## Potential Supervisors

**Professor Frank von Delft**

Frank's overall research project is to establish methods to ensure that X-ray structures can serve as a routine and predictive tool for generating novel chemistry for targeting proteins - as opposed to them being only occasionally and retrospectively useful descriptively, as is currently generally the case.

He is jointly Principal Investigator of the Protein Crystallography group in the SGC (Oxford University), as well as Principal Beamline Scientist of beamline I04-1 at Diamond Light Source synchrotron (Harwell). After his PhD in protein crystallography with Tom Blundell in Cambridge, he has focused on methodology and high throughput techniques for crystallography, first in San Diego (academically at JCSG, and industrially at Syrrx, Inc), and since 2004 at the SGC, where his group has to date helped solve over 600 crystal structures of human proteins.

In late 2012 he set up the partnership with Diamond, in order to configure beamline I04-1 as a user facility for routine medium-throughput fragment screening by X-ray structures: this XChem facility has been live since 2015 to users from academia and industry. Accordingly, his focus and collaborations at the SGC address both ends of this facility: how to generate crystals that are suitable for such screening, and afterwards, how to proceed routinely from such a screen to compounds with good affinity.

The research approach is two-pronged: developing the infrastructure (robotics, hardware, beamline) required to drive the throughput necessary for identifying the most appropriate samples at each step in the experimental process; and improving the methodology available at each step.

## Software Tools Developed

TeXRank - consists of 2 components, Ranker - the algorithm for ranking droplets, and Viewer, the GUI for viewing droplets in the ranked order, and ideally integrated with your database and imaging infrastructure. DTC student: Jia Tsing Ng (2012-15)

XChemExplorer - Tool for batch refinement and deposition of 100s of protein-ligand crystal structures

soakDB - Excel plugin for logistics of experimental soaking of 100s of protein-ligand crystals

PanDDA - Pan-Dataset Density Analysis. Multi-dataset crystallographic analysis for the identification of ligand binding and structural events. DTC student: Nicholas Pearce (2013-16)

CCF - Source code for WONKA and OOMMPPAA tools for analysis and integration of protein-ligand activity and structural data. Written in Python Django and using the RDKit. DTC student: Anthony Bradley (2012-15)

XPoise – Knime-based workflow to enumerate compounds that can be made based on poised fragment hits. DTC student: Oakley Cox (2013-16)

Fragalysis - Lightweight package for protein-ligand complex analysis and generation of Astex fragment network package. Uses TravisCI for continuous integration and Docker for packaging.

Fragalysis-stack – Web application to enable visualisation of analysis from fragalysis suite.

Pipeline - Python Luigi pipeline for post-processing of experimental X-ray structures from XChem project.

Opentrons - Library of tools to make opentrons based liquid handling for reactions simple

## Involvement of DTC Students

Contributions already in continuous use:

- Jia Tsing Ng
- Nicholas Pearce
- Oakley Cox
- Radoslaw Novak

Ongoing developments:

- Hannah Patel
- Susan Leung
- Elliot Nelson
- Mpho Makola
- Yuliya Dubianok

## Industrial links

- Novartis
- Pfizer
- Takeda
- Abbvie
- Boehringer-Ingelheim
- Bayer
- MSD
- Merck
- Janssen
- UCB
- Informatics Matters
- Mitegen
- Evotec
- Enamine
- Bruker
- Exscientia
- Crysalin