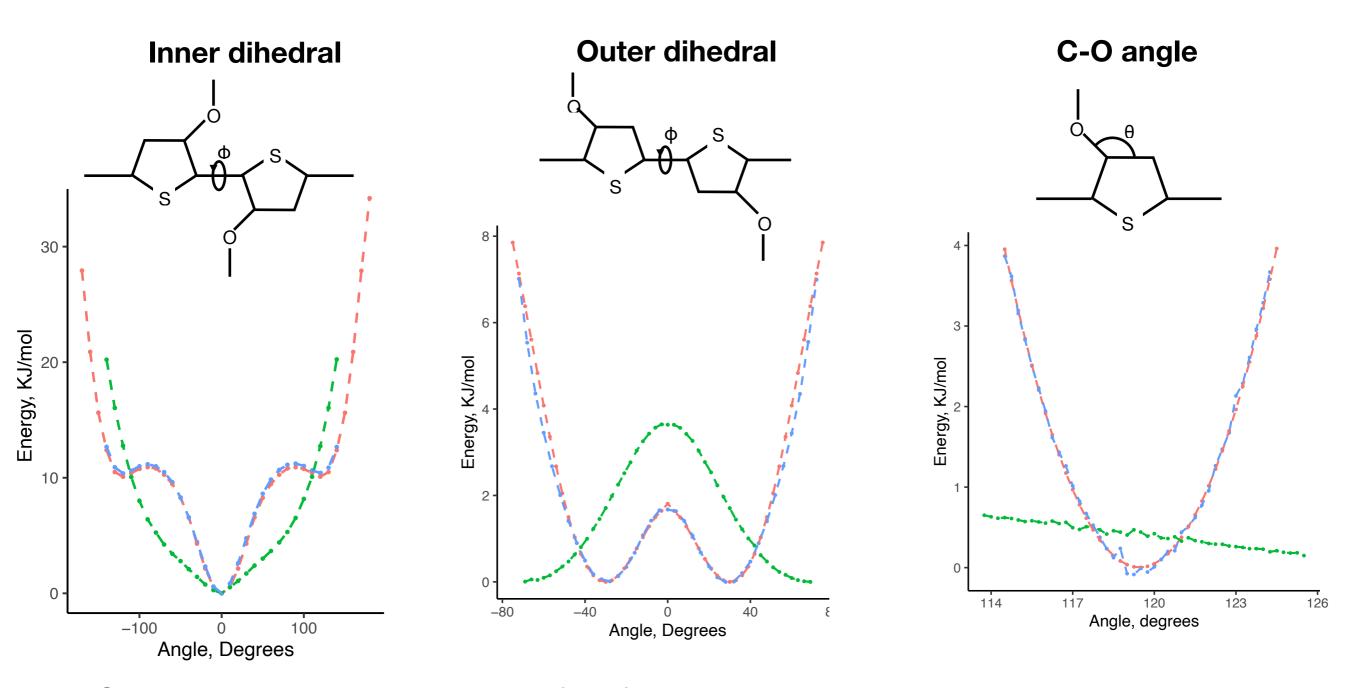
Force Field Design Principles

- Forcefield based on OPLS
- 2) 'Important' DOFs re-parameterised. These are -
 - 1) 'inner dihedral'
 - 2) 'outer dihedral'
 - 3) C-O angle
- 3) Electrostatic parameters taken from mixture of OPLS and density functional theory (see next slide)



