form an angle of 120 degrees due to the crystallgraphic symmetry, indicating a possible DNA looping mechanism during transcription activation and inhibition.

Keywords: crystal_structure, circadian_rhythm, transcription_control

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Crystal structure analysis of release factor 3

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Translation of an mRNA is terminated when a stop codon is encountered. Since tRNAs do not recognize stop codons, this event is performed by proteins called release factors. Prokaryotes have two class I release factors (RFs), RF1 and RF2, and one class II release factor, the G protein RF3. RF1 and RF2 hydrolyze and release the completed polypeptide from the peptidyl-tRNA at the ribosomal P-site in response to a stop codon. RF3 binds to the ribosome to promote rapid dissociation of RF1 or RF2 from the A-site in a GTP-dependent manner. We have studied the structure-function relationship of the RF3 from sulfate-reducing bacterium, *Desulfovibrio vulgaris* Miyazaki F. Here we present the high resolution crystal structures of RF3 complexd with GDP and guanosine 3',5'-(bis) diphosphate (ppGpp).

ppGpp is known as an alarmone which is involved in stringent response in bacteria. In cells growing under optimal conditions, the concentration of GDP is much dominant over that of ppGpp. Under stress conditions, however, the concentration of ppGpp increases strikingly, and attains levels over that of GDP. In the structure of RF3 complexed with ppGpp, ppGpp binds at the same nucleotide-binding site in an almost identical manner with GDP, suggesting that GDP and ppGpp is two alternative physiologically relevant ligands to RF3. We have found that ppGpp blocks the recycling of RF1 or RF2 by RF3 in bacterial ribosome. It is probably because ppGpp interferes either binding of RF3 to ribosome or replacement of GDP by GTP in the RF3 ribosome complex. These lines of evidences suggest that RF3 would have functions of a cellular metabolic sensor and/or regulator that switches between the active GDP-bound form which allows active protein syntheses under the normal condition and the low-active ppGpp-bound form when shortage of nutrients are detrimental.

Keywords: structure_function_relationship, stress, translation_factor

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Electron crystallography: harder, better, faster, stronger

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The stronger interaction of electrons with matter allows nanoscale crystals to be investigated, which is of increasing importance, academically and commercially, given the growth of nanotechnology research and application during the last decade. Electron crystallography fills the void between crystals which are too small for single crystal X-ray studies and powder diffraction experiments that fail to yield a structure. However, it is often viewed as a technically difficult and time-consuming method for structure solution.

The development of the Automated Diffraction Tomography (ADT) [1] for electron crystallography has led to a number of distinct advantages over traditional methods, in terms of data collection, quality, quantity and the ability to solve structures *ab initio via* direct methods. The most appealing advantage, when compared to traditional approaches which require zonal diffraction data and complementary real space image, is the vastly reduced time it takes to solve a structure from diffraction intensities only, in favourable cases data collection and structure solution can be completed within a single day.

The details of how ADT methodology performs data collection from nanocrystals shall be outlined. The new data collection geometry has some striking advantages, it provides a vastly improved coverage of reciprocal space, when compared to zone axis data sets, as well as reduced dynamical effects. The new processing requirements [2], for extracting the intensities for structure solution, these will be discussed in detail.

The improvements in data quality gained by using ADT for electron crystallography have two distinct advantages. 1. Direct Methods can be used routinely for structure solution [3]. 2. Structures more difficult and complex can be solved by electron diffraction data alone than previously thought possible. Examples of structures solved using ADT, which were not possible by any other method, will be presented.

We hope to convey the benefits of using the ADT approach for electron crystallography and appeal to crystallographers who would not normally consider using electron crystallography that it may be a viable approach to consider in the future for solving problematic nanocrystals which would not yield an answer to their tried and trusted methods.

[1] U. Kolb, T. Gorelik, C. Kübel, M.T. Otten, D. Hubert, *Ultramicroscopy* **2007**, *107*, 507-513. [2] U. Kolb, T. Gorelik, M.T, Otten, *Ultramicroscopy* **2008,** *108*, 763-772. [3] E. Munaioli, T. Gorelik, U. Kolb, *Ultramicroscopy* **2009,** *109*, 758-765.

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Modulated structures and TEM's: from relaxor ferroelectrics to nano-chessboards

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Functionally useful materials are often modulated and frequently inherently flexible [1] *i.e.* materials whose local structures and properties are finely balanced and hence able to respond to the application of external signals *e.g.* electric and/or magnetic fields, strains, changes in temperature, composition *etc*. Materials of this type (piezoelectrics, relaxor ferroelectrics, ionic conductors, solid solutions *etc.*) are ubiquitous in devices all around us *e.g.* mobile phones, sensors, solid oxide fuel cells. A detailed understanding of structure, both average as well as local (on the relevant length and time scales, see *e.g.* Fig.1 below) of such materials is essential for an understanding of their properties and of methods to optimize and manipulate them.