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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.<sup>1</sup> However, only 27% of nonolfactory GPCRs are currently targeted by an approved drug and 15% are currently in clinical trials, leaving 232 nonolfactory GPCRs that remain entirely unexploited as drug targets.<sup>2</sup> Despite the central importance of GPCRs, we still have a very rudimentary understanding of the structure and function of this family of membrane-spanning receptors, particularly with respect to how GPCRs interact with intracellular proteins to achieve signal transduction and physiological responses. GPCR ligands generally bind to the extracellular side of the receptor and target the orthosteric or allosteric binding sites, or both as bivalent ligands.<sup>3</sup> On the other hand, the intracellular

# $G_s$ protein peptidomimetics as allosteric modulators of the $\beta_2$ -adrenergic receptor $\dagger$

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A series of  $G_s$  protein peptidomimetics were designed and synthesised based on the published X-ray crystal structure of the active state  $\beta_2$ -adrenergic receptor ( $\beta_2AR$ ) in complex with the  $G_s$  protein (PDB 3SN6). We hypothesised that such peptidomimetics may function as allosteric modulators that target the intracellular  $G_s$  protein binding site of the  $\beta_2AR$ . Peptidomimetics were designed to mimic the 15 residue C-terminal  $\alpha$ -helix of the  $G_s$  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  $\beta_2AR$ . 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  $\beta_2AR$ . Overall, the obtained pharmacological data suggest that some of the peptidomimetics may be able to compete with the native  $G_s$  protein for the intracellular binding site to block ISO-induced cAMP formation, but are unable to stabilise an active-like receptor conformation.

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  $\beta_2$ adrenergic receptor ( $\beta_2 AR$ ) using a combinatorial approach with DNA encoded libraries.4 The allosteric ligand was found to bind to the intracellular surface of the receptor and inhibit both G protein and arrestin mediated signalling. Kobilka and coworkers crystallised a closely related analogue of the same ligand in complex with the  $\beta_2$ AR-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.5

Based on recent bio-structural data of active state GPCRs in complex with GPCR interacting proteins  $(GIP)^{6,7}$  or mimics thereof<sup>8-12</sup> we wondered if it would be possible to rationally



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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  $\alpha$  subunits (G $\alpha$ ) are capable of reducing cAMP accumulation by blocking G protein coupling.13-15 Moreover, Scheerer et al. have reported the X-ray crystal structure of rhodopsin in complex with an 11-mer C-terminal peptide from the Gt protein.10 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 β<sub>2</sub>AR that binds at the same site of the receptor as the native G<sub>s</sub> protein.9,16

Using the X-ray crystal structure of the  $\beta_2AR$  in complex with the  $G_s$  protein  $(\beta_2AR\text{-}G_s)$  as a template (PDB 3SN6)^7 we

embarked on a project to identify such allosteric modulators for the  $\beta_2 AR$  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  $G\alpha_s$  Cterminus ( $G\alpha_s CT_{12}$ ) was capable of inhibiting  $G_s$  protein coupling to the  $\beta_2 AR$  and increased agonist affinity for the receptor.<sup>15</sup> However, in our hands the corresponding proteinogenic 15-mer peptide ( $G\alpha_s CT_{15}$ ) did not block agonist induced cAMP formation in  $\beta_2 AR$  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  $\beta_2 AR$ .<sup>17</sup> 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



Fig. 1 (a) The native  $G\alpha_sCT_{15}$  peptide sequences. Red: residues with no or weak receptor contacts. Blue: reverse turn, not helical, (b) the structure of  $G\alpha_sCT_{15}$  extracted from PDB entry 3SN6, (c) the  $G\alpha_sCT_{15}$  peptide does not inhibit agonist induced cAMP formation of the  $\beta_2AR$ . Isoproterenol (ISO) concentration–response curves of cAMP accumulation were generated in the absence and presence of 50  $\mu$ M peptide using HEK293 cell membranes overexpressing the  $\beta_2AR$ . Data represents mean  $\pm$  SEM from 3–4 independent experiments carried out in duplicates. The known  $\beta_2AR$ -interacting nanobody 80 (Nb80) was included for comparison at 10  $\mu$ M.<sup>9</sup> (d) Helical wheel projection showing important contacts determined by MD simulation<sup>26</sup> and X-ray crystallography.<sup>7</sup> Dashed boxes: polar contacts involving side chains, solid boxes: polar contacts involving backbone carbonyls, bold box: cation– $\pi$  interaction, (e) CD spectrum of  $G\alpha_sCT_{15}$  indicating a random coil structure (at 50  $\mu$ M in 10 mM NaH<sub>2</sub>PO<sub>4</sub> buffer, pH 6.0).