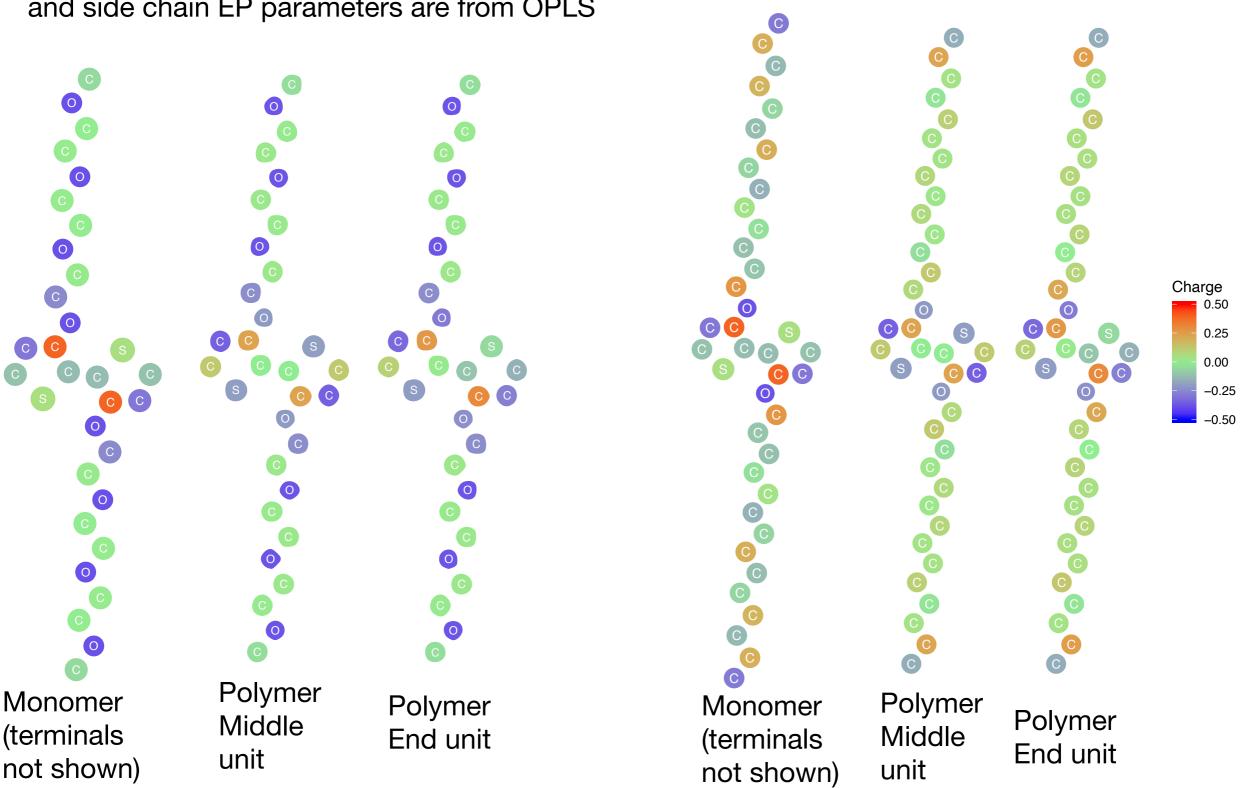
Green - Background potential in MD forcefield, Red - DFT energy scan, Blue - MD potential after parameterisation

Electrostatic parameters (EP)

- Alkoxylated monomer EP parameters for entire molecule calculated using DFT
- Alkoxylated polymer EP parameters calculated for a set of representative oligomers using DFT 2)
- 3) Glycoxylated monomer - EP parameters for the backbone are the same as for Alkoxylated monomer, and side chain EP parameters are from OPLS

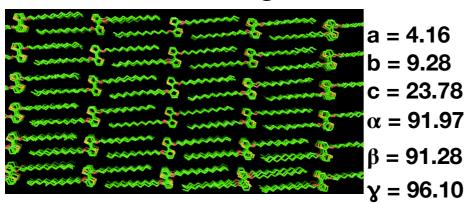
Glycoxylated polymer - EP parameters for the backbone are the same as for Alkoxylated polymer,

