Gs protein peptidomimetics as allosteric modulators of the 2-adrenergic receptor

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**Introduction**

The importance of G protein-coupled receptors (GPCRs) within drug discovery is undisputed. It is estimated that >25% of FDA approved drugs act via GPCRs. However, only 27% of non-olfactory GPCRs are currently targeted by an approved drug and 15% are currently in clinical trials, leaving 232 non-olfactory GPCRs are currently targeted by an approved drug. These authors contributed equally as principal investigators.

A series of G\textsubscript{s} protein peptidomimetics were designed and synthesised based on the published X-ray crystal structure of the active state \(\beta\textsubscript{2}\text{-adrenergic receptor} (\beta\textsubscript{2}AR)\) in complex with the G\textsubscript{s} protein (PDB 3SN6). We hypothesised that such peptidomimetics may function as allosteric modulators that target the intracellular G\textsubscript{s} protein binding site of the \(\beta\textsubscript{2}AR\). Peptidomimetics were designed to mimic the 15 residue C-terminal \(\alpha\)-helix of the G\textsubscript{s} protein and were pre-organised in a helical conformation by \((i, i + 4)\)-stapling using copper catalysed azide alkyne cycloaddition. Linear and stapled peptidomimetics were analysed by circular dichroism (CD) and characterised in a membrane-based cAMP accumulation assay and in a bimane fluorescence assay on purified \(\beta\text{2}AR\). Several peptidomimetics inhibited agonist isoproterenol (ISO) induced cAMP formation by lowering the ISO maximal efficacy up to 61%. Moreover, some peptidomimetics were found to significantly decrease the potency of ISO up to 39-fold. In the bimane fluorescence assay none of the tested peptidomimetics could stabilise an active-like conformation of \(\beta\text{2}AR\). Overall, the obtained pharmacological data suggest that some of the peptidomimetics may be able to compete with the native G\textsubscript{s} protein for the intracellular binding site to block ISO-induced cAMP formation, but are unable to stabilise an active-like receptor conformation.

The structure of the active state \(\beta\text{2}AR\) was determined in complex with the G\textsubscript{s} protein (PDB 3SN6). We hypothesised that such peptidomimetics may function as allosteric modulators that target the intracellular G\textsubscript{s} protein binding site of the \(\beta\text{2}AR\). Peptidomimetics were designed to mimic the 15 residue C-terminal \(\alpha\)-helix of the G\textsubscript{s} protein and were pre-organised in a helical conformation by \((i, i + 4)\)-stapling using copper catalysed azide alkyne cycloaddition. Linear and stapled peptidomimetics were analysed by circular dichroism (CD) and characterised in a membrane-based cAMP accumulation assay and in a bimane fluorescence assay on purified \(\beta\text{2}AR\). Several peptidomimetics inhibited agonist isoproterenol (ISO) induced cAMP formation by lowering the ISO maximal efficacy up to 61%. Moreover, some peptidomimetics were found to significantly decrease the potency of ISO up to 39-fold. In the bimane fluorescence assay none of the tested peptidomimetics could stabilise an active-like conformation of \(\beta\text{2}AR\). Overall, the obtained pharmacological data suggest that some of the peptidomimetics may be able to compete with the native G\textsubscript{s} protein for the intracellular binding site to block ISO-induced cAMP formation, but are unable to stabilise an active-like receptor conformation.

The allosteric ligand was found to bind to the intracellular surface of the receptor and inhibit both G\textsubscript{s} protein and arrestin mediated signalling. Kobilka and co-workers reported the discovery of an intracellular small molecule-like allosteric modulator for the \(\beta\text{2}AR\) using a combinatorial approach with DNA encoded libraries. The allosteric ligand was found to bind to the intracellular surface of the receptor and inhibit both G\textsubscript{s} protein and arrestin mediated signalling. Kobilka and co-workers crystallised a closely related analogue of the same ligand in complex with the \(\beta\text{2}AR\T4\text{-lysozyme fusion protein}\) with the orthosteric inverse agonist carazolol bound. The structure (PDB 5X7D) clearly shows the ligand occupying the G protein binding pocket.