Fig. 2 Stapling positions and unnatural amino acid building blocks. According to our analysis the red residues represent the best (i, i + 4)-stapling positions by appropriate substitution with amino acids 1–4 (staples A–C). Staple position D was included to validate the design (a negative control). To circumvent oxidation problems the norleucine building block 5 was employed as a substitute for methionine (stapling positions B and D).

et al. were not able to observe any effect of the 20-mer  $G\alpha_s CT_{20}$ peptide on  $\beta_2$ AR receptor function and complex formation with  $\beta_2$ AR.<sup>7</sup> However, when  $G\alpha_s CT_{20}$  was fused to the carboxy terminus of the  $\beta_2$ 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 GasCT20 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  $G\alpha_s CT_{15}$  that showed a random coil structure (Fig. 1e). Also, the affinity of a linear  $G\alpha_s CT$  peptide for  $\beta_2 AR$  is likely significantly lower than the full G<sub>s</sub> 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 GasCT15 peptide to improve binding to the  $\beta_2$ AR. In the  $\beta_2$ AR-G<sub>s</sub> X-ray crystal structure the C-terminus of G<sub>s</sub> adopts an α-helix terminated by a 3-residue reverse turn (Fig. 1b).<sup>7</sup> Thus, we set out to chemically modify  $G\alpha_s CT_{15}$  to preorganise the peptide in a similar conformation. Peptide stapling is a commonly applied technique for the synthesis of helical peptides.<sup>18-20</sup> Among the many available methods for peptide stapling we favour CuAAC-stapling between amino acids with azido- and alkynyl-modified side chains.<sup>21,22</sup> This methodology was originally developed by Tornoe et al.23 and later optimised by

Table 1Synthesis 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. Theremaining purified (or crude) linear peptides were stapled by CuAAC and purified by preparative RP-HPLC

	i) Fmoc-AA-OH, DMF H₂N-Leu ────────────────────────────────────		SO <sub>4</sub> , NaAsc uOH, H <sub>2</sub> O	V	
	iii) TFA, TIPS, H <sub>2</sub> O	6A-D, 7A-D	10A-C, 11A	10A-C, 11A-C	
		8A-D, 9A-D	12A-C, 13A-C		
Linear	Amino acid sequence	Stapled	Yield <sup><i>a</i></sup> /NPC <sup><i>b</i></sup> (%)	Reaction time	
$G\alpha_s CT_{15}$	H-R-D-I-I-Q-R-M-H-L-R-Q-Y-E-L-L-OH	NA	NA	NA	
6A	Ac-R-D-1-I-Q-R-3-H-L-R-Q-Y-E-L-L-OH	10A	36 <sup>c</sup> /84	15 min	
6B	Ac-R-D-I-1-Q-R-5-3-L-R-Q-Y-E-L-L-OH	10B	$10^{d}/63$	Overnight <sup>e</sup>	
6C	Ac-R-D-I-I-Q-R-1-H-L-R-3-Y-E-L-L-OH	10C	$10^{d}/45$	3 h	
6D	Ac-R-1-I-I-Q-3-5-H-L-R-Q-Y-E-L-L-OH	NA	NA	NA	
7 <b>A</b>	Ac-R-D-2-I-Q-R-3-H-L-R-Q-Y-E-L-L-OH	11A	56 <sup>c</sup> /77	15 min	
7 <b>B</b>	Ac-R-D-I-2-Q-R-5-3-L-R-Q-Y-E-L-L-OH	11B	$11^{d}/72$	Overnight <sup>e</sup>	
7C	Ac-R-D-I-I-Q-R-2-H-L-R-3-Y-E-L-L-OH	11C	$26^{d}/71$	1 h	
7 <b>D</b>	Ac-R-2-I-I-Q-3-5-H-L-R-Q-Y-E-L-L-OH	NA	NA	NA	
8A	Ac-R-D-1-I-Q-R-4-H-L-R-Q-Y-E-L-L-OH	12A	69 <sup>c</sup> /60	1 h	
8B	Ac-R-D-I-1-Q-R-5-4-L-R-Q-Y-E-L-L-OH	12B	$15^{d}/74$	1 h	
8C	Ac-R-D-I-I-Q-R-1-H-L-R-4-Y-E-L-L-OH	12C	$14^{d}/53$	2 h	
8D	Ac-R-1-I-I-Q-4-5-H-L-R-Q-Y-E-L-L-OH	NA	NA	NA	
9A	Ac-R-D-2-I-Q-R-4-H-L-R-Q-Y-E-L-L-OH	13A	40 <sup>c</sup> /67	Overnight <sup>e</sup>	
9B	Ac-R-D-I-2-Q-R-5-4-L-R-Q-Y-E-L-L-OH	13B	13 <sup>d</sup> /77	Overnight <sup>e</sup>	
9C	Ac-R-D-I-I-Q-R-2-H-L-R-4-Y-E-L-L-OH	13C	$11^{d}/60$	3 h	
9D	Ac-R-2-I-I-Q-4-5-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. <sup>*d*</sup> Synthesised from crude linear peptide. Overall yield based on resin loading. <sup>*e*</sup> Presumably finished in <3 hours but left overnight for practical reasons.



