03-Crystallography of Biological Macromolecules

03.10 – Macromolecular Assemblies

PS-03.10.01 STUDY OF GUANOSINE DERIVATIVES BY X-RAY DIFFRACTION

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In a recent paper on the H phase in a micellar system (L.Q. Amaral et al., Phys. Rev., A, 1992, 45, 5482-5500) we analysed the distance d0 between bilayer axis in the H phase as a function of the volume concentration of solute c0, obtaining a c0,43 typical of finite cylinders, while a c0,43 is expected for infinite cylinders. This method of analysis is now used to study a series of guanosine derivatives, with following results:

- the dinucleotide phosphate G2 presents a N* - H transition and a change of functional behavior a c0,65 at the transition (n = 0 in N* phase and n = 1/2 in H phase), evidencing cylinder growth.
- the derivatives G1, G3 and G6 show instead n = 1/3 in the H phase, evidencing smaller aggregation process.
- the derivative G2 cyclic presents n = 1/2 in H phase.
- results obtained in folic acid salt, that forms aggregates similar to the four-stranded helix, as given by guanosine derivatives, evidence a direct I - H transition and n = 1/3 in H phase.

These results are discussed in terms of differences in the aggregation process of the several derivatives and the phase transitions analysed in terms of recent, statistical mechanical theories that take self-association into account (M.D. Taylor and J. Hersfeld, Phys. Rev., 1991, A43, 1952-1960).

PS-03.10.03 DATA COLLECTED AND EVALUATED FROM CRYSTALS OF RIBOSOMAL PARTICLES. By S. Agmon2, B. Pastula, H.S. Groenert3, A. Ben-Nabavi, E. H. Semmelweis, E. Pr鲣olczak1, H.A.S. Happaer1, J. Happaer1, G. Knyper1, J. Levin1, E. Schlunzer2, A. Shur1, J. Truppers2, N. Volkman3, A. Wraith1,2 and A. Zaytzev-Bashan1. 1 Dep. of Structural Biology, Weizmann Institute, Rehovot, Israel. 2 Max-Planck-Institute for Biophysical Structure, Hamburg, Germany. 3 Max-Planck-Institute for Molecular Genetics, Berlin, Germany.

X-ray diffraction data have been collected at cryotemperatures, using intense synchrotron radiation sources, from crystals of different ribosomes, their complexes with components of protein biosynthesis and their natural, mutated, selectively depleted and modified subunits, as well as from ribosomal particles specifically labeled with a gold cluster (composed of 11 gold atoms). The best crystals, those of the large subunit (30S) of Haloarcula marismortui, the most compact atomic resolution (2.5 A). The best resolution to date of the whole ribosome (70S) is 15 Å and that of the small subunit (30S) is 7.5 Å, both from Thermus Thermophilus.

Crystals of ribosomal particles exhibit special features: large unit cells, high mosaicity, extremely weak diffraction, low sensitivity, a limited internal order and an extremely steep descent of the intensity of the reflection as a function of resolution.