Based on recent bio-structural data of active state GPCRs in complex with GPCR interacting proteins (GIPs) or mimics thereof, we wondered if it would be possible to rationally surface of GPCRs has largely been ignored in the development of allosteric modulators. Such allosteric modulators could conceivably be designed to target the receptor surface responsible for recruiting intracellular transducers such as the G proteins and arrestins and thus be useful pharmacological tool compounds for studying GPCR signal transduction and possibly provide a new avenue for drug discovery. Moreover, such compounds could be useful compounds for X-ray crystallography to stabilise GPCRs in their active state conformation, which is particularly difficult to crystallise due to the high degree of receptor flexibility in the receptor active state. Recently, Lefkowitz and co-workers reported the discovery of an intracellular small molecule-like allosteric modulator for the \(\beta\text{2}AR\) using a combinatorial approach with DNA encoded libraries. The allosteric ligand was found to bind to the intracellular surface of the receptor and inhibit both G\textsubscript{s} protein and arrestin mediated signalling. Kobilka and co-workers crystallised a closely related analogue of the same ligand in complex with the \(\beta\text{2}AR\text{T4-lysozyme fusion protein}\) with the orthosteric inverse agonist carazolol bound. The structure (PDB 5X7D) clearly shows the ligand occupying the G protein binding pocket.
design peptidomimetics that target the GIP interface. Such allosteric ligands could be beneficial for stabilisation of GPCRs in various conformational states for structural studies, as pharmacological tool compounds, and could possibly provide a new avenue for therapeutic molecules. There have been some reports in the literature on using proteinogenic peptides as GPCR ligands. Hamm and co-workers have published several papers describing that peptides derived from the C-terminus of various G protein α subunits (Gα) are capable of reducing cAMP accumulation by blocking G protein coupling. Moreover, Scheerer et al. have reported the X-ray crystal structure of rhodopsin in complex with an 11-mer C-terminal peptide from the G protein. More recently, we reported our efforts to develop a peptidomimetic that mimics the function of nanobody 80 (Nb80) a well-known allosteric modulator of the β2AR that binds at the same site of the receptor as the native Gα protein.

Using the X-ray crystal structure of the β2AR in complex with the Gα protein (β2AR-Gα) as a template (PDB 3SN6) we embarked on a project to identify such allosteric modulators for the β2AR by a structure-based design approach.

Results and discussion

Peptidomimetic design

Hamm and co-workers previously reported that a peptide comprised of the last 12 amino acid residues from the Gα C-terminus (GαCT12) was capable of inhibiting Gα protein coupling to the β2AR and increased agonist affinity for the receptor. However, in our hands the corresponding proteinogenic 15-mer peptide (GαCT15) did not block agonist induced cAMP formation in β2AR cell membranes, whereas Nb80 significantly inhibited the maximal efficacy of ISO (Fig. 1c). Whereas Hamm and co-workers used saponin-permeabilised C6 glioma cells, all peptides reported herein were evaluated in HEK293 membranes overexpressing the β2AR. We selected to work in a cell membrane-based assay setup to render the intracellular surface freely accessible to the ligands and eliminate issues related to cell permeability. Likewise, Rasmussen...
et al. were not able to observe any effect of the 20-mer $\text{G}_{\text{z,C}}\text{T}_{\text{CT}_{15}}$ peptide on $\beta_2\text{AR}$ receptor function and complex formation with $\beta_2\text{AR}$. However, when $\text{G}_{\text{z,C}}\text{T}_{\text{CT}_{20}}$ was fused to the carboxy terminus of the $\beta_2\text{AR}$ and expressed as a fusion protein a 27-fold increase in agonist affinity was observed. Based on the results by Rasmussen et al. we speculate that $\text{G}_{\text{z,C}}\text{T}_{\text{CT}_{20}}$ mainly adopts a random coil structure in solution rendering binding to the receptor less favourable. This is consistent with our circular dichroism (CD) analysis of $\text{G}_{\text{z,C}}\text{T}_{\text{CT}_{15}}$ that showed a random coil structure (Fig. 1e). Also, the affinity of a linear $\text{G}_{\text{z,C}}\text{T}$ peptide for $\beta_2\text{AR}$ is likely significantly lower than the full $\text{G}_s$ protein complex, which has several additional contacts with the receptor. Based on these observations, we hypothesised that it would be necessary to chemically modify the native $\text{G}_{\text{z,C}}\text{T}_{\text{CT}_{15}}$ peptide to improve binding to the $\beta_2\text{AR}$. In the $\beta_2\text{AR}$-$\text{G}_s$ X-ray crystal structure the C-terminus of $\text{G}_s$ adopts an $\alpha$-helix terminated by a 3-residue reverse turn (Fig. 1b). Thus, we set out to chemically modify $\text{G}_{\text{z,C}}\text{T}_{\text{CT}_{15}}$ to pre-organise the peptide in a similar conformation. Peptide stapling is a commonly applied technique for the synthesis of helical peptides. Among the many available methods for peptide stapling we favour CuAAC-stapling between amino acids with azido- and alkynyl-modified side chains. This methodology was originally developed by Tornoe et al. and later optimised by

