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## An integrated platform approach enables discovery of potent, selective and ligand-competitive cyclic peptides targeting the GIP receptor†

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In any drug discovery effort, the identification of hits for further optimisation is of crucial importance. For peptide therapeutics, display technologies such as mRNA display have emerged as powerful methodologies to identify these desired *de novo* hit ligands against targets of interest. The diverse peptide libraries are genetically encoded in these technologies, allowing for next-generation sequencing to be used to efficiently identify the binding ligands. Despite the vast datasets that can be generated, current downstream methodologies, however, are limited by low throughput validation processes, including hit prioritisation, peptide synthesis, biochemical and biophysical assays. In this work we report a highly efficient strategy that combines bioinformatic analysis with state-of-the-art high throughput peptide synthesis to identify nanomolar cyclic peptide (CP) ligands of the human glucose-dependent insulinotropic peptide receptor (hGIP-R). Furthermore, our workflow is able to discriminate between functional and remote binding non-functional ligands. Efficient structure–activity relationship analysis (SAR) combined with advanced *in silico* structural studies allow deduction of a thorough and holistic binding model which informs further chemical optimisation, including efficient half-life extension. We report the identification and design of the first *de novo*, GIP-competitive, incretin receptor family-selective CPs, which exhibit an *in vivo* half-life up to 10.7 h in rats. The workflow should be generally applicable to any selection target, improving and accelerating hit identification, validation, characterisation, and prioritisation for therapeutic development.

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In recent years, peptides have emerged as powerful therapeutic agents<sup>1</sup> and the most prominent examples can match antibodies in selectivity and potency. This development has been greatly aided by breakthroughs in half life extension

technologies by formulation or chemical modification. A key advantage of engineered peptides is their ease of production, and while antibodies are generally considered to be too large for efficient oral uptake in therapeutically relevant amounts, the small size of peptides allows the potential for oral dosing with significant progress made in recent years.<sup>2,3</sup> Despite these advantages, most drug development projects heavily rely on antibodies, most likely due to the ease of *de novo* antibody discovery by evolutionarily optimised methods. Modern *in vivo* or *in vitro* display technologies, such as phage display and mRNA display, allow for the identification of potent and specific peptide ligands through iterative screening of peptide pools containing trillions of randomised sequences.<sup>4,5</sup> These technologies have the potential to yield a plethora of *de novo* peptides which could be engineered into powerful therapeutics. However, these techniques are surprisingly scarce in clinical pipelines (compared to antibodies or small molecules) despite being known for decades and most peptides in late-stage discovery are derivatives of naturally occurring molecules.<sup>1</sup>

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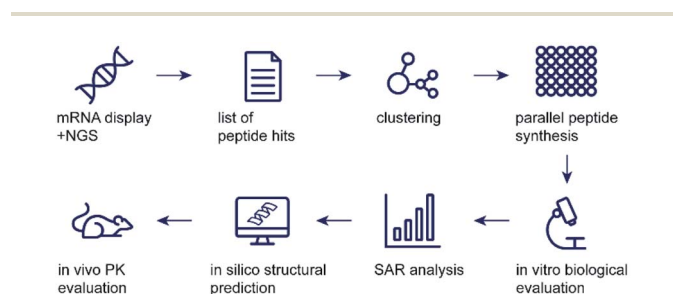
Challenges in hit prioritisation and time-consuming validation could at least partly be responsible for this observation. While classical approaches would rely on Sanger sequencing of the most abundant clones (yielding very few hits), the advent of next generation sequencing (NGS) has revolutionized the information content available from *de novo* peptide screens.<sup>4</sup> In the majority of studies, however, this information is unused and only a handful of the most abundant sequences are followed up by chemical synthesis for testing of biological activity.<sup>5</sup> We rationalized that powerful bioinformatic data mining methods would best utilise the vast information contained in peptide display datasets. To prove this, we combined chemical synthesis and high throughput binding analysis on data from mRNA display. We show that these methods identify more diverse series of hits with different modes of binding as starting points for peptide drug discovery efforts, especially when a functional binder to a specific binding pocket is desired (Scheme 1).