Fig. 3 CD spectra of linear (blue curves) and corresponding stapled (red curves) peptidomimetics at a concentration of  $50 \mu$ M (10 mM NaH<sub>2</sub>PO<sub>4</sub> buffer, pH 6.0). The first row compares stapling at position A (Fig. 2), the second row shows stapling position B and the third row shows a comparison of stapling position C. The columns show a comparison of the different combinations of stapling residues 1 + 3, 2 + 3, 1 + 4 and 2 + 4, respectively. The helicity of the most helical peptidomimetic **10C** as determined by the induced minima at 222 nm and maxima at 190 nm was set to 100% and the helicity of all other peptidomimetics were determined relative to that of **10C**.

Cantel *et al.*<sup>24</sup> and has been applied extensively in (i, i + 4)-peptide stapling in recent years.<sup>25</sup>

By visual inspection of the  $\beta_2$ AR-G<sub>s</sub> X-ray crystal structure we concluded that the 15 C-terminal residues of  $G\alpha_s$  participate in important interactions with  $\beta_2$ AR. This is consistent with the conclusions drawn by Hildebrand and co-workers based on MD simulations.<sup>26</sup> 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 (*i*, *i* + 4)-staples and four stapling positions would be evaluated in the present study (Fig. 2). Moreover, four different staple designs utilising D- and L- $\varepsilon$ -azidolysine (1–2), L-propargyl glycine (3) and *O*-propargylated Lserine (4) would be explored.

#### 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<sup>27</sup> using the diazotransfer reagent imidazole sulfonyl azide.<sup>28,29</sup> Alkyne **4** was synthesised in three steps from Bocprotected serine according to the published procedure.<sup>27</sup>

prone methionine residue.<sup>30</sup> With amino acids 1-5 in hand the linear peptidomimetics 6-9 were synthesised by standard Fmocbased solid-phase peptide synthesis (SPPS) on chlorotrityl resin and the N-terminus was acylated (Table 1). The synthesis of linear peptides 6-9 A-C 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 <sup>t</sup>BuOH and water (1 : 2 v/v) using  $CuSO_4 \cdot 5H_2O$  (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  $\sim 2100 \text{ cm}^{-1}$ ) is clearly seen to disappear after completion of the stapling reaction (see ESI<sup>†</sup>).

Finally, for stapling positions **B** and **D** commercially available

norleucine (5) was employed as a replacement for the oxidation

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**Table 2** Effect of  $G_s$  peptidomimetics on the cAMP accumulation induced by isoproterenol (ISO) at the  $\beta_2$ -adrenergic receptor ( $\beta_2AR$ ) in a cell membrane-based cyclic adenosine monophosphate (cAMP) accumulation assay. Basal cAMP level, maximum efficacy, pEC<sub>50</sub>(-log(EC<sub>50</sub>)) and Hill slope of the concentration–response curve of ISO in absence and presence of 100  $\mu$ M peptidomimetic (10  $\mu$ M for **8C**) were calculated by non-linear regression using GraphPad Prism. Nb80 was tested at 10  $\mu$ M. Data are given as mean values of *n* number of experiments  $\pm$  SEM. Significance level *P* < 0.05 (\*) calculated by statistical analysis with a one-way ANOVA in GraphPad Prism