Table 1 Synthesis of linear and stapled peptidomimetics. Linear peptides were synthesised on 2-chlorotritylresin preloaded with leucine. The N-termini of all peptides were acylated. Peptides 6D–9D were poorly soluble in a variety of solvent systems and were not purified/stapled. The remaining purified (or crude) linear peptides were stapled by CuAAC and purified by preparative RP-HPLC.

| Linear Amino acid sequence | Stapled | Yield (mass%)<sup>a</sup> | Reaction time |
|---------------------------|----------|--------------------------|---------------|
| $\text{G}_{\text{z,C}}\text{T}_{15}$ | $\text{H-R-I-Q-R-M-H-L-R-Q-Y-E-L-L-OH}$ | NA | NA | NA |
| 6A | $\text{Ac-R-D-I-R-Q-R-M-H-L-R-Q-Y-E-L-L-OH}$ | 10A | 36<sup>b</sup>/84 | 15 min |
| 6B | $\text{Ac-R-D-I-R-Q-R-M-H-L-R-Q-Y-E-L-L-OH}$ | 10B | 10<sup>b</sup>/63 | Overnight<sup>d</sup> |
| 6C | $\text{Ac-R-D-I-Q-R-I-H-L-R-Q-Y-E-L-L-OH}$ | 10C | 10<sup>b</sup>/45 | 3 h |
| 6D | $\text{Ac-R-D-I-Q-R-I-H-L-R-Q-Y-E-L-L-OH}$ | NA | NA | NA |
| 7A | $\text{Ac-R-D-I-Q-R-I-H-L-R-Q-Y-E-L-L-OH}$ | 11A | 56<sup>b</sup>/77 | 15 min |
| 7B | $\text{Ac-R-D-I-Q-R-I-H-L-R-Q-Y-E-L-L-OH}$ | 11B | 11<sup>b</sup>/72 | Overnight<sup>d</sup> |
| 7C | $\text{Ac-R-D-I-Q-R-I-H-L-R-Q-Y-E-L-L-OH}$ | 11C | 26<sup>b</sup>/71 | 1 h |
| 7D | $\text{Ac-R-D-I-Q-R-I-H-L-R-Q-Y-E-L-L-OH}$ | NA | NA | NA |
| 8A | $\text{Ac-R-D-I-Q-R-I-H-L-R-Q-Y-E-L-L-OH}$ | 12A | 69<sup>b</sup>/60 | 1 h |
| 8B | $\text{Ac-R-D-I-Q-R-I-H-L-R-Q-Y-E-L-L-OH}$ | 12B | 15<sup>b</sup>/74 | 1 h |
| 8C | $\text{Ac-R-D-I-Q-R-I-H-L-R-Q-Y-E-L-L-OH}$ | 12C | 14<sup>b</sup>/53 | 2 h |
| 8D | $\text{Ac-R-D-I-Q-R-I-H-L-R-Q-Y-E-L-L-OH}$ | NA | NA | NA |
| 9A | $\text{Ac-R-D-I-Q-R-I-H-L-R-Q-Y-E-L-L-OH}$ | 13A | 40<sup>b</sup>/67 | Overnight<sup>d</sup> |
| 9B | $\text{Ac-R-D-I-Q-R-I-H-L-R-Q-Y-E-L-L-OH}$ | 13B | 13<sup>b</sup>/77 | Overnight<sup>d</sup> |
| 9C | $\text{Ac-R-D-I-Q-R-I-H-L-R-Q-Y-E-L-L-OH}$ | 13C | 11<sup>b</sup>/60 | 3 h |
| 9D | $\text{Ac-R-D-I-Q-R-I-H-L-R-Q-Y-E-L-L-OH}$ | NA | NA | NA |