We chose the type 2 GPCR glucose-dependent insulinotropic peptide receptor (GIP-R) as a challenging and clinically relevant test case.<sup>6</sup> Its natural ligand GIP and the close relative glucagon-like peptide 1 (GLP-1) are incretins, *i.e.*, hormones which are secreted after oral nutrient uptake and which augment glucose-dependent insulin release from pancreatic beta cells.<sup>7</sup> GLP-1 receptor agonists have been reported to not only have effects in metabolic disease through increasing insulin release, but also promote satiety by delaying gastric emptying, and are being investigated for their protective effects in obesity,<sup>8,9</sup> heart disease,<sup>10</sup> and diabetic kidney disease.<sup>11</sup> Conversely, the biology of GIP is less clearly understood, and both GIP-R agonists<sup>12</sup> as well as antagonists<sup>13,14</sup> are under investigation as potential therapeutics in the fields of type 2 diabetes and obesity. Previous approaches to target the GIP-R thus far have made use of analogues of GIP itself,<sup>15,16</sup> or GIP R specific antibodies<sup>14,17–20</sup> and peptide display work was based on dual GIP-GLP-1 analogue libraries.<sup>14,19,20</sup> As such, the GIP-R represented an ideal target for our mRNA based workflow as we strived to identify potent, ligand competitive, and subfamily selective *de novo* binders, which could provide valuable tools to understand GIP-R biology and serve as starting points for drug discovery efforts.

We employed mRNA display to identify cyclic peptide ligands towards the biotinylated extracellular domain (ECD) of the human GIP receptor (residues 22–138 of hGIP-R), which has been shown to retain binding to GIP.<sup>21</sup> Initially, we established

conditions for efficient cyclisation by disulphide bond formation for representative library peptides (Fig. S3†), before conducting iterative rounds of mRNA display<sup>5,22</sup> using a nucleotide library encoding two conserved cysteines for macrocyclization flanking a region of 4 to 12 random amino acid sequence. Negative selections were performed against biotin-loaded streptavidin-functionalised magnetic beads, followed by positive selection against bead-immobilised hGIP-R ECD. Sufficient library enrichment was obtained for hGIP-R after five rounds of selections (percentage recovery relative to input > 0.1%) (Fig. S4a†). NGS of enriched output cDNA was carried out and peptides were clustered by similarity for each selection round (R1–R5). All sequences exceeding six reads in R5 (the top 3160 sequences) were compared against each other using pairwise local alignments in order to derive a complete distance matrix. Single-linkage hierarchical clustering was then performed on the distance matrix, choosing a threshold for cutting the relative dendrogram into clusters based on a statistical optimality criterion.<sup>23</sup> For this dataset, the sequence similarity threshold for assigning a sequence to a cluster was set at 0.38, and the fewest number of members that a cluster was allowed to contain was 20. This generated 13 clusters (assigned letters A through M), where the largest cluster, A, contained 1880 sequences, while the two least populated clusters L and M contained 21 sequences each, and the unclustered sequences were assigned to a “noise” cluster (termed cluster 0), encompassing 263 sequences (Fig. 1).

In the next step, we selected peptides from each cluster (A–M, 0) based on sequence diversity and abundance in R5 for parallel solid-phase peptide synthesis (SPPS) in a 96 well format. The N-terminus was capped with an acetyl group (Ac) to mimic the fMet in mRNA-display and a C-terminal FLAG tag was added to each peptide to ensure peptide solubility in buffer by serving as a source of negative charge, analogous to C-terminal mRNA that is present during the selection screens.<sup>24</sup> Peptides were assigned identifiers with cluster ID and their rank order based on their



**Scheme 1** Workflow of peptide hit identification, prioritisation, and validation.



**Fig. 1** High throughput pairwise clustering analysis of 3160 Round 5 output sequences selected against hGIP-R ECD. Lighter colour indicates closer similarity between individual sequences (ESI Data 1†).



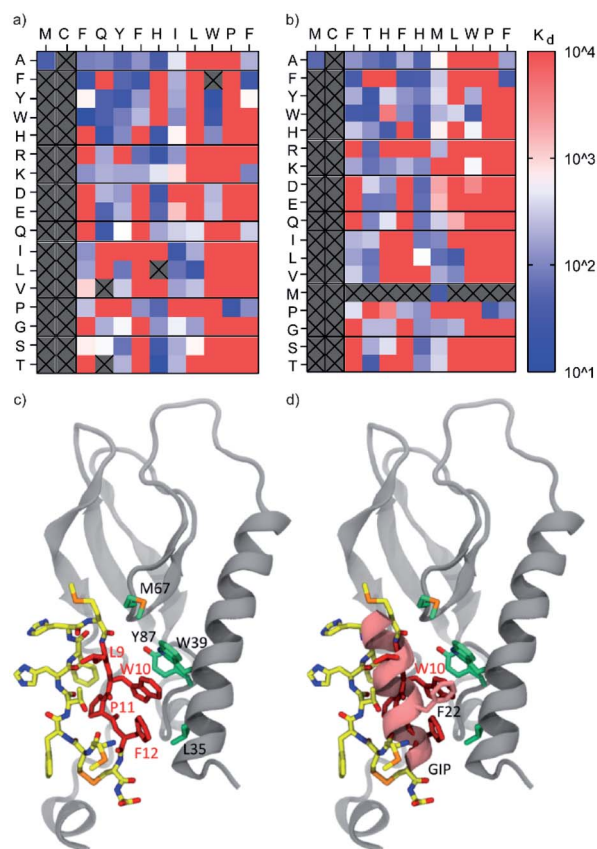


throughput binding assay but was included in the follow up. Further analysis of the sequence list showed another structurally diverse member of cluster B, B\_1275, which we hypothesized would also exhibit potent binding and GIP competition, despite the low levels of sequencing reads. These four sequences were scaled up by traditional SPPS and further investigated in multi-concentration BLI and competitive binding assays. All purified peptides showed nanomolar binding and competition of the  $^{125}\text{I}$ -GIP from BHK cells stably expressing hGIP-R (Fig. 4). Furthermore, none of these ligands were found to displace radiolabelled GLP-1 from GLP-1R, nor glucagon from GCG-R (Fig. S11†). The parent CP sequences also do not bear any significant sequence homology with native GIP, nor any known interactors of hGIP-R, suggesting that these are the first reported examples of *de novo* incretin receptor selective and competitive peptides for hGIP-R.

To optimise the biophysical and physicochemical properties of the CPs, and to identify a suitable attachment point for half-life extending moieties, such as albumin binders, we sought to establish a detailed structure–activity relationship (SAR) on cluster B. We chose the most and least abundant of our cluster B lead peptides (B\_3 and B\_1275) as starting points for full amino acid mutation scans.<sup>24,26</sup> We focussed on natural amino acids only to keep the option for (semi-)recombinant expression of the compounds, should large amounts be needed for further development stages. Single mutation variant peptides were synthesised in a 96 well format for each amino acid in the variable region contained between the two conserved cysteine residues C2 and C13. Methionine and cysteine were not included in the mutational scan due to potential oxidation, and asparagine was not included due to the risk of deamidation and isomerisation to iso-aspartate. Additionally, scrambled peptides were included in the panel. The binding affinities of these mutant peptides to hGIP-R ECD were then determined by single concentration BLI experiments.

As shown in Fig. 3a and b, the consensus sequence of cluster B (positions 9–12, LWPF) was found to be the most intolerant to mutation, confirming this region to be critical for binding. Proline at position 11 was found to be completely intolerant to replacement by any other amino acid, suggesting that this residue is critical for maintaining conformationally restricted binding interface of CPs. While residues 9–12 are hydrophobic in both parent peptides, it is unlikely that the interaction of the peptides to hGIP-R ECD is unspecific, as none of the scrambled peptides (e.g. LWPF) were found to bind, including the transposed mutants of B\_3 and B\_1275, with interchanged L9 and W10. The data shows some general trends for both B\_3 and B\_1275. In general, positions 3 and 6 (both F in the parent peptides) favour aromatic residues, position 8 favours aliphatic residues, while residues 4, 5, and 7 are fairly tolerant to mutation. The single amino acid scan did not reveal any substitutions that led to remarkable improvements in binding, suggesting that these peptides may either already be optimised for binding through several rounds of mRNA-display selection, or that further binding improvements would only be achieved by synergistic action of multiple substituted residues. The latter could ideally be investigated by mRNA display based affinity maturation experiments in follow up studies.<sup>24,26</sup> To gain insight into the binding mode of