Peptide	Basal level	Maximum efficacy	pEC <sub>50</sub>	Hill slope	n
Vehicle	$0.0\pm0.0$	$100.0\pm0.0$	$8.64\pm0.03$	$0.81\pm0.05$	6
Nb80	$-1.2\pm0.7$	$11.3\pm0.6^*$	$8.98\pm0.16$	$0.88\pm0.29$	3
6A	$0.7\pm1.1$	$90.8\pm6.0$	$8.68\pm0.04$	$0.81\pm0.07$	3
6B	$-2.9\pm4.2$	$81.5\pm4.5$	$8.48\pm0.08$	$0.81\pm0.12$	3
6C	$4.6 \pm 1.9$	$89.7 \pm 1.5$	$8.33 \pm 0.02$	$0.83\pm0.06$	3
7 <b>A</b>	$-0.5\pm1.5$	$88.8\pm8.0$	$8.74\pm0.01$	$0.83\pm0.10$	3
7 <b>B</b>	$-4.2\pm1.8$	$79.9 \pm 2.0^*$	$8.58\pm0.03$	$0.84\pm0.04$	3
7C	$8.4 \pm 4.3$	$88.1\pm3.6$	$8.17\pm0.11$	$0.87\pm0.06$	3
8A	$-1.1\pm0.7$	$97.7\pm5.3$	$8.67\pm0.04$	$0.72\pm0.02$	3
8B	$-8.8\pm2.8$	$77.1 \pm 3.9^*$	$8.46 \pm 0.15$	$0.82\pm0.07$	3
8C	$-3.7\pm2.3$	$78.0\pm5.2^*$	$8.65\pm0.06$	$0.71\pm0.07$	3
9A	$0.4\pm0.7$	$92.7\pm7.5$	$8.73 \pm 0.08$	$0.83\pm0.04$	3
9B	$3.3\pm4.6$	$84.1\pm2.4$	$7.05 \pm 0.38^{*}$	$0.89\pm0.05$	3
9C	$5.7\pm2.1$	$88.1\pm4.5$	$8.21\pm0.33$	$0.92\pm0.06$	3
10A	$3.0\pm0.4$	$82.8\pm3.3$	$8.67\pm0.05$	$0.78\pm0.03$	3
10B	$-5.0\pm2.6$	$80.5\pm2.2$	$8.45\pm0.04$	$0.72\pm0.05$	3
10C	$-11.0 \pm 4.3$	$61.0 \pm 4.1^*$	$7.87 \pm 0.01$	$0.63\pm0.06$	3
11A	$-1.4\pm0.7$	$90.7\pm4.6$	$8.53\pm0.05$	$0.74\pm0.03$	3
11B	$-5.8\pm3.0$	$88.0\pm4.1$	$8.46 \pm 0.07$	$0.72\pm0.06$	3
11C	$-1.9\pm8.4$	$78.4 \pm 2.6^*$	$8.10\pm0.12$	$0.85\pm0.06$	3
12A	$0.6\pm0.4$	$94.5\pm 6.3$	$8.68\pm0.03$	$0.73\pm0.04$	3
12B	$-2.8\pm4.0$	$74.0 \pm 3.3^{*}$	$7.87 \pm 0.53$	$0.88\pm0.09$	3
12C	$-6.0\pm2.1$	$71.7\pm3.0^{*}$	$8.52\pm0.05$	$0.90\pm0.06$	3
13A	$2.4\pm0.3$	$90.0\pm 6.4$	$8.71\pm0.05$	$0.85\pm0.03$	3
13B	$7.1\pm5.7$	$85.1\pm3.0$	$7.72\pm0.30^{*}$	$0.89\pm0.04$	3
13C	$2.3\pm1.2$	$82.8\pm3.8$	$8.46\pm0.43$	$0.80\pm0.04$	3

#### 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<sup>†</sup>).

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 D-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  $\beta_2AR$  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  $\beta_2AR$  expressing membranes with various

concentrations of the agonist (–)-isoproterenol (ISO) increased cAMP formation in a concentration-dependent manner (mean pEC<sub>50</sub> = 8.64  $\pm$  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  $\mu$ M, except for **8C**, which was tested at 10  $\mu$ M 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  $200 \ \mu$ M, and This article is licensed under a Creative Commons Attribution 3.0 Unported Licence.

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Fig. 4 Representative graphs of the most effective peptidomimetics on the cyclic adenosine monophosphate (cAMP) production induced by the full agonist isoproterenol (ISO) at the  $\beta_2$ -adrenergic receptor ( $\beta_2$ AR). The stapled peptidomimetic **10C** inhibited the maximal response of ISO to 61% whereas its linear precursor **6C** had no significant effect on the ISO-induced cAMP production (A). The linear **7B** (B) and stapled peptidomimetic **11C** (C) inhibited ISO efficacy to a smaller degree (~80%) but significantly. Their stapled (**11B**) and linear counterparts (**7C**) had a minor (~90%) albeit non-statistically significant effects. The linear **8B** and stapled peptidomimetic **12B** pair decreased the maximum response of ISO to 70–80% (D), which is also the case for the linear and stapled pair **8C** and **12C** (E). The linear **9B** and stapled peptidomimetic **13B**, decreased the potency of ISO by 39- and 8-fold, respectively, whereas the efficacy was not affected (F). In presence of ISO corresponding to EC<sub>75</sub>, the IC<sub>50</sub> of **10C** was estimated to 55  $\mu$ M, and the IC<sub>50</sub> of Nb80 was estimated to 0.40  $\mu$ M (G).