<sup>a</sup> Yield after preparative HPLC purification to >95% purity (non-NPC corrected).<sup>b</sup> Net peptide content (NPC) (mass% of peptide, the remainder being constituted by counter ions and water). Determined by qNMR (see ESI for details).<sup>c</sup> Synthesised from pure linear peptide. Synthesised from crude linear peptide. Overall yield based on resin loading.<sup>d</sup> Presumably finished in <3 hours but left overnight for practical reasons.
Cantel et al. and has been applied extensively in (i, i + 4)-peptide stapling in recent years.

By visual inspection of the β2AR-Gs X-ray crystal structure we concluded that the 15 C-terminal residues of Gs participate in important interactions with β2AR. This is consistent with the conclusions drawn by Hildebrand and co-workers based on MD simulations. In terms of design, it is important that the staple position does not disrupt binding to the target. By visual inspection and based on the MD simulation study by Hildebrand and co-workers 5 residues were identified as potential staple anchoring points (Fig. 1). These 5 residues are ideally positioned for introduction of staples and four stapling positions would be evaluated in the present study (Fig. 2). Moreover, four different staple designs utilising D- and L-norleucine (5) was employed as a replacement for the oxidation prone methionine residue. With amino acids 1–5 in hand the linear peptidomimetics 6–9 were synthesised by standard Fmoc-based solid-phase peptide synthesis (SPPS) on chlorotrityl resin and the N-terminus was acylated (Table 1). The synthesis of linear peptides 6–9 was uneventful and they were all purified by standard preparative RP-HPLC. However, the synthesis of peptides 6D–9D where two polar residues (D and R) were replaced proved complicated due to poor solubility after cleavage and deprotection. Because peptides 6D–9D were intended as inactive negative controls we eventually abandoned their purification and stapling due to their poor solubility, which would also translate to problems for pharmacological characterisation. Stapling of purified or crude 6–9 A–C (see ESI† for details) was carried out in tBuOH and water (1 : 2 v/v) using CuSO4·5H2O (1 eq.) and sodium ascorbate (5 eq.) as the in situ reducing agent. In general, the CuAAC reaction was clean and went to completion fast (1–3 h) to give stapled peptidomimetics 10–13 A–C that were purified by preparative RP-HPLC to >95% purity in reasonable yields. Full conversion of linear to stapled peptidomimetic was monitored by RP-HPLC by spiking the reaction sample with the linear starting material, and by FT-IR where the azide stretch (at ~2100 cm⁻¹) is clearly seen to disappear after completion of the stapling reaction (see ESI†).