and side chain EP parameters are from OPLS

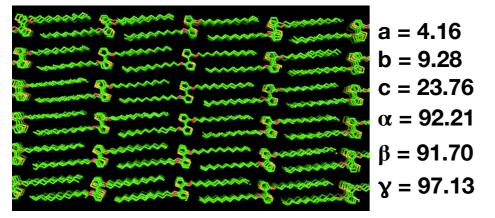


Alkoxylated monomer crystal structure - testing stability

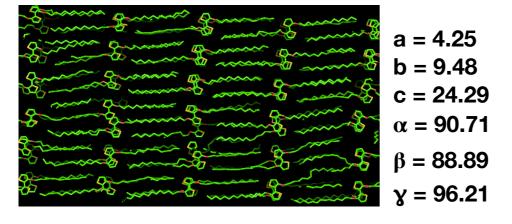
Without annealing



Annealed at 350K



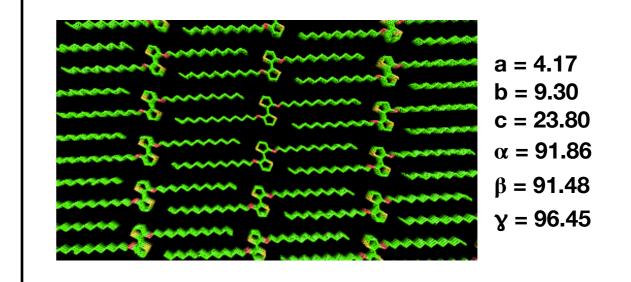
Annealed at 400K

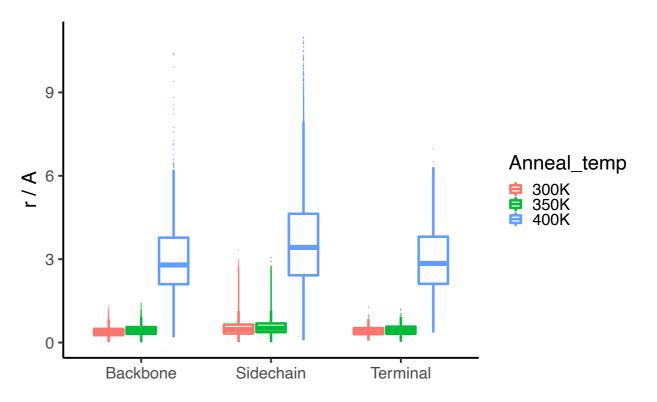


Annealing protocol -

- 1) Heat from 300K to annealing temperature over 1ns
- 2) Cool from annealing temperature to 300K at a rate of 10K/1ns

Before MD (structure from Andrew)





Distribution of atomic displacement vectors, r, for each component of the system at the different temperatures

Annealing protocol Structure is stable at room temp, and after annealing at 350K. It still holds together after annealing at 400K, but some disorder is introduced into the system. Overall the alkoxylated monomer crystal is well reproduced.

Alkyl Monomer Crystal

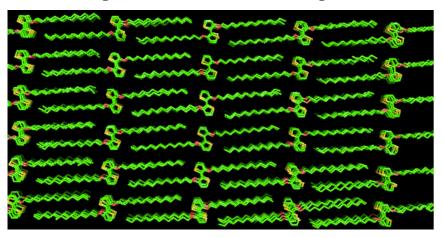
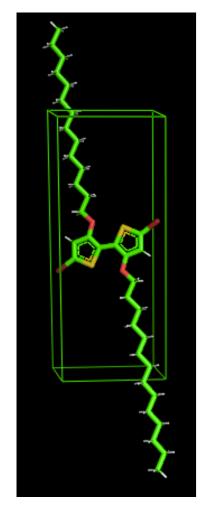


Image of super cell stabilised in MD



Parameters after MD

a = 4.16

b = 9.28

c = 23.78

 $\alpha = 91.97$

 $\beta = 91.28$

y = 96.10

Strong agreement seen between the experiment, the theoretical structure factor and the calculated structure factor after equilibration in MD. Additionally the level of crystallinity seems to be in good agreement.