Nb80 as a control were applied in the presence of an ISO concentration corresponding to  $EC_{75}$ . The  $IC_{50}$  of **10**C was estimated to 55  $\mu$ M whereas the  $IC_{50}$  of Nb80 was estimated to 0.40  $\mu$ M (Fig. 4).

**Bimane fluorescence shift assay.** To further investigate their pharmacological profiles, selected peptidomimetics were tested in a bimane fluorescence shift assay (see ESI<sup>†</sup>). Labelling of cysteine residue 265 (C265) located in the lower part of the TM6

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Fig. 5 Representative bimane emission spectra of isoproterenol (ISO), nanobody 80 (Nb80) and ICI-118,551 (ICI) at the  $\beta_2$ -adrenergic receptor ( $\beta_2$ AR). ISO induces an active receptor conformation in a concentration-dependent manner. ISO displays saturating effects at 250  $\mu$ M and 500  $\mu$ M (A). Nb80 (5  $\mu$ M) potentiates the 10  $\mu$ M ISO-induced bimane-fluorescence response to that of ISO at 250  $\mu$ M and 500  $\mu$ M (B). At 10  $\mu$ M, ICI prevents the receptor activation induced by 10  $\mu$ M ISO and has a similar effect on the bimane-fluorescence response alone (C).

of  $\beta_2$ AR with a bimane-fluorophore allows detection of conformational changes associated with receptor activation.31 Stimulation of purified, C265 fluorophore-labelled  $\beta_2AR$  with increasing concentrations of ISO results in a concentrationdependent decrease in the fluorescence intensity (FI) and a red-shift of the maximum emission wavelength ( $\lambda_{max}$ ) of the bimane-fluorophore probe (Fig. 5A). The active receptor conformation may be further stabilised in the presence of G protein<sup>31</sup> and G protein mimetics such as Nb80.9 Indeed, in presence of a partial equilibrium shifting ISO concentration (10  $\mu$ M), Nb80 is capable of decreasing FI and red-shifting  $\lambda_{max}$ 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  $\beta_2AR$ , blocks the 10 µM ISO-induced response and also slightly increase FI and blue-shifts  $\lambda_{max}$  on its own (Fig. 5C). Thus, the bimane fluorescence shift assay can identify active and inactiveconformation stabilising ligands of the  $\beta_2$ AR.

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  $\mu$ M (Fig. 6). The peptidomimetics were tested for possible effects on receptor conformation alone and in the presence of 10  $\mu$ M ISO, which allows detection of peptidomimetic-induced active conformation stabilisation as seen for Nb80. Bimanefluorescence 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  $\lambda_{max}$  on their own or by potentiating the response beyond that of 10  $\mu$ M 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  $\mu$ M 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  $\lambda_{max}$  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 *D*-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  $\beta_2$ AR. 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<sup>†</sup>). 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

1.1-

1.0-

0.9

0.8

0.7

0.6

0.5

0.4

1.1-

1.0-

0.9

0.8

0.7

0.6

0.5

0.4

440

Fluorescence intensity

440

Vehicle

460

Vehicle

460

ISO (10 µM)

10C (20 µM) ISO (10 µM)

+ 10C (20 µM)

480

ISO (10 µM)

6C (20 µM)

ISO (10 µM)

+ 6C (20 μM)

wavelength [nm]

480

500

500

Fluorescence intensity

1.1

1.0

0.9

0.8

0.7

0.6

0.5

0.4

1.1

1.0

0.9

0.8 0.7

0.6

0.5

0.4

440

Fluorescence intensity

440

Vehicle

460

Vehicle

460

ISO (10 µM)

12C (20 µM)

ISO (10 µM)

+ 12C (20 µM)

480

ISO (10 µM)

8C (20 µM)

ISO (10 µM)

+ 8C (20 µM)

wavelength [nm]

