L-09 **Tue. 17. 06., 15^{00}-15^{45}**

Serial crystallography with X-ray Free Electron Lasers

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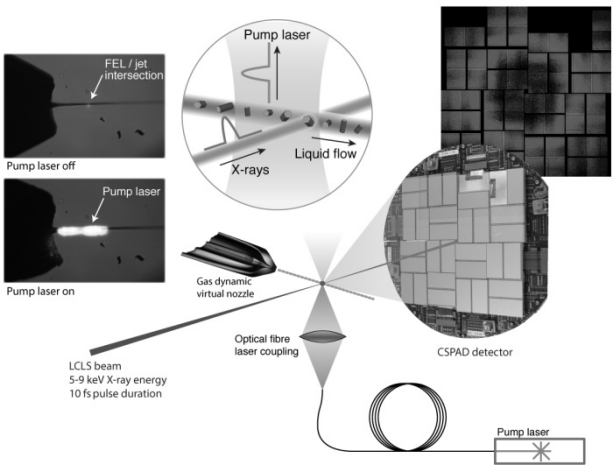
The extremely intense, femtosecond duration X-ray pulses provided by X-ray free electron laser sources enable the measurement of diffraction patterns from sub-micron sized crystals before each crystal is vaporised. This has enabled a new approach to collecting X-ray diffraction data from many hundreds of thousands of microcrystals flowing across a pulsed X-ray beam. Although each crystal is destroyed in a single pulse, the X-ray pulse duration is so short that the measured diffraction data is apparently free of signs of radiation damage, while the flowing suspension provides a continual source of fresh crystals for the next pulse. Referred to as serial crystallography, this technique permits room temperature measurement of radiation sensitive microcrystals too small for study at synchrotron sources, including microcrystals grown *in vivo* [1,2] and membrane proteins embedded in lipidic phase growth medium [3]. Serial femtosecond crystallography is particularly suited to the study of time-resolved biochemistry, including the study of non-reversible or non-cyclic processes [4]. Serial crystallography requires an intense X-ray beam, a fast detector system, and the computational infrastructure to process large data volumes. Indeed, recent experiments demonstrate that serial crystallography can be performed at synchrotron sources [5].



[1] R. Koopmann *et al.*, *Nature Methods* **9** (2012) 259–262.
[2] L. Redecke *et al., Science* **339** (2013) 227–230.
[3] W. Liu, *et al. Science* **342** (2013) 1521–1524 (2013).
[4] A. Aquila *et al. Opt Express* **20** (2012) 2706–2716.
[5] C. Gati, C. *et al.* research papers. *IUCrJ* **1** (2014) 87-94.

L-10 **Tue. 17. 06., 15^{45}-16^{30}**

Crystallography of CNG repeats – RNA molecules relevant to human health

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CNG repeats (N denotes one of the four natural nucleotides) are abundant in the human genome. Their abnormal expansion is the cause of twenty deurodegenerative disorders, such as Huntington's diesease, myotonic dystrophy, spinocerebellar ataxias and fragile X syndrome, together known as TREDs (Trinucleotide Repeat Disorders). The toxic factor can be protein expressed from the abnormal gene or it can be mRNA containing the extended CNG tracts, which tend to fold into long hairpin structures and precipitate in the cell nucleus.

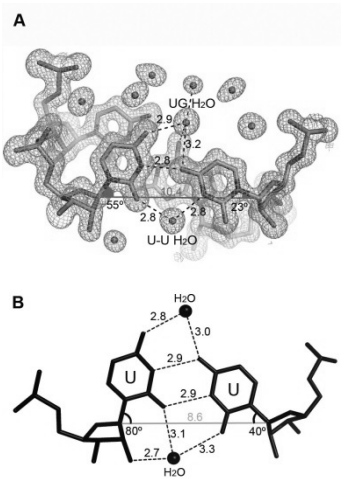

Figure 1. Non-canonical pairing of uridine residues in CUG repeats (A) and in other RNA molecules (B)

We have characterised by X-ray crystallography all four types of CNG repeats [1, 2, 3, 4] with the aim to build their detailed structural profiles to be used in structure-based drug design

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[2] A. Kiliszek, R. Kierzek, W. Krzyżosiak, W. Rypniewski, *Nucleic Acids Res.* **39** (2011) 7308.
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