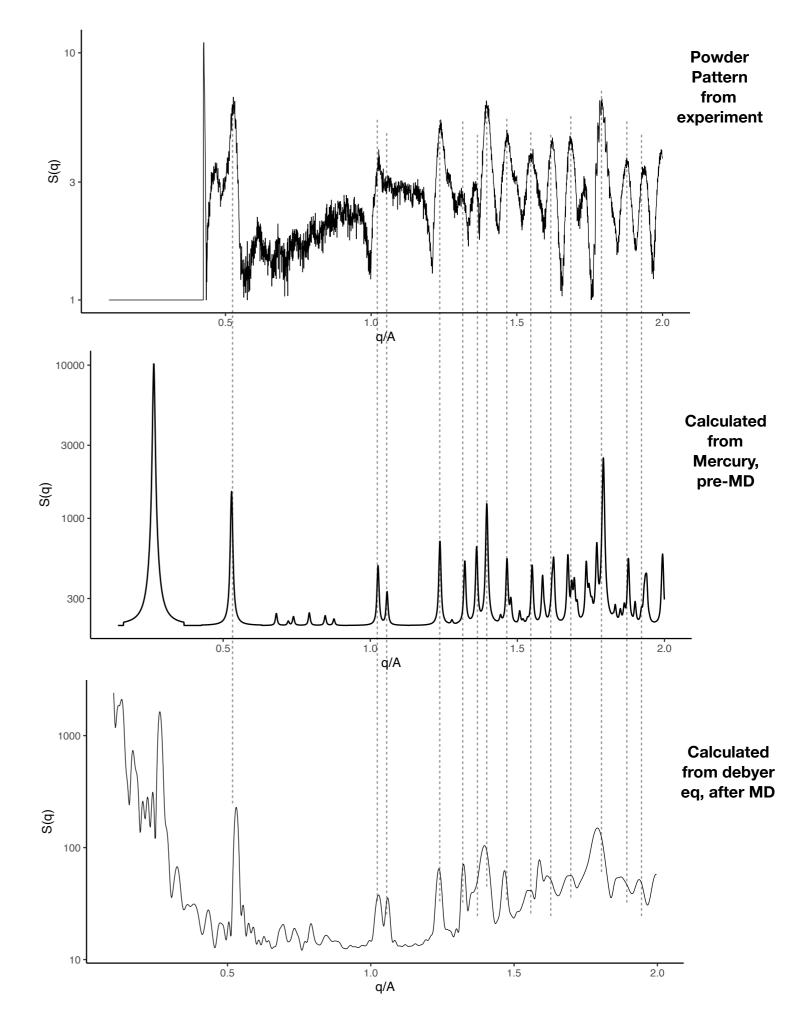
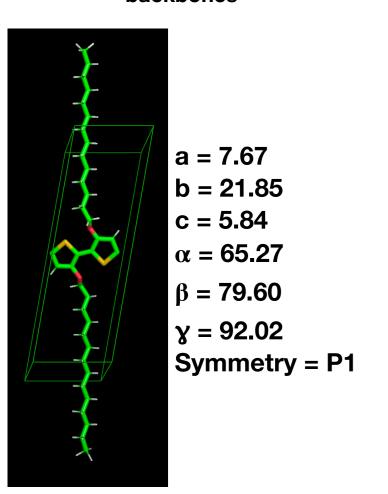
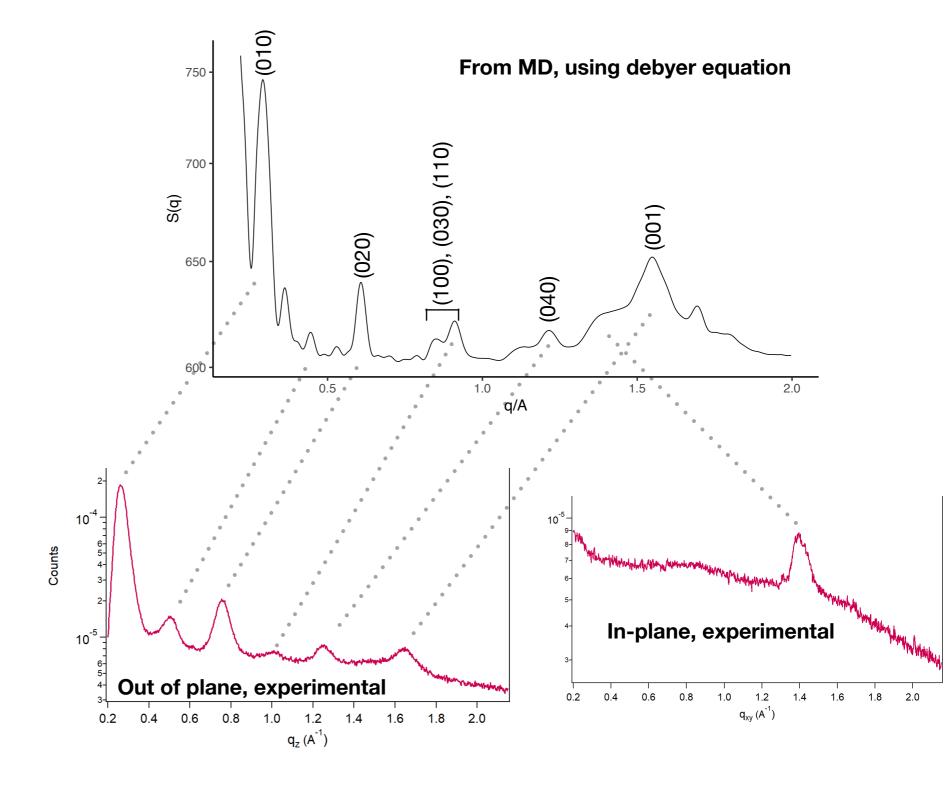