480

500

500

Fluorescence intensity

wavelength [nm] wavelength [nm] wavelength [nm] 1.1-1.1 1.0 1.0 Fluorescence intensity Fluorescence intensity 0.9 0.9 0.8 0.8 0.7 Vehicle 0.7 Vehicle ISO (10 µM) ISO (10 µM) 0.0 0.6 9B (20 µM) 8B (20 µM) ISO (10 µM) ISO (10 µM) 0.5 0.5 + 9B (20 µM) + 8B (20 µM) 0.4 0.4 440 460 500 440 460 480 500 480 wavelength [nm] wavelength [nm] 1.17 1.1 1.0 1.0 Fluorescence intensity Fluorescence intensity 0.9 0.9 0.8 0.8 Vehicle 0.7 Vehicle 0.7 ISO (10 µM) ISO (10 µM) 0.6 0.6 12B (20 µM)

1.1

1.0

0.9

0.8

0.7

0.6

0.5

0.4

1.1-

1.0

0.9

0.8

0.7

0.6

0.5

0.4

440

Fluorescence intensity

440

Vehicle

460

Vehicle

460

ISO (10 µM)

11C (20 µM)

ISO (10 µM)

+ 11C (20 µM)

480

ISO (10 µM)

7C (20 µM)

ISO (10 µM)

+ 7C (20 μM)

wavelength [nm]

480

500

500

Fluorescence intensity



0.5

0.4

440

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).

0.5

0.4

440

ISO (10 µM)

460

+ 12B (20 µM)

wavelength [nm]

480

500

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.

13B (20 µM)

ISO (10 µM)

460

+ 13B (20 µM)

wavelength [nm]

480

500

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However, a small tendency to increase the fluorescence intensity (FI) and blue-shift  $\lambda_{max}$  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  $(G\alpha_s CT_{15})$  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  $G\alpha_s$  protein were synthesised as potential allosteric modulators of the  $\beta_2AR$ . 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<sub>50</sub> for blocking ISO induced cAMP formation was determined to 55 µM. 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 activelike  $\beta_2 AR$  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<sub>s</sub> 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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## References

- 1 J. P. Overington, B. Al-Lazikani and A. L. Hopkins, How many drug targets are there?, *Nat. Rev. Drug Discovery*, 2006, 5, 993–996.
- 2 A. S. Hauser, M. Attwood, M. Rask-Andersen, H. B. Schiöth and D. E. Gloriam, Trends in GPCR Drug Discovery – New Targets and Indications, *Nat. Rev. Drug Discovery*, 2017, **16**, 829–842.
- 3 P. Fronik, B. I. Gaiser and D. S. Pedersen, Bitopic Ligands and Metastable Binding Sites: Opportunities for G Protein-Coupled Receptor (GPCR) Medicinal Chemistry, *J. Med. Chem.*, 2017, **60**, 4126-4134.
- 4 S. Ahn, A. W. Kahsai, B. Pani, Q. T. Wang, S. Zhao, A. L. Wall, R. T. Strachan, D. P. Staus, L. M. Wingler, L. D. Sun, J. Sinnaeve, M. Choi, T. Cho, T. T. Xu, G. M. Hansen, M. B. Burnett, J. E. Lamerdin, D. L. Bassoni, B. J. Gavino, G. Husemoen, E. K. Olsen, T. Franch, S. Costanzi, X. Chen and R. J. Lefkowitz, Allosteric  $\beta$ -blocker isolated from a DNA-encoded small molecule library, *Proc. Natl. Acad. Sci. U. S. A.*, 2017, **114**, 1708–1713.
- 5 X. Liu, S. Ahn, A. W. Kahsai, K. C. Meng, N. R. Latorraca, B. Pani, A. J. Venkatakrishnan, A. Masoudi, W. I. Weis, R. O. Dror, X. Chen, R. J. Lefkowitz and B. K. Kobilka, Mechanism of intracellular allosteric  $\beta_2 AR$  antagonist revealed by X-ray crystal structure, *Nature*, 2017, **548**, 480–484.
- 6 Y. Kang, X. E. Zhou, X. Gao, Y. He, W. Liu, A. Ishchenko, A. Barty, T. A. White, O. Yefanov, G. W. Han, Q. Xu, P. W. de Waal, J. Ke, M. H. Tan, C. Zhang, A. Moeller, G. M. West, B. D. Pascal, E. N. Van, L. N. Caro, S. A. Vishnivetskiy, R. J. Lee, K. M. Suino-Powell, X. Gu, K. Pal, J. Ma, X. Zhi, S. Boutet, G. J. Williams, M. Messerschmidt, C. Gati, N. A. Zatsepin, D. Wang, D. James, S. Basu, S. Roy-Chowdhury, C. E. Conrad, J. Coe, H. Liu, S. Lisova, C. Kupitz, I. Grotjohann, R. Fromme, Y. Jiang, M. Tan, H. Yang, J. Li, M. Wang, Z. Zheng, D. Li, N. Howe, Y. Zhao, J. Standfuss, K. Diederichs, Y. Dong, C. S. Potter, B. Carragher, M. Caffrey, H. Jiang, H. N. Chapman, J. C. Spence, P. Fromme, U. Weierstall, O. P. Ernst, V. Katritch, V. V. Gurevich, P. R. Griffin, W. L. Hubbell, R. C. Stevens, V. Cherezov, K. Melcher and