**Synthesis**

Fmoc-protected propargylglycine (3) is commercially available and the remaining azide and alkyne modified building blocks were synthesised in house. Azides 1–2 were synthesised from the corresponding Fmoc-protected amines as previously reported using the diazotransfer reagent imidazole sulfonyl azide. Alkyne 4 was synthesised in three steps from Boc-protected serine according to the published procedure. Finally, for stapling positions B and D commercially available norleucine (5) was employed as a replacement for the oxidation prone methionine residue. With amino acids 1–5 in hand the linear peptidomimetics 6–9 were synthesised by standard Fmoc-based solid-phase peptide synthesis (SPPS) on chlorotrityl resin and the N-terminus was acylated (Table 1). The synthesis of linear peptides 6–9 was uneventful and they were all purified by standard preparative RP-HPLC. However, the synthesis of peptides 6D–9D where two polar residues (D and R) were replaced proved complicated due to poor solubility after cleavage and deprotection. Because peptides 6D–9D were intended as inactive negative controls we eventually abandoned their purification and stapling due to their poor solubility, which would also translate to problems for pharmacological characterisation. Stapling of purified or crude 6–9 A–C (see ESI† for details) was carried out in tBuOH and water (1 : 2 v/v) using CuSO4·5H2O (1 eq.) and sodium ascorbate (5 eq.) as the in situ reducing agent. In general, the CuAAC reaction was clean and went to completion fast (1–3 h) to give stapled peptidomimetics 10–13 A–C that were purified by preparative RP-HPLC to >95% purity in reasonable yields. Full conversion of linear to stapled peptidomimetic was monitored by RP-HPLC by spiking the reaction sample with the linear starting material, and by FT-IR where the azide stretch (at ~2100 cm⁻¹) is clearly seen to disappear after completion of the stapling reaction (see ESI†).
Structural analysis by circular dichroism (CD)

All purified linear and stapled peptides were subjected to structural analysis by CD. Prior to recording CD spectra, the net peptide content (NPC) for all peptidomimetics was determined by quantitative NMR (qNMR, see ESI†). The CD data in Fig. 3 shows that stapling in general leads to peptidomimetics with a more helical structure when compared to the linear counterparts. However, the magnitude of the induced helicity varies significantly. While the position of the staple (A, B or C, Fig. 2) does not have a significant effect on the induced helicity, the employed amino acid residues (1–4) that form the staple have a tremendous effect. Employing residues 1 and 3 clearly increases the helicity of the peptide the most at all three stapling positions. The use of residues 1 and 4 likewise shows strong induction of helicity. In contrast, the use of the ω-amino acid 2 in combination with either 3 or 4 lowers the helical induction markedly.

Pharmacology

Membrane-based cAMP accumulation assay. Initially, the stapled peptidomimetics (10–13) and their linear precursors (6–9) were tested for their ability to modulate β2AR agonist-induced cAMP formation. To allow the peptidomimetics to interact with the intracellular G protein binding pocket they were tested in a membrane-based cAMP accumulation assay (see ESI†). In this setup stimulation of β2AR expressing membranes with various concentrations of the agonist (−)isoproterenol (ISO) increased cAMP formation in a concentration-dependent manner (mean pEC50 = 8.64 ± 0.03). To test the effect of the peptidomimetics on the ISO-induced cAMP formation, similar ISO concentration response curves (CRCs) were generated in presence of a constant concentration of peptidomimetic (100 μM, except for 8C, which was tested at 10 μM due to poor solubility). The cAMP levels in absence of peptidomimetics were normalised to the basal (0%) and maximal efficacy (100%) of ISO in presence of vehicle (DMSO).

All peptidomimetics stapled at position A had little to no effect on the maximum efficacy of ISO (Table 2). Several of the peptidomimetics stapled at positions B and C displayed a small effect on the maximum efficacy of ISO; 7B, 8B, 8C and 11C all significantly decreased the maximal efficacy to approximately 80% (Table 2 and Fig. 4). Peptidomimetics 12B and 12C had a more pronounced effect and inhibited the maximal efficacy to ~73% on average. Finally, peptidomimetic 10C affected the maximal ISO efficacy the most by lowering ISO maximal efficacy to 61%. With respect to peptidomimetic-induced effects on ISO potency, 9B and 13B significantly decreased the potency by 39- and 8-fold, respectively, but not the efficacy of ISO (Fig. 4). No significant effects of the peptidomimetics were observed on the basal cAMP levels or on the Hill-slope of the fitted curves.

To estimate the potency of the most efficacious peptidomimetic 10C, increasing concentrations of 10C up to 200 μM, and
Nb80 as a control were applied in the presence of an ISO concentration corresponding to EC75. The IC50 of 10C was estimated to 55 μM whereas the IC50 of Nb80 was estimated to 0.40 μM (Fig. 4).

