjected to dissociation experiments to identify the agonist with the slowest rate of dissociation. In these experiments, 100 nM mBB-β2AR was incubated with 1 μM lead compound in DDM buffer for 2 h at room temperature before obtaining the emission scan at τ = 0 (example in Supplementary Fig. 2d, green spectra). An excess amount (200 μM) of the neutral antagonist alprenolol (ALP) was added to identical samples followed by measurement of bimane emission at various time points in a period up to 7 days or until complete dissociation of agonist.

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