H. E. Xu, Crystal structure of rhodopsin bound to arrestin by femtosecond X-ray laser, *Nature*, 2015, **523**, 561.

- 7 S. G. F. Rasmussen, B. T. DeVree, Y. Zou, A. C. Kruse, K. Y. Chung, T. S. Kobilka, F. S. Thian, P. S. Chae, E. Pardon, D. Calinski, J. M. Mathiesen, S. T. A. Shah, J. A. Lyons, M. Caffrey, S. H. Gellman, J. Steyaert, G. Skiniotis, W. I. Weis, R. K. Sunahara and B. F. Kobilka, Crystal structure of the  $\beta_2$  adrenergic receptor-G<sub>s</sub> protein complex, *Nature*, 2011, 477, 549.
- 8 B. Carpenter, R. Nehmé, T. Warne, A. G. W. Leslie and C. G. Tate, Structure of the adenosine A2A receptor bound to an engineered G protein, *Nature*, 2016, **536**, 104.
- 9 S. G. F. Rasmussen, H. J. Choi, J. J. Fung, E. Pardon, P. Casarosa, P. S. Chae, B. T. DeVree, D. M. Rosenbaum, F. S. Thian, T. S. Kobilka, A. Schnapp, I. Konetzki, R. K. Sunahara, S. H. Gellman, A. Pautsch, J. Steyaert, W. I. Weis and B. K. Kobilka, Structure of a nanobodystabilized active state of the  $\beta_2$  adrenoceptor, *Nature*, 2011, **469**, 175.
- 10 P. Scheerer, J. H. Park, P. W. Hildebrand, Y. J. Kim, N. Krauss, H. W. Choe, K. P. Hofmann and O. P. Ernst, Crystal structure of opsin in its G-protein-interacting conformation, *Nature*, 2008, 455, 497.
- A. K. Shukla, A. Manglik, A. C. Kruse, K. Xiao, R. I. Reis,
  W. C. Tseng, D. P. Staus, D. Hilger, S. Uysal, L. Y. Huang,
  M. Paduch, P. Tripathi-Shukla, A. Koide, S. Koide,
  W. I. Weis, A. A. Kossiakoff, B. K. Kobilka and
  R. J. Lefkowitz, Structure of active β-arrestin-1 bound to
  a G-protein-coupled receptor phosphopeptide, *Nature*, 2013, 497, 137.
- 12 M. Szczepek, F. Beyrière, K. P. Hofmann, M. Elgeti, R. Kazmin, A. Rose, F. J. Bartl, D. von Stetten, M. Heck, M. E. Sommer, P. W. Hildebrand and P. Scheerer, Crystal structure of a common GPCR-binding interface for G protein and arrestin, *Nat. Commun.*, 2014, 5, 4801.
- 13 E. L. Martin, S. Rens-Domiano, P. J. Schatz and H. E. Hamm, Potent peptide analogues of a G protein receptor-binding region obtained with a combinatorial library, *J. Biol. Chem.*, 1996, **271**, 361.
- 14 M. R. Mazzoni, S. Taddei, L. Giusti, P. Rovero, C. Galoppini,
  A. D'Ursi, S. Albrizio, A. Triolo, E. Novellino, G. Greco,
  A. Lucacchini and H. E. Hamm, A galpha(s) carboxylterminal peptide prevents G(s) activation by the A(2A) adenosine receptor, *Mol. Pharmacol.*, 2000, 58, 226.
- 15 M. M. Rasenick, M. Watanabe, M. B. Lazarevic, S. Hatta and H. E. Hamm, Synthetic peptides as probes for G protein function. carboxyl-terminal G alpha s peptides mimic  $G_s$ and evoke high affinity agonist binding to beta-adrenergic receptors, *J. Biol. Chem.*, 1994, **269**, 21519.
- 16 C. Martin, S. Moors, M. Danielsen, C. Betti, C. Fabris,
  D. Sejer Pedersen, E. Pardon, M. Peyressatre, K. Fehér,
  J. C. Martins, J. Mosolff Mathiesen, M. Morris,
  N. Devoogdt, V. Caveliers, F. De Proft, J. Steyaert and
  S. Ballet, Rational Design of Nanobody80 Loop
  Peptidomimetics: Towards Biased β<sub>2</sub> Adrenergic Receptor
  Ligands, *Chem.-Eur. J.*, 2017, 23, 9632.