**Bimane fluorescence shift assay.** To further investigate their pharmacological profiles, selected peptidomimetics were tested in a bimane fluorescence shift assay (see ESI†). Labelling of cysteine residue 265 (C265) located in the lower part of the TM6...
of β2AR with a bimane-fluorophore allows detection of conformational changes associated with receptor activation.\(^\text{31}\) Stimulation of purified, C265 fluorophore-labelled β2AR with increasing concentrations of ISO results in a concentration-dependent decrease in the fluorescence intensity (FI) and a red-shift of the maximum emission wavelength (\(\lambda_{\text{max}}\)) of the bimane-fluorophore probe (Fig. 5A). The active receptor conformation may be further stabilised in the presence of G protein\(^\text{34}\) and G protein mimetics such as Nb80.\(^\text{8}\) Indeed, in presence of a partial equilibrium shifting ISO concentration (10 μM), Nb80 is capable of decreasing FI and red-shifting \(\lambda_{\text{max}}\) beyond that of ISO (10 μM) or Nb80 (5 μM) alone (Fig. 5B). Conversely, ICI-118,551 (ICI), an inverse agonist capable of stabilising an inactive conformation of β2AR, blocks the 10 μM ISO-induced response and also slightly increase FI and blue-shifts \(\lambda_{\text{max}}\) on its own (Fig. 5C). Thus, the bimane fluorescence shift assay can identify active and inactive-conformation stabilising ligands of the β2AR.

Based on the results obtained with the cAMP assay, the linear and cyclic peptidomimetic pairs 6C/10C, 7C/11C, 8C/12C, 8B/12B and 9B/13B were tested in the bimane assay at 20 μM (Fig. 6). The peptidomimetics were tested for possible effects on receptor conformation alone and in the presence of 10 μM ISO, which allows detection of peptidomimetic-induced active conformation stabilisation as seen for Nb80. Bimane-fluorescence curves in presence of agonist or peptidomimetic alone or in combination were normalised to that of the receptor alone.

Unlike Nb80, none of the tested peptidomimetic were observed to stabilise an active-like conformation by decreasing FI and red-shifting \(\lambda_{\text{max}}\) on their own or by potentiating the response beyond that of 10 μM ISO alone. Although there was a tendency for several peptidomimetics to shift the bimane-fluorescence in the opposite direction (8B, 7–8C and 10–11C), the peptidomimetics did not affect the response of 10 μM ISO alone. Interestingly, with the exception of peptidomimetic 8B only the peptidomimetics stapled at position C closest to the C-terminal were able to increase FI and blue-shift \(\lambda_{\text{max}}\) in a similar way to that seen for the inverse agonist ICI (Fig. 5C).

### Discussion

As anticipated CD analysis revealed that the stapled peptidomimetics generally had a higher helical content than their linear counterparts and the native G\(_{\alpha}\)s 15-mer. The staples comprised of building blocks 1, 3 and 4 had the highest helical content, whereas the peptidomimetics stapled with \(\gamma\)-amino acid 2 and alkynes 3 and 4 contained significantly less helicity. There was no trend regarding the helical content and the stapling positions A–C.

The peptidomimetics were evaluated for their ability to block agonist-induced cAMP formation in cell membranes overexpressing the β2AR. Stapling the peptidomimetics at position A was not optimal for blocking cAMP formation by ISO. Thus, both stapled peptidomimetics 12A–13A and linear peptidomimetics 8A–9A were essentially inactive, indicating that this stapling position is not ideal for binding to the receptor using the present chemistry. Moving the staple towards the C-terminus (position B and C) was more favourable. The linear peptidomimetics 7B and 8B had a slight, yet significant effect on the maximal ISO response, lowering the efficacy to approximately 80%. Stapled peptidomimetic 12B had a more pronounced effect on the maximum efficacy with a lowering to 74%. Unexpectedly the 9B/13B pair red-shifted the ISO CRC comparable to that of a competitive antagonist rather than decreasing the maximal agonist efficacy as would be expected for a non-competitive antagonist. The linear 8C and stapled peptidomimetic 11C both lowered the maximum efficacy of ISO to approximately 80%. On the other hand, stapled 12C lowered the efficacy to 72%, whereas stapled 10C lowered the efficacy to approximately 61%. Thus, 10C clearly gave the most significant decrease in the maximum efficacy of ISO. In general, the stapled peptidomimetics gave the highest reduction in efficacy and a small tendency for peptidomimetics with a high helical content to have a greater effect was observed (ESI Fig. S1\(^\text{T}\)). Thus, stapled peptidomimetics 10C, 12B and 12C with a relatively high helical content were found to lower the efficacy the most (61–74%). However, the data

![Fig. 5](https://example.com/f5.png)
also shows that a high degree of helicity on its own is not sufficient to give a notable reduction in the formation of cAMP (e.g. stapled peptidomimetic 10B).

When tested in the conformational bimane fluorescence shift assay none of the peptidomimetics stabilised an active-like conformation similar to that of the G protein mimetic Nb80.

Fig. 6 Representative bimane emission spectra of selected peptidomimetics with significant effects in the cAMP assay. The responses of the linear and cyclic peptidomimetic pairs 6C/10C, 7C/11C, 8C/12C, 8B/12B and 9B/13B were normalised to that of the unliganded β2AR alone (black solid line). The peptides were tested at 20 μM (n = 2 of measurements in triplicate) in the absence (pink solid line) and the presence (blue solid line) of ISO 10 μM (grey solid line).
However, a small tendency to increase the fluorescence intensity (FI) and blue-shift $\lambda_{\text{max}}$ similar to that for the inverse agonist ICI was seen. The effect was most pronounced for peptidomimetics stapled at position C but no correlation between the degree of helicity and the effect on the FI was observed. It cannot be excluded that the concentration tested in the bimane assay was too low to induce a more significant effect.

One interpretation of the obtained pharmacological data is that some of the peptidomimetics (e.g. 10C) are capable of modulating ISO-induced cAMP formation by binding to and thus overlapping with the intracellular binding site of the G protein. However, unlike Nb80, none of the peptidomimetics reported herein stabilise an active-like receptor conformation. Although only small effects of the peptidomimetics were observed it does support the idea of developing intracellular modulators of GPCR signalling derived from hotspot domains of GPCR interacting proteins (e.g. the C-termini of G proteins). However, the native C-terminal peptide sequence (Gz$_2$CT$_{15}$) that was employed as a template herein clearly does not provide potent peptidomimetic analogues despite stapling these in a helical conformation. Thus, to render this class of ligands of use for pharmacological and biophysical studies significant optimisation is required. It should be noted that the present study does not provide data that demonstrates that the peptidomimetics are binding in the intended G protein binding pocket. In principle, the peptidomimetics could be engaging the $\beta_2$AR elsewhere. Further studies with more potent analogues will be required to determine the mode of action.

**Conclusion**

In the present study, a series of peptidomimetics that mimic the C-terminal $\alpha$-helix of the Gz$_2$ protein were synthesised as potential allosteric modulators of the $\beta_2$AR. The peptidomimetics were characterised pharmacologically in a cAMP accumulation assay and bimane fluorescence assay. Several peptidomimetics inhibited agonist ISO induced cAMP formation by lowering the maximal efficacy of ISO up to 61%. For the most potent peptidomimetic 10C the IC$_{50}$ for blocking ISO induced cAMP formation was determined to 55 $\mu$M. Moreover, some peptidomimetics could decrease the potency of ISO significantly (up to 39-fold). In the bimane fluorescence assay none of the tested peptidomimetics could stabilise an active-like $\beta_2$AR conformation. However, we observed a tendency to shift the bimane assay in the opposite direction for some peptidomimetics. Taken together, the data suggests that some of the peptidomimetics can compete with the native G$_i$ protein for the intracellular binding site, but are unable to stabilise an active-like receptor conformation.

To render the peptidomimetics of use as pharmacological tool compounds significant optimisation is required to increase ligand potency. Likewise, to elucidate the mode of action for this class of ligands more potent ligands are required. To this end we are in the process of strengthening ligand–receptor interactions by substitution with natural and unnatural amino acids aided by computational design. The results from these endeavours will be reported elsewhere in due course.

**Conflicts of interest**

There are no conflicts to declare.

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