

SAXS STUDIES OF d(TTAGGG)<sub>4</sub> OLIGOMER IN SOLUTIONMaciej Kozak<sup>1\*</sup>, Agnieszka Włodarczyk<sup>2</sup>, and Andrzej Dobek<sup>2</sup><sup>1</sup> Department of Macromolecular Physics, Faculty of Physics, A. Mickiewicz University, Umultowska 85, 61-614 Poznań, Poland;<sup>2</sup> Department of Molecular Biophysics, A. Mickiewicz University, Umultowska 85, 61-614 Poznań, Poland.

Keywords: small angle X-ray scattering, low resolution structure, DNA

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Telomeres are specialized DNA structures located at the end of eukaryotic chromosomes. They consist of small, repeated DNA sequences (*e.g.*, TTGGGG in Tetrahymene, TTAGGG in human). Telomeres play an essential role in maintenance of eukaryotic chromosome within a cell by specifically binding to structural proteins. These proteins cap the ends of linear chromosomes, preventing nucleolytic degradation, end-to-end fusion, irregular recombination, and other events that are normally lethal to a cell. Chromosomal ends progressively shorten with each replication cycle, a process that seems to be linked to the limited proliferative ability of normal somatic cells. The loss of the telomeric tandem eventually leads to the cell death [1–3].

The aim of our studies was the characterisation of low resolution structure and conformational changes of a synthetic d(TTAGGG)<sub>4</sub> oligomer in solution with the presence of different monovalent cations.

The small angle X-ray scattering measurements were performed on the X33 camera of the EMBL on the DORIS storage ring at DESY, Hamburg using linear gas proportional detector with delay line readout. The d(TTAGGG)<sub>4</sub> oligomer (2, 4, 6, 8 and 10 mg/ml) was measured in 10 mM Tris/HCl pH 7.3 solution with and without K<sup>+</sup> cations (0.1 – 100 mM KCl). The sample-to-detector distance was 1.7 m. The data were normalized to

the incident beam intensity, corrected for detector response and the scattering of the buffer was subtracted using the computer program PRIMUS.

The radius of gyration  $R_G$ , calculated for d(TTAGGG)<sub>4</sub> oligomer (10 mg/ml in 10 mM Tris/HCl) was 1.42 nm. The pair distance distribution function,  $P(r)$ , yielded a maximum dimension of 4.4 nm. On the basis of SAXS data, the low-resolution structure in solution has been reconstructed using *ab initio* methods and program DAMMIN [4].

**Acknowledgements:** The data collection was supported by European Community - EMBL Hamburg Outstation, contract number: RII3-CT-2004-506008.

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