- 17 J. M. Mathiesen, L. Vedel and H. Bräuner-Osborne, cAMP biosensors applied in molecular pharmacological studies of G protein-coupled receptors, *Methods Enzymol.*, 2013, 522, 191.
- 18 T. A. Hill, N. E. Shepherd, F. Diness and D. P. Fairlie, Constraining Cyclic Peptides To Mimic Protein Structure Motifs, Angew. Chem., Int. Ed., 2014, 53, 13020.
- 19 Y. H. Lau, P. de Andrade, Y. Wu and D. R. Spring, Peptide stapling techniques based on different macrocyclisation chemistries, *Chem. Soc. Rev.*, 2015, **44**, 91.
- 20 C. J. White and A. K. Yudin, Contemporary strategies for peptide macrocyclization, *Nat. Chem.*, 2011, 3(7), 509.
- 21 P. T. Tran, C. Ø. Larsen, T. Røndbjerg, M. De Foresta, M. B. A. Kunze, A. Marek, J. H. Løper, L.-E. Boyhus, A. Knuhtsen, K. Lindorff-Larsen and D. S. Pedersen, Diversity-Oriented Peptide Stapling: A Third Generation Copper-Catalysed Azide—Alkyne Cycloaddition Stapling and Functionalisation Strategy, *Chem.-Eur. J.*, 2017, 23, 3490.
- 22 A. D. Pehere, M. Pietsch, M. Gutschow, P. M. Neilsen,
  D. S. Pedersen, S. Nguyen, O. Zvarec, M. J. Sykes,
  D. F. Callen and A. D. Abell, Synthesis and Extended Activity of Triazole-Containing Macrocyclic Protease Inhibitors, *Chem.-Eur. J.*, 2013, **19**, 7975.
- 23 C. W. Tornoe, C. Christensen and M. Meldal, Peptidotriazoles on solid phase: [1,2,3]-triazoles by regiospecific copper(I)-catalyzed 1,3-dipolar cycloadditions of terminal alkynes to azides, *J. Org. Chem.*, 2002, **67**, 3057.
- 24 S. Cantel, A. L. C. Isaad, M. Scrima, J. J. Levy, R. D. DiMarchi, P. Rovero, J. A. Halperin, A. M. D'Ursi, A. M. Papini and M. Chorev, Synthesis and conformational analysis of a cyclic peptide obtained *via i* to *i* + 4 intramolecular sidechain to side-chain azide – alkyne 1,3-dipolar cycloaddition, *J. Org. Chem.*, 2008, 73, 5663.
- 25 D. S. Pedersen and A. Abell, 1,2,3-Triazoles in Peptidomimetic Chemistry, *Eur. J. Org. Chem.*, 2011, 2399.
- 26 A. S. Rose, M. Elgeti, U. Zachariae, H. Grubmüller, K. P. Hofmann, P. Scheerer and P. W. Hildebrand, Position of Transmembrane Helix 6 Determines Receptor G Protein Coupling Specificity, *J. Am. Chem. Soc.*, 2014, **136**, 11244–11247.
- 27 T. J. Sminia and D. S. Pedersen, Azide- and Alkyne-Functionalised  $\alpha$ - and  $\beta$ 3-Amino Acids, *Synlett*, 2012, **23**, 2643.
- 28 E. D. Goddard-Borger and R. V. Stick, An Efficient, Inexpensive, and Shelf-Stable Diazotransfer Reagent: Imidazole-1-sulfonyl Azide Hydrochloride, *Org. Lett.*, 2007, 9, 3797.
- 29 H. Johansson and D. S. Pedersen, Azide- and Alkyne-Derivatised α-Amino Acids, *Eur. J. Org. Chem.*, 2012, 4267.
- 30 A. M. Gilles, P. Marlière, T. Rose, R. Sarfati, R. Longin, A. Meier, S. Fermandjian, M. Monnot, G. N. Cohen and O. Bârzu, Conservative replacement of methionine by norleucine in Escherichia coli adenylate kinase, *J. Biol. Chem.*, 1988, 263, 8204.
- 31 X. J. Yao, G. Vélez-Ruiz, M. R. Whorton, S. G. F. Rasmussen, B. T. DeVree, X. Deupi, R. K. Sunahara and B. Kobilka, The effect of ligand efficacy on the formation and stability of a GPCR-G protein complex, *Proc. Natl. Acad. Sci. U. S. A.*, 2009, **106**, 9501.