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. Amara et al., Phys. Rev. A, 1992, 46, 3548-3550) we analysed the distance $\alpha$ between cylinder axis in the H phase as a function of the volume concentration of solute $c_n$, obtaining a $\alpha \approx 0.5$ for a typical of finite cylinders, while a $\alpha \approx 0.45$ is expected for infinite cylinders. This method of analysis is now used to study a series of guanosine derivatives, with following results:

- the dinucleoside phosphate G2 presents a $N^* - H$ transition and a change of functional behavior in $c_n$ at the transition (n = 1 in $N^*$ phase and n = 1/2 in H phase), evidencing cylinder grow.

- the derivatives G1, G3 and G6 grow 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 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 analyzed in terms of recent statistical mechanical theories that take self-association into account (M.D. Taylor and J. Hersfeld, Phys. Rev., 1991, A43, 1892-1909).

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**PS-03.10.03 DATA COLLECTED AND EVALUATED FROM CRYSTALS OF RBONUCLEOPROTEINS**


X-ray diffraction data have been collected at cryotemperatures, using intense synchrotron radiation sources, from crystals of ribonucleosides, their complexes with components of protein biosynthesis and their natural, modified, selectively depleted and modified subunits, as well as from ribonuclease particles specifically labeled with a gold cluster (composed of 11 gold atoms). The best crystals, those of the large subunit (MAL), from Bacillus marinus, diffract to almost atomic resolution (2.9 Å). The best resolution to date of the whole ribosome (70S) is 15Å and that of the small subunit (30S) is 7.8Å, both from Thermus Thermophilus.

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

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