Image of crystal looking along backbones



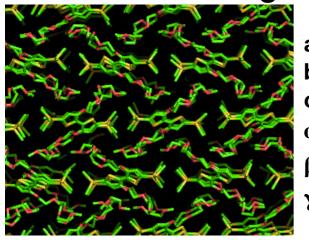
Alkoxylated Polymer Crystal



In general the lamellar peaks, (0n0), seem to be at lower q's than in the data, suggesting the model over-predicts the lamellar stack distance. The pi-stack peak, (001), is also at lower q value than the data, showing that it over-predicts the pi-stack distance. Peaks that I haven't labelled are because in the structure factor calculations there are many peaks in that area, so it is unclear which are showing peaks.

Glycoxylated monomer crystal structure - testing stability

Without annealing



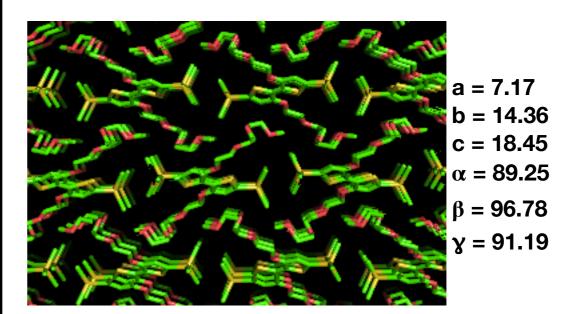
Annealed at 350K

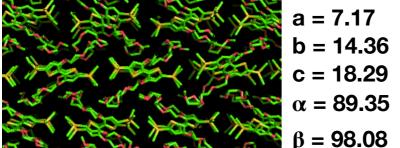
- a = 7.17
- b = 14.36c = 18.45
- $\alpha = 89.25$
- $\beta = 96.78$
- y = 91.19

Annealing protocol -

- Heat from 300K to annealing temperature over 1ns
- 2) Cool from annealing temperature to 300K at a rate of 10K/1ns

Before MD (structure from Andrew)



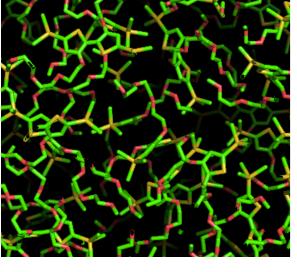


- y = 90.23

12.5 -10.0 7.5 Annealling_temp r/A ⇒ 300K⇒ 350K⇒ 400K 5.0 2.5

Terminal

Annealed at 400K



Too amorphous to characterise A unit cell

Distribution of atomic displacement vectors, r, for each component of the system at the different temperatures

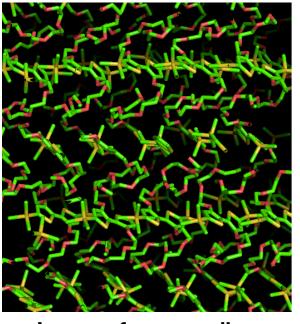
Sidechain

Same as alkoxylated crystal structure. Holds together well at 300K and 350K, with average atomic displacements around 2A. The crystal melts and fails to reform after annealing at 400K. Overall, crystal structure is well reproduces.

0.0

Backbone

Glycol Monomer Crystal



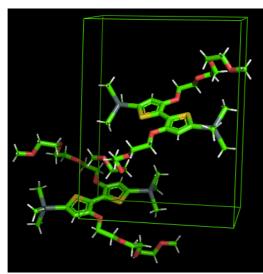
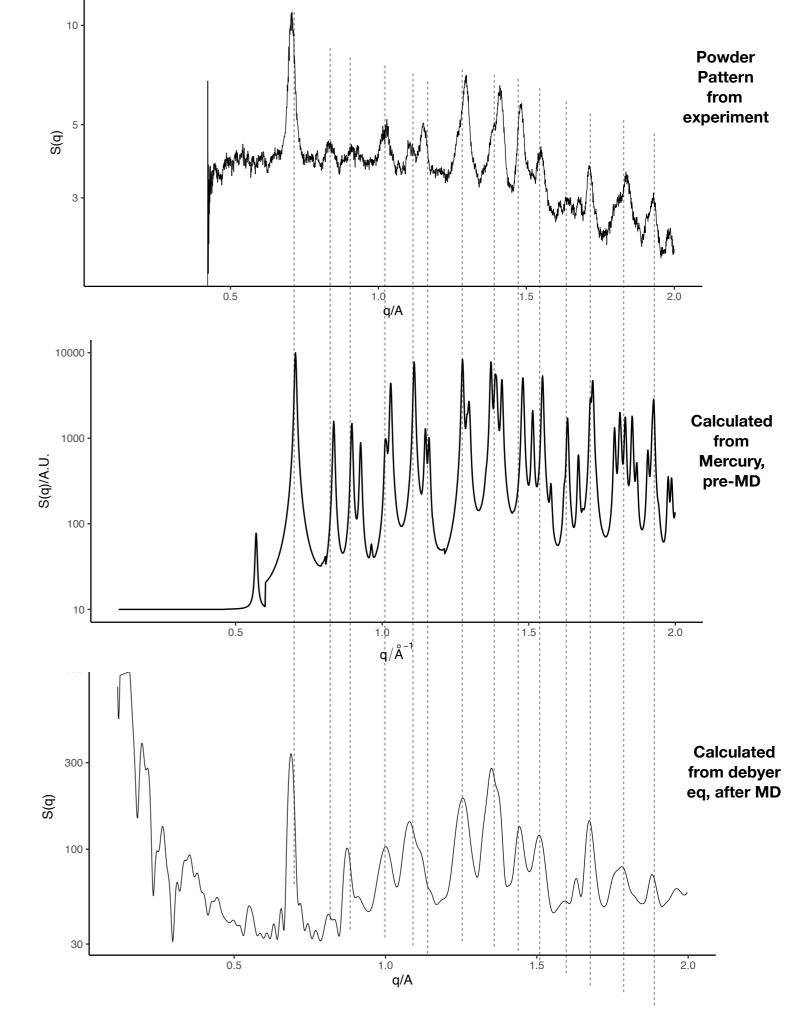


Image of super cell stabilised in MD

 $\begin{array}{c} a = 7.17 \\ b = 14.36 \\ c = 18.45 \\ \text{after MD} \\ \alpha = 89.25 \\ \beta = 96.78 \\ \gamma = 91.19 \end{array}$

Strong agreement seen between the experiment, the theoretical structure factor and the calculated structure factor after equilibration in MD.



Glycoxylated Bithiophene Polymer Crystal

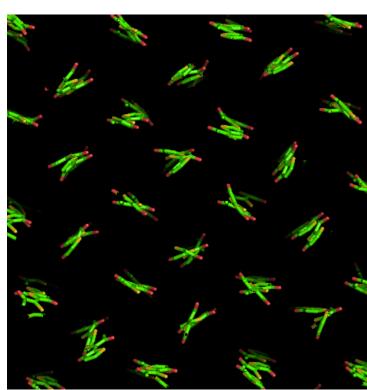
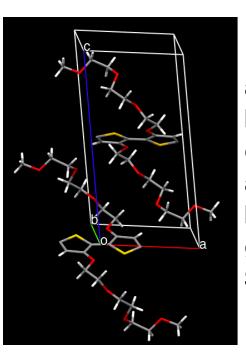
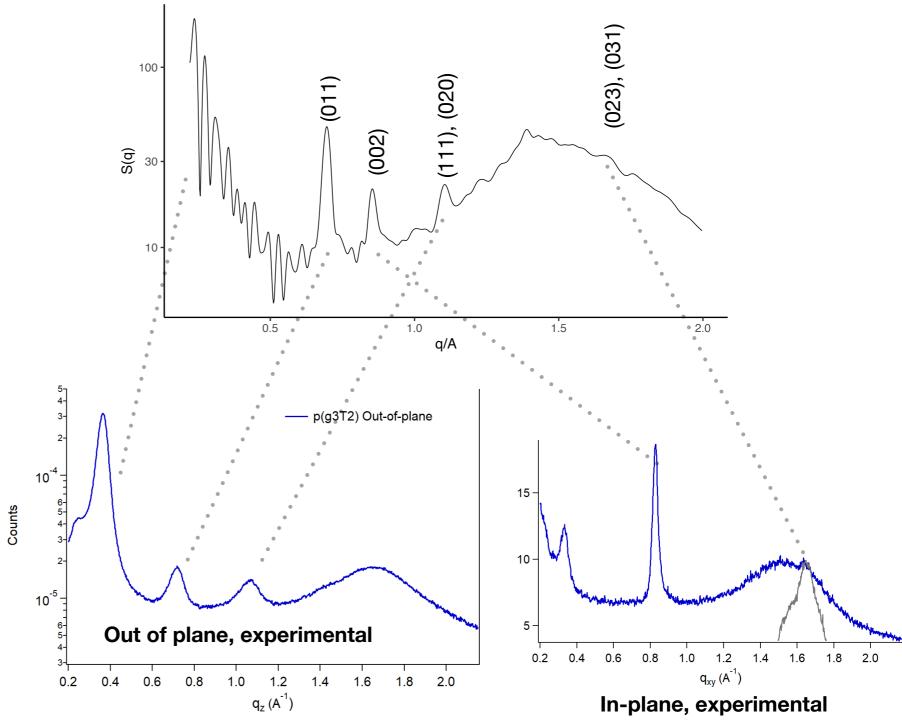


Image of crystal looking along backbones. Only backbone structure shown for clarity



a = 7.96 b = 12.2 c = 15.7 alpha = 90.00 beta = 97.71 gamma = 90.00 Symmetry = P21/n



Oscillations at low-q in the simulated pattern may be occurring due to artefacts from the limited size of the box that is simulated. The lattice parameters are only approximate, as further analysis of the MD structure files are needed to extract the exact ones. The polymer crystal adopts a herringbone structure, as opposed to a pi stack. Worthwhile to keep testing other structures with pic stacks to see if good agreement is reached with other structures. So far these haven't been stable in MD however.

Questions moving forward -

- 1) How can we screen for other possible crystal structures for the polymers? I am currently working on some other structures for the glycoxylated polymer which contain a more traditional pi-stack, however so far these have shown to be unstable in MD (thats not to say its the pi-stack thats making them unstable).
- 2) Is there significant side chain-backbone interactions occurring in the glycoxylated polymers? For example some sort of weak hydrogen-bonding that could influence redox potentials?
- 3) How do these crystal structures affect the interaction with an aqueous electrolyte (subject of future simulations)
- 4) What is the implications of these crystal structures for devices? Both in terms of hole transport and ion penetration into the bulk.