# Simulation and experimental analysis of the structure and antimicrobial activity of linear peptoids

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## 1. Introduction

We use a range of approaches both experimental and computational to link the primary structure of linear peptoids to their biological activity by investigating their interactions with lipid membranes.

Peptoids are poly-N-substituted glycines: a class of synthetic peptide mimics with side chains substituted onto the amide nitrogen atom,



Substitution of the side chain (R) onto the amide nitrogen prevents hydrogen

### 4. Results

### CD in PBS and octanol

- Phosphate buffered saline and octanol act as human isotonic conditions and bilayer interior mimics respectively,
- **Spectral differences indicate** peptoid structural differences and are qualitatively similar for all peptoids in library,



bonding in peptoid backbone, affecting secondary structure stabilisation,

- Peptoids can be designed to have structural similarities to natural antimicrobial peptides (AMPs) with antimicrobial activity and selectivity believed to originate from their ability to form cationic, amphipathic secondary structures,<sup>1</sup>
- Small structural differences afford peptoids better in vivo properties than AMPs and therefore greater potential for clinical use in the future.<sup>2</sup>

### Membrane disruption mechanisms



wavelength (nm)

Spectra indicate helical structures, similar but not identical to the alphahelix seen in peptides.



Spectral changes indicate that interactions with SUVs induce structural changes in peptoids and possible insertion into bilayer interior, Presence of isodichoric point indicates that the system could be described by a two state model with spectra in PBS and octanol representative of the free in solution and fully membrane bound states.

#### stable pore formation

## 2. Peptoid library

- □ 3 different structural motifs, each a combination of residues with charged and aromatic side chains,
- Each motif is repeated until the peptoid is 12 residues in total *e.g.* (NLysNspe)<sub>6</sub> (motif 1),
- Peptoids active against range of bacterial and parasitic pathogens.<sup>3</sup>



Motif 2 Motif 3

### 3. Methods

#### Experimental

Peptoid secondary structure characterised by circular dichroism spectroscopy (CD) in different solvent environments and the presence

#### Concentration dependent CD



CD indicates peptoids in library have good thermal stability,  $\Box$  One peptoid, (NaeNspeNspeNspe)<sub>3</sub> shows concentration dependent CD, indicating the occurrence of some aggregation or self-assembly, □ Further work is currently being carried out to characterise this.



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### Simulations in water and octanol

of small unilamellar vesicles (SUVs) which act as model biomembranes,

 Here we use far UV CD to probe electronic transitions in the peptoid backbone.



Computational

Differential absorption of right and left handed polarised light by optically active sample

- Molecular dynamics simulations are used here to predict and analyse peptoid secondary structure,
- Peptoids are simulated in GROMACS, using modified AMBER forcefields with parameters obtained through ANTECHAMBER software.
- Secondary structure defined by the backbone dihedral angles  $\omega$ ,  $\Phi$  and  $\psi$ ,
- Simulations in water and octanol can be used to map structural differences with Ramachandran plots of  $\Phi vs \psi$ ,

 $(N_{ae} N_{spe} N_{spe})_4$  in water simulated over 10 ns. Frequency of angle occurrence increases from purple to yellow

Further computational work will involve simulating peptoids with an atomistic lipid bilayer in order to understand the mechanism of insertion and analyse peptoid structural changes during this process.

#### References

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