CPs to hGIP-R on the atomistic level we employed a two-step modelling protocol that first generates multiple conformations of the complex and then selects the final conformation based on stability (for details, see ESI†). As our peptides were demonstrated to be  $^{125}\text{I}$ -GIP-competitive, we directly folded them inside the GIP binding site of hGIP-R using Rosetta (Fig. 3c and d; results for B\_1275 shown). Briefly, each of the four crucial residues according to the SAR data (Leu9, Trp10, Pro11 or Phe12) was placed in the GIP binding site and the rest of the peptide was grown around it. The obtained conformations (24 000 in total) were further clustered and the representative poses of the four most populated clusters were submitted to molecular dynamics (MD) simulations



**Fig. 3** Heat maps showing  $K_d$  (nM) values for binding of single-residue mutant peptides derived from B3 (a) and B1275 (b) to biotinylated hGIP-R ECD as determined by single-concentration BLI. The columns indicate the amino acid changes compared to the parent sequence (displayed at the top of the table). All peptides featured a C-terminal Cys and were tested in crude form. Peptides that were not tested or those where synthesis failed are marked as grey boxes. None of the scrambled mutant peptides showed any binding. (c) Atomistic model of the cyclic peptide B\_1275 and GIP receptor complex suggested by molecular modelling. The LWPF sequence of the peptide is shown in red, while the rest of the molecule is coloured by the atom name (carbon in yellow, nitrogen in blue, oxygen in red, and sulphur in orange). The receptor is shown in grey; the binding site residues (L35, W39, M67 and Y87) are highlighted in green. (d) Overlay of the crystal structure of GIP complexed with hGIP receptor (PDB 2QKH) and atomistic model of cyclic peptide B\_1275 in the binding site of the GIP receptor. Note that the positions of W10 of the cyclic peptide and F22 of GIP overlap.





and the optimised B\_1275 variants with FLAG tag (B\_1275.4), without FLAG tag (B\_1275.5) and with protractor but without FLAG tag (B\_1275.6). The two non-protracted peptides exhibit very short half-lives (B\_1275.4 = 3.5 min, B\_1275.5 = 1.8 min), whereas the peptides carrying an albumin binder show significant plasma exposure over a long period of time ( $t_{1/2}$ , B\_3.1 = 9.8 h, B\_1275.1 = 10.7 h, B\_1275.6 = 4.2 h), with half-lives being increased by more than 100 fold (Fig. 4d) (as a comparison, the GLP-1 analogue semaglutide, which is dosed once-weekly in humans has a  $t_{1/2}$  in rats of 7 h.)<sup>28</sup>

## Conclusions

In conclusion, we have developed a powerful and efficient workflow to identify and prioritize hit peptides from display screens and to rapidly progress them to functional lead molecules. These can be used to decipher biological questions *in vitro* and *in vivo* or be used as starting points to initiate drug development programmes. Our results show that peptide display technologies coupled to NGS-guided clustering and high-throughput hit validation offers a fast, powerful, and robust strategy for identification of *de novo* ligands against targets of interest, and additionally allows the rapid construction of meaningful and data based structural models *in silico*. As the crucial aspect of our workflow, it allows holistic and unbiased analysis of binding sequence mapping of CPs against the target of interest. This enables thorough investigation of the different possible binding motifs – and possibly different binding sites – in the selection for further validation, rather than limiting the follow up to the most enriched sequences (which could be dominated by a handful of binding motifs). We believe that this prioritisation and optimisation approach holds great promise for future lead identification campaigns both in an academic and industrial setting.

## Data availability

Next generation sequencing data including cluster information, measured kd values and experimental data on synthesized peptides are available as ESI.†

## Author contributions

B. B. investigation and data curation, D. G. software and data curation, C. S. K. investigation and data curation, M. A. K. software, data curation and visualisation, Q. R. investigation, C. N. C. investigation, M. D. W. investigation, A. M. K. H. investigation, C. F. investigation, G. I. investigation, K. D. software and data curation, O. D. C. investigation, X. Z. investigation, X. Q. investigation, H. L. investigation, S. S. Z. investigation, J. T. K. supervision, A. K. conceptualisation, methodology, supervision, funding acquisition, M. M. conceptualisation, funding acquisition, data curation and visualisation, methodology, supervision, writing original draft. All authors have reviewed the final draft.

## Conflicts of interest

All authors apart from B. B., O. D. C., and A. K. are or were employees and shareholders of Novo Nordisk A/S. A. K. has received consultancy fees from Novo Nordisk